

REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-90

Query Match 50.0%; Score 5; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
DB 8 PLPPT 12

RESULT 10  
US-08-602-999A-93  
Sequence 93, Application US/08602999A  
Patent No. 6184205

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESS: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/602,999A  
FILING DATE: 16-FEB-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-93

Query Match 50.0%; Score 5; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
DB 5 PLPPT 9

## RESULT 11

US-08-278-865-93  
Sequence 93, Application US/08278865  
Patent No. 6303574  
GENERAL INFORMATION:  
APPLICANT: KAY, BRIAN K.  
APPLICANT: SPARKS, ANDREW B.  
APPLICANT: THORN, JUDITH M.  
APPLICANT: QUILLIAM, LAWRENCE A.  
APPLICANT: DER, CHANNING J.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,865  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Villacorta, Gilberto M.  
REGISTRATION NUMBER: 34,038  
REFERENCE/DOCKET NUMBER: 4980-007-0  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 93:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-278-865-93

Query Match 50.0%; Score 5; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
DB 5 PLPPT 9

## RESULT 12

US-09-500-124-90  
Sequence 90, Application US/09500124  
Patent No. 6432920

GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.

;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
;/ TITLE OF INVENTION: ISOLATING AND USING SAME  
;/ NUMBER OF SEQUENCES: 467  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/500,124  
;/ FILING DATE:  
;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/602,999  
;/ FILING DATE: 16-FEB-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Mirock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 1101-202  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 869-9741/8864  
;/ TELEFAX: (212) 869-9741/8864  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 90:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 13 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: peptide  
;/  
;/ US-09-500-124-93  
;/  
;/ Query Match 50.0%; Score 5; DB 4; Length 13;  
;/ Best Local Similarity 100.0%; Pred. No. 12;  
;/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/  
;/ Qy 2 PLPPT 6  
;/ Db 8 PLPPT 12  
;/  
;/ RESULT 13  
;/ US-09-500-124-93  
;/ Sequence 93, Application US/09500124  
;/ Patent No. 6432920  
;/ GENERAL INFORMATION:  
;/ APPLICANT: SPARKS, Andrew B.  
;/ APPLICANT: KAY, Brian K.  
;/ APPLICANT: THORN, Judith M.  
;/ APPLICANT: QUILLIAM, Lawrence A.  
;/ APPLICANT: DER, Channing J.  
;/ APPLICANT: FOWLKES, Dana M.  
;/ APPLICANT: RIDER, James E.  
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
;/ TITLE OF INVENTION: ISOLATING AND USING SAME  
;/ NUMBER OF SEQUENCES: 467  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/09/500,124  
;/ FILING DATE:  
;/ CLASSIFICATION:  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER: 08/602,999  
;/ FILING DATE: 16-FEB-1996  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Mirock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 1101-202  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 790-9090  
;/ TELEFAX: (212) 869-9741/8864  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 93:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 13 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: peptide  
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;/ US-09-500-124-93  
;/  
;/ Query Match 50.0%; Score 5; DB 4; Length 13;  
;/ Best Local Similarity 100.0%; Pred. No. 12;  
;/ Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
;/  
;/ Qy 2 PLPPT 6  
;/ Db 5 PLPPT 9  
;/  
;/ RESULT 14  
;/ US-08-602-999A-355  
;/ Sequence 355, Application US/08602999A  
;/ Patent No. 6184205  
;/ GENERAL INFORMATION:  
;/ APPLICANT: SPARKS, Andrew B.  
;/ APPLICANT: KAY, Brian K.  
;/ APPLICANT: THORN, Judith M.  
;/ APPLICANT: QUILLIAM, Lawrence A.  
;/ APPLICANT: DER, Channing J.  
;/ APPLICANT: FOWLKES, Dana M.  
;/ APPLICANT: RIDER, James E.  
;/ TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
;/ TITLE OF INVENTION: ISOLATING AND USING SAME  
;/ NUMBER OF SEQUENCES: 467  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Pennie & Edmonds  
;/ STREET: 1155 Avenue of the Americas  
;/ CITY: New York  
;/ STATE: New York  
;/ COUNTRY: U.S.A.  
;/ ZIP: 10036-2711  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.30  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/602,999A  
;/ FILING DATE: 16-FEB-1996  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Mirock, S. Leslie  
;/ REGISTRATION NUMBER: 18,872  
;/ REFERENCE/DOCKET NUMBER: 1101-202  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (212) 790-9090  
;/ TELEFAX: (212) 869-9741/8864  
;/ TELEX: 66141 PENNIE  
;/ INFORMATION FOR SEQ ID NO: 355:



; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-355

Query Match 50.0%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
|||||  
DB 9 PLPPT 13

RESULT 15  
US-08-602-999A-437  
; Sequence 437, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 437:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-437

Query Match 50.0%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
|||||  
DB 2 QPLPP 6

RESULT 16

US-09-500-124-355  
; Sequence 355, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 355:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-09-500-124-355

Query Match 50.0%; Score 5; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
|||||  
DB 9 PLPPT 13

RESULT 17  
US-09-500-124-437  
; Sequence 437, Application US/09500124  
; Patent No. 6432920  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467



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; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-500-124-213

Query Match      50.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPPT 6
Db      5 PLPPT 9

RESULT 20
US-09-026-276-17
; Sequence 17, Application US/09026276
; Patent No. 6319503
; GENERAL INFORMATION:
; APPLICANT: Kenten, John H
; APPLICANT: Tramontano, Alfonso
; APPLICANT: Pilon, Aprile L
; APPLICANT: Lohnas, Gerald L
; APPLICANT: Roberts, Steven F
; TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
; FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276
; CURRENT APPLICATION NUMBER: US/09/026,276
; CURRENT FILING DATE: 1998-02-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-026-276-17

Query Match      50.0%; Score 5; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLPP 5
Db      6 QPLPP 10

RESULT 21
US-08-363-276B-11
; Sequence 11, Application US/08363276B
; Patent No. 5969109
; GENERAL INFORMATION:
; APPLICANT: BONA ET AL
; TITLE OF INVENTION: CHIMERIC ANTIBODIES
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10112-0228
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,276B
; FILING DATE: 22-DECEMBER-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 07/486,546
; FILING DATE: 28-FEBRUARY-1990 (ABANDONED)

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; APPLICATION NUMBER: USN 07/687,376
; FILING DATE: 18-APRIL-1991 (ABANDONED)
; APPLICATION NUMBER: USN 08/327,636
; FILING DATE: 24-OCTOBER-1994 (ABANDONED)
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Richard S
; REGISTRATION NUMBER: 26,154
; REFERENCE/DOCKET NUMBER: 29889-165/29528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2558
; TELEFAX: 212-765-2519
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Mycobacteria
; FEATURE:
; NAME/KEY:
; LOCATION: 350...369
; OTHER INFORMATION: Heat Shock Protein
US-08-363-276B-11

Query Match      50.0%; Score 5; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QPLPP 5
Db      6 QPLPP 10

RESULT 22
US-08-602-999A-147
; Sequence 147, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090

```

TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-147

Query Match 50.0%; Score 5; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
DB 7 PLPPT 11

RESULT 23  
US-08-755-034-11  
Sequence 11, Application US/08755034  
Patent No. 6204250  
GENERAL INFORMATION:  
APPLICANT: BOT and BONA  
TITLE OF INVENTION: IMMUNIZATION OF INFANTS  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Brumbaugh, Graves, Donohue &  
ADDRESSEE: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10112-0228

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/755,034  
FILING DATE: 22-NOVEMBER-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Richard S  
REGISTRATION NUMBER: 26,154  
REFERENCE/DOCKET NUMBER: 29889-165/29528  
TELEPHONE: 212-408-2558  
TELEFAX: 212-765-2519  
TELEX:

INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Mycobacteria  
FEATURE:  
NAME/KEY:  
LOCATION: 350...369  
OTHER INFORMATION: Heat Shock Protein  
US-08-755-034-11

Query Match 50.0%; Score 5; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPLPP 5  
DB 6 QPLPP 10

RESULT 24  
US-09-500-124-147  
Sequence 147, Application US/09500124  
Patent No. 6432920  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: QUILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
TITLE OF INVENTION: ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/500,124  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/602,999  
FILING DATE: 16-FEB-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Mistock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-09-500-124-147

Query Match 50.0%; Score 5; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPPT 6  
DB 7 PLPPT 11

RESULT 25  
PCT-US95-16718-11  
Sequence 11, Application PC/TUS9516718  
GENERAL INFORMATION:  
APPLICANT: MOUNT SINAI SCHOOL OF MEDICINE OF THE  
APPLICANT: CITY UNIVERSITY OF NEW YORK  
TITLE OF INVENTION: CHIMERIC ANTIBODIES  
TITLE OF INVENTION: COMPRISING ANTIGEN BINDING SITES AND B AND T CELL EPITOPES



Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Searliss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jave, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (PatentIn)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-40  
  
Query Match 40.0%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 PLPP 5  
Db 3 PLPP 6  
  
RESULT 29  
US-08-340-283-38  
; Sequence 38, Application US/08340283  
; Patent No. 5861318  
; GENERAL INFORMATION:  
; APPLICANT: Elhammer, Ake P.  
; TITLE OF INVENTION: A SCINTILLATION PROXIMITY ASSAY FOR  
; TITLE OF INVENTION: N-ACETYL GALACTOSAMINYLTRANSFERASE ACTIVITY  
; NUMBER OF SEQUENCES: 205  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pharmacia and Upjohn, Inc., Intellectual. Prop. Law  
; STREET: 301 Henrietta Street  
; CITY: Kalamazoo  
; STATE: Michigan  
; COUNTRY: U.S.A.  
; ZIP: 49001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/340,283  
; FILING DATE:

CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wootton, Thomas A.  
; REGISTRATION NUMBER: 35,004  
; REFERENCE/DOCKET NUMBER: 4828  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (616) 385-7914  
; TELEFAX: (616) 385-6897  
; TELEX: 224401  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-340-283-38  
  
Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 PLPP 5  
Db 4 PLPP 7  
  
RESULT 30  
US-08-769-745-7  
; Sequence 7, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Rat  
US-08-769-745-7  
  
Query Match 40.0%; Score 4; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 2 PLPP 5  
Db 2 PLPP 5  
  
RESULT 31  
US-08-602-999A-9  
; Sequence 9, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF

;; TITLE OF INVENTION: ISOLATING AND USING SAME  
;; NUMBER OF SEQUENCES: 467  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Pennie & Edmonds  
;; STREET: 1155 Avenue of the Americas  
;; CITY: New York  
;; STATE: New York  
;; COUNTRY: U.S.A.  
;; ZIP: 10036-2711  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; FILING DATE: 16-FEB-1996  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-602-999A-9

Query Match 40.0%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
Db 2 PLPP 5

RESULT 32  
US-08-278-865-9  
; Sequence 9, Application US/08278865  
; Patent No. 6303574  
; GENERAL INFORMATION:  
; APPLICANT: KAY, BRIAN K.  
; APPLICANT: SPARKS, ANDREW B.  
; APPLICANT: THORN, JUDITH M.  
; APPLICANT: QUILLIAM, LAWRENCE A.  
; TITLE OF INVENTION: DER, CHANNING J.  
; TITLE OF INVENTION: SIC SH3 BINDING PEPTIDES AND METHODS OF  
; ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C.  
; STREET: 1755 S. Jefferson Davis Highway, Suite 400  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE:  
; CLASSIFICATION: 514

;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Villacorta, Gilberto M.  
;; REGISTRATION NUMBER: 34,038  
;; REFERENCE/DOCKET NUMBER: 4980-007-0  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703) 413-3000  
;; TELEFAX: (703) 413-2220  
;; TELEX: 248855 OPAT UR  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-08-278-865-9

Query Match 40.0%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
Db 2 PLPP 5

RESULT 33  
US-08-630-915A-45  
; Sequence 45, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-45

Query Match 40.0%; Score 4; DB 4; Length 7;

```
Best Local Similarity 100.0%; Pred. No. 2.5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 34
US-09-500-124-9
; Sequence 9, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOMLKE, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-09-500-124-9

Query Match 40.0%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 2 PLPP 5

RESULT 35
PCT-US94-01840-11
; Sequence 11, Application PC/TUS9401840
; GENERAL INFORMATION:
; APPLICANT: Christopher E. Rudd
; APPLICANT: Praesad Kanteti
```

```
; APPLICANT: Lewis Cantley
; TITLE OF INVENTION: CD4 MEDIATED MODULATION OF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01840
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/023,915
; FILING DATE: February 26, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00530/063001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: Linear
; PCT-US94-01840-11

Query Match 40.0%; Score 4; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
Db 3 PLPP 6

RESULT 36
US-09-641-640-8
; Sequence 8, Application US/09641640
; Patent No. RE37952
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/641,640
; FILING DATE: 15-Aug-2000
; CLASSIFICATION: <Unknown>
```



```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,857
; FILING DATE: <Unknown>
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-641-640-8

Query Match 40.0%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
DB 3 PLPP 6

RESULT 37
US-08-612-857-8
; Sequence 8, Application US/08612857
; Patent No. 5831048
; GENERAL INFORMATION:
; APPLICANT: SCHWEIGHOFFER, Fabien
; APPLICANT: TOCQUE, Bruno
; TITLE OF INVENTION: GRB3-3 GENE, VARIANTS AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd. 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,857
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 93-10971
; FILING DATE: 15-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR94/00542
; FILING DATE: 09-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 38,619
; REFERENCE/DOCKET NUMBER: ST93044-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)454-3839
```

```
; TELEFAX: (610)454-3808
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..8
; OTHER INFORMATION: /note= "3BP1 peptide"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-612-857-8

Query Match 40.0%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5
DB 3 PLPP 6

RESULT 38
US-08-747-221B-43
; Sequence 43, Application US/08747221B
; Patent No. 6063610
; GENERAL INFORMATION:
; APPLICANT: Silver, Gary W.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: No. 6063610el Carboxylesterase Nucleic Acid
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Wordperfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,221B
; FILING DATE: No. 6063610ember 12, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: FC-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-08-747-221B-43

Query Match 40.0%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7
DB 2 PPTV 5
```

RESULT 39  
US-09-005-051-43  
; Sequence 43, Application US/09005051  
; Patent No. 6291222  
; GENERAL INFORMATION:  
; APPLICANT: Silver, Gary W.  
; APPLICANT: Wisniewski, Nancy  
; TITLE OF INVENTION: No. 6291222el Carboxylesterase Nucleic Acid  
; TITLE OF INVENTION: Molecules, Proteins and Uses Thereof  
; NUMBER OF SEQUENCES: 66  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol Talkington Verser, Ph.D.  
; ADDRESSEE: Heska Corporation  
; STREET: 1825 Sharp Point Drive  
; CITY: Fort Collins  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80525  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: WordPerfect for Windows, Version 7.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/005,051  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/747,221  
; FILING DATE: No. 6291222ember 12, 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Verser, Carol Talkington  
; REGISTRATION NUMBER: 37,459  
; REFERENCE/DOCKET NUMBER: PC-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 970/493-7272  
; TELEFAX: 970/484-9505  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-005-051-43  
Query Match 40.0%; Score 4; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPTV 7  
Db 2 PPTV 5  
RESULT 40  
US-08-214-650-43  
; Sequence 43, Application US/08214650  
; Patent No. 5709995  
; GENERAL INFORMATION:  
; APPLICANT: Chisari, Francis V.  
; APPLICANT: Cerny, Andreas  
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T  
; TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leydig, Voigt & Mayer  
; STREET: Two Prudential Plaza, Suite 4900  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/214,650  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Silvert, Donald J.  
; REGISTRATION NUMBER: 37552  
; REFERENCE/DOCKET NUMBER: 61230  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (312) 616-5600  
; TELEFAX: (312) 616-5700  
; TELEX: 25-3533  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-214-650-43  
Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 PLPP 5  
Db 1 PLPP 4  
RESULT 41  
US-08-615-181-110  
; Sequence 110, Application US/08615181  
; Patent No. 5756666  
; GENERAL INFORMATION:  
; APPLICANT: MASAFUMI, TAKIGUCHI  
; APPLICANT: MIWA, KIYOSHI  
; TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE  
; TITLE OF INVENTION: RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
; TITLE OF INVENTION: CURING AIDS  
; NUMBER OF SEQUENCES: 115  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; ADDRESSEE: P.C. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
; CITY: ARLINGTON  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/615,181  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP94/01756  
; FILING DATE: 19-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 261302/1993  
; FILING DATE: 19-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OBLON, NORMAN F.  
; REGISTRATION NUMBER: 24,618  
; REFERENCE/DOCKET NUMBER: 10-796-0 PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-110

Query Match 40.0%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LPPT 6  
|||  
Db 1 LPPT 4

## RESULT 42

US-08-146-028-441  
Sequence 441, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 441:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-441

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
|||  
Db 6 PLPP 9

## RESULT 43

US-08-146-028-442  
Sequence 442, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 442:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-442

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
|||  
Db 5 PLPP 8

## RESULT 44

US-08-146-028-443  
Sequence 443, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/146,028  
INFORMATION FOR SEQ ID NO: 443:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-146-028-443

Query Match 40.0%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
|||  
Db 4 PLPP 7

## RESULT 45

US-08-146-028-445  
Sequence 445, Application US/08146028  
Patent No. 5891640  
GENERAL INFORMATION:  
APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES  
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
NUMBER OF SEQUENCES: 453

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 445:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-445

Query Match          40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 46
US-08-146-028-446
Sequence 446, Application US/08146028
Patent No. 5891640
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES.
TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
NUMBER OF SEQUENCES: 453
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/146,028
INFORMATION FOR SEQ ID NO: 446:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-146-028-446

Query Match          40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      1 PLPP 4

RESULT 47
US-08-318-856A-49
Sequence 49, Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
```

```
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068.8
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP1R1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-856A-49

Query Match          40.0%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      5 PLPP 8

RESULT 48
US-08-723-425A-441
Sequence 441, Application US/08723425A
Patent No. 6165730
GENERAL INFORMATION:
APPLICANT: DELEYS, ROBERT
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
NUMBER OF SEQUENCES: 453
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHIE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,425A
```

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;
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-441

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 6 PLPP 9

RESULT 49
US-08-723-425A-442
; Sequence 442, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723.425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-442

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 6 PLPP 9

US-09-641-801-25.oligo.ra1
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Qy 2 PLPP 5
Db 5 PLPP 8

RESULT 50
US-08-723-425A-443
; Sequence 443, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/723.425A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 1487-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 443:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-723-425A-443

Query Match 40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5
Db 4 PLPP 7

RESULT 51
US-08-723-425A-445
; Sequence 445, Application US/08723425A
; Patent No. 6165730
; GENERAL INFORMATION:
; APPLICANT: DELEYS, ROBERT
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF
; TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...
; NUMBER OF SEQUENCES: 453
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE, P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: Arlington
```

STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 445:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-445

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
Db 2 PLPP 5

## RESULT 52

US-08-723-425A-446  
Sequence 446, Application US/08723425A  
Patent No. 6165730  
GENERAL INFORMATION:  
APPLICANT: DELEYS, ROBERT  
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF  
PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF  
ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...  
NUMBER OF SEQUENCES: 453  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIXON & VANDERHYE, P.C.  
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR  
CITY: Arlington  
STATE: VA  
COUNTRY: USA  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/723,425A  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: SADOFF, B.J.  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 1487-13  
TELEPHONE: 703-816-4000  
TELEFAX: 703-816-4100  
INFORMATION FOR SEQ ID NO: 446:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-723-425A-446

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
Db 1 PLPP 4

## RESULT 53

US-08-602-999A-11  
Sequence 11, Application US/08602999A  
Patent No. 6184205  
GENERAL INFORMATION:  
APPLICANT: SPARKS, Andrew B.  
APPLICANT: KAY, Brian K.  
APPLICANT: THORN, Judith M.  
APPLICANT: O'ILLIAM, Lawrence A.  
APPLICANT: DER, Channing J.  
APPLICANT: FOWLKES, Dana M.  
APPLICANT: RIDER, James E.  
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
ISOLATING AND USING SAME  
NUMBER OF SEQUENCES: 467  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/602,999A  
APPLICATION NUMBER: 16-FEB-1996  
FILING DATE: 435  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Misrock, S. Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 1101-202  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-602-999A-11

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PLPP 5  
Db 2 PLPP 5

## RESULT 54

US-09-112-206-441  
; Sequence 441, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 441:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-441

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
|||  
Db 6 PLPP 9

RESULT 55  
US-09-112-206-442  
; Sequence 442, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 442:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-442

Query Match 40.0%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 PLPP 5  
|||  
Db 5 PLPP 8  
RESULT 56  
US-09-112-206-443  
; Sequence 443, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 443:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-112-206-443

Query Match 40.0%; Score 4; DB 3; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5  
|||  
Db 4 PLPP 7

RESULT 57  
US-09-112-206-445  
; Sequence 445, Application US/09112206  
; Patent No. 6210903  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR  
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,  
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
; NUMBER OF SEQUENCES: 453  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/112,206  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/146,028  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 445:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-445

Query Match          40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 58
US-09-112-206-446
; Sequence 446, Application US/09112206
; Patent No. 6210903
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES
; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR
; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,
; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM
; NUMBER OF SEQUENCES: 453
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/112,206
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,028
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 446:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-112-206-446

Query Match          40.0%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      1 PLPP 4

RESULT 59
US-08-278-865-11
; Sequence 11, Application US/08278865
; Patent No. 6303574
; GENERAL INFORMATION:
; APPLICANT: KAY, BRIAN K.
; APPLICANT: SPARKS, ANDREW B.
; APPLICANT: THORN, JUDITH M.
; APPLICANT: QUILLIAM, LAWRENCE A.
; APPLICANT: DER, CHANNING J.
; TITLE OF INVENTION: SRC SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
```

```
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,865
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-007-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-278-865-11

Query Match          40.0%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 PLPP 5
Db      2 PLPP 5

RESULT 60
US-09-500-124-11
; Sequence 11, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
```



;; FILING DATE: 16-FEB-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Mistrock, S. Leslie  
;; REGISTRATION NUMBER: 18,872  
;; REFERENCE/DOCKET NUMBER: 1101-202  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-9741/8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: peptide  
US-09-500-124-11

Query Match 40.0%; Score 4; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PLPP 5  
Db 2 PLPP 5

RESULT 61  
US-08-230-047-12  
;; Sequence 12, Application US/08230047  
;; Patent No. 5541109  
;; GENERAL INFORMATION:  
;; APPLICANT: Searfoss III, George H.  
;; APPLICANT: Ivashchenko, Yuri D.  
;; APPLICANT: Jaye, Michael C.  
;; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
;; STREET: 500 Arcola Road, 3043  
;; CITY: Collegeville  
;; STATE: PA  
;; COUNTRY: USA  
;; ZIP: 19426

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-12

Query Match 40.0%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PLPP 5

Db 7 PLPP 10

RESULT 62  
US-08-212-190A-8  
;; Sequence 8, Application US/08212190A  
;; Patent No. 5652223  
;; GENERAL INFORMATION:  
;; APPLICANT: KOHN, Elise C.  
;; APPLICANT: LIOTTA, Lance A.  
;; APPLICANT: KIM, Young Sook  
;; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
;; TITLE OF INVENTION: USES THEREOF  
;; NUMBER OF SEQUENCES: 10  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew  
;; STREET: Steuart Street Tower, One Market Plaza  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: US  
;; ZIP: 94105-1493  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/212,190A  
FILING DATE: 14-MAR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunter, Tom  
REGISTRATION NUMBER: 38,498  
REFERENCE/DOCKET NUMBER: 15280-204US  
REFERENCE/DOCKET NUMBER: DHHS Ref. No. 5652223 E-112-94/0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-212-190A-8

Query Match 40.0%; Score 4; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 PLPP 5  
Db 7 PLPP 10

RESULT 63  
US-08-146-028-444  
;; Sequence 444, Application US/08146028  
;; Patent No. 5891640  
;; GENERAL INFORMATION:  
;; APPLICANT:  
;; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES  
;; TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEI  
;; TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED  
;; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES  
;; TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM  
;; NUMBER OF SEQUENCES: 453  
;; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/146,028  
; INFORMATION FOR SEQ ID NO: 444:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-146-028-444

Query Match 40.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5  
|||  
Db 3 PLPP 6

RESULT 64  
US-08-769-745-5  
; Sequence 5, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Rat  
US-08-769-745-5

Query Match 40.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5  
|||  
Db 4 PLPP 7

RESULT 65  
US-08-769-745-6  
; Sequence 6, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; TITLE OF INVENTION: Channel Activity  
; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-08-769-745-6

Query Match 40.0%; Score 4; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5  
|||  
Db 4 PLPP 7

RESULT 66  
US-08-900-321-8  
; Sequence 8, Application US/08900321  
; Patent No. 5981712  
; GENERAL INFORMATION:  
; APPLICANT: Kohn, Elise C.  
; APPLICANT: Liotta, Lance A.  
; APPLICANT: Kim, Young S.  
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and  
; TITLE OF INVENTION: Uses Thereof  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/900,321  
; FILING DATE: 25-JUL-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,190  
; FILING DATE: 14-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hunter, Tom  
; REGISTRATION NUMBER: 38,498  
; REFERENCE/DOCKET NUMBER: 015280-204100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-900-321-8

Query Match 40.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 PLPP 5  
|||  
Db 7 PLPP 10

RESULT 67  
US-08-336-553A-12  
; Sequence 12, Application US/08336553A  
; Patent No. 6054264  
; GENERAL INFORMATION:  
; APPLICANT: CHIEN, DAVID Y.  
; APPLICANT: KUO, GEORGE  
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
; TITLE OF INVENTION: REAGENTS FOR USE THEREIN  
; NUMBER OF SEQUENCES: 75

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; QUERY MATCH 40.0%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 PPTV 7
; DB 5 PPTV 8
;
; RESULT 68
; US-08-336-553A-43
; Sequence 43, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-12
;
; Query Match 40.0%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 PPTV 7
; DB 5 PPTV 8
;
; RESULT 68
; US-08-336-553A-43
; Sequence 43, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
```

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-43
;
; Query Match 40.0%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 PPTV 7
; DB 5 PPTV 8
;
; RESULT 69
; US-08-336-553A-65
; Sequence 65, Application US/08336553A
; Patent No. 6054264
; GENERAL INFORMATION:
; APPLICANT: CHIEN, DAVID Y.
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
;
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-336-553A-65
;
; Query Match 40.0%; Score 4; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.1e+02;
; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 PPTV 7  
 Db 5 PPTV 8

## RESULT 70

US-08-723-425A-444  
 ; Sequence 444, Application US/08723425A

Patent No. 6165730

GENERAL INFORMATION:

APPLICANT: DELEYS, ROBERT

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT

TITLE OF INVENTION: EPITOPES AND THEIR USE IN A PROCESS FOR DETERMINATION OF

TITLE OF INVENTION: ANTIBODIES OR BIOTINYLATED PEPTIDES CORRESPONDING ...

NUMBER OF SEQUENCES: 453

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHUYE, P.C.

STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/723.425A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: SADOFF, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 1487-13

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-723-425A-444

Query Match 40.0%; Score 4; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5

Db 3 PLPP 6

## RESULT 71

US-09-112-206-444

; Sequence 444, Application US/09112206

Patent No. 6210903

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES

TITLE OF INVENTION: CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR

TITLE OF INVENTION: IN A PROCESS FOR DETERMINATION OF ANTIBODIES OR BIOTINYLATED

TITLE OF INVENTION: PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT EPITOPES,

TITLE OF INVENTION: PROCESS FOR PREPARING THEM AND COMPOSITIONS CONTAINING THEM

NUMBER OF SEQUENCES: 453

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/112,206

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/146,028

FILING DATE:

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-112-206-444

Query Match 40.0%; Score 4; DB 3; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PLPP 5

Db 3 PLPP 6

## RESULT 72

US-08-439-157-12

; Sequence 12, Application US/08439157

Patent No. 6416944

GENERAL INFORMATION:

APPLICANT: CHIEN, DAVID Y.

KUO, GEORGE

TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND

REAGENTS FOR USE THEREIN

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/439,157

FILING DATE: 11-May-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/336,553A

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/060,400

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: LEHNHARDT, SUSAN K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 22300-20947.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-08-439-157-12

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7  
 ||||  
 Db 5 PPTV 8

RESULT 73  
 US-08-439-157-43  
 ; Sequence 43, Application US/08439157  
 ; Patent No. 6416944  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIEN, DAVID Y.  
 ; KUO, GEORGE  
 ; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
 ; REAGENTS FOR USE THEREIN

NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/439,157  
 FILING DATE: 11-May-1995  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/336,553A  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/060,400  
 FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 22300-20947.00  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
 US-08-439-157-43

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7  
 ||||  
 Db 5 PPTV 8

RESULT 74  
 US-08-439-157-65  
 ; Sequence 65, Application US/08439157  
 ; Patent No. 6416944  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIEN, DAVID Y.

; KUO, GEORGE  
 ; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
 ; REAGENTS FOR USE THEREIN

NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/439,157  
 FILING DATE: 11-May-1995  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/336,553A  
 FILING DATE: <Unknown>  
 APPLICATION NUMBER: US 08/060,400  
 FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: LEHNHARDT, SUSAN K.  
 REGISTRATION NUMBER: 33,943  
 REFERENCE/DOCKET NUMBER: 22300-20947.00

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 65:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 65:  
 US-08-439-157-65

Query Match 40.0%; Score 4; DB 4; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PPTV 7  
 ||||  
 Db 5 PPTV 8

RESULT 75  
 US-09-437-895-12  
 ; Sequence 12, Application US/09437895  
 ; Patent No. 6416946  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHIEN, DAVID Y.  
 ; KUO, GEORGE

; TITLE OF INVENTION: METHODS OF TYPING HEPATITIS C VIRUS AND  
 ; REAGENTS FOR USE THEREIN

NUMBER OF SEQUENCES: 75  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/437,895
; FILING DATE: 09-No. 6416946-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,553
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/060,400
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: LEHNHARDT, SUSAN K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 22300-20947.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-437-895-12

Query Match      40.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PPTV 7
        |||||
Db       5 PPTV 8

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Search completed: November 25, 2003, 20:30:01  
Job time : 9.0814 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.11628 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

- 1: PIR1:\*
- 2: PIR2:\*
- 3: PIR3:\*
- 4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	66.7	11	F33098	214K exoantigen (v
2	3	50.0	6	PT0560	T-cell receptor be
3	3	50.0	9	I57650	hemoglobin alpha c
4	3	50.0	12	A42324	cytochrome P450c27
5	3	50.0	12	S69095	ubiquinol-cytochro
6	3	50.0	13	S47361	T-cell antigen rec
7	3	50.0	13	B56864	dipeptidyl-peptida
8	3	50.0	14	QWAPF	polistes mastopara
9	3	50.0	14	S11074	alcohol dehydrogen
10	3	50.0	15	PN0117	hemoglobin alpha c
11	3	50.0	15	S62620	protein disulfide-
12	3	50.0	15	PA0075	fructose-bisphosph
13	3	50.0	15	PA0102	fructose-bisphosph
14	3	50.0	15	S71300	ICL3 protein - far
15	3	50.0	15	C84035	hypothetical prote
16	3	50.0	16	S11290	matrix protein M1
17	3	50.0	16	A44352	candidapepsin (EC
18	3	50.0	16	C61414	chymotrypsin (EC 3
19	3	50.0	16	G24687	T-cell receptor be
20	3	50.0	16	C28587	T-cell receptor be
21	3	50.0	16	G53284	T-cell receptor be
22	3	50.0	17	A34835	ribosomal protein
23	3	50.0	17	B44873	caldesmon - rabbit
24	3	50.0	17	B61414	chymotrypsin (EC 3
25	3	50.0	18	S74195	epoxide hydrolase
26	3	50.0	19	S54848	succinyl-CoA synth
27	3	50.0	19	B53145	high conductance c
28	3	50.0	19	S20274	quinoline oxidized
29	3	50.0	20	S46205	comosain (EC 3.4.2

30	3	50.0	20	S46204	ananain (EC 3.4.22
31	3	50.0	20	C49164	chromogranin-B - r
32	3	50.0	20	B46174	RNA-binding protei
33	3	50.0	20	S18582	hypothetical prote
34	3	50.0	20	T50757	pufk protein (impo
35	3	50.0	20	JU0330	hypothetical prote
36	3	50.0	20	A61414	chymotrypsin (EC 3
37	3	50.0	20	A90991	hypothetical prote
38	2	33.3	4	I40505	hypothetical prote
39	2	33.3	4	S17255	ribosomal protein
40	2	33.3	4	T30569	hypothetical prote
41	2	33.3	5	A60521	glycogen phosphory
42	2	33.3	5	T14908	hypothetical prote
43	2	33.3	5	S55237	zinc-binding prote
44	2	33.3	5	A60803	neuropeptide - sea
45	2	33.3	5	PT0278	Ig heavy chain CRD
46	2	33.3	5	S69237	surface protein te
47	2	33.3	5	A58728	serrawettin W2 - S
48	2	33.3	6	A35890	RNA-directed DNA p
49	2	33.3	6	B34835	dnaA protein - Pae
50	2	33.3	6	A37765	hypothetical prote
51	2	33.3	6	S29637	jacalin beta-II ch
52	2	33.3	6	A49792	acylaminoacyl-pept
53	2	33.3	6	B26206	alpha-1,4-glucan-p
54	2	33.3	6	I59142	platelet-derived g
55	2	33.3	7	JN0859	peptidyl-dipeptida
56	2	33.3	7	PQ6663	membrane protein -
57	2	33.3	7	PT0087	ribulose-bisphosph
58	2	33.3	7	PN0150	omega-gliadine 1'
59	2	33.3	7	S70335	endosperm protein,
60	2	33.3	7	S71299	ICL2 protein - Far
61	2	33.3	7	S33244	neuromodulatory pe
62	2	33.3	7	S33245	neuromodulatory pe
63	2	33.3	7	S33246	neuromodulatory pe
64	2	33.3	7	PT0246	Ig heavy chain CRD
65	2	33.3	7	E30608	Ig kappa chain V-I
66	2	33.3	7	I48086	DNA topoisomerase
67	2	33.3	7	S29735	polysphosphate-gluc
68	2	33.3	8	B24749	neuropeptide B - b
69	2	33.3	8	PC4131	hypothetical prote
70	2	33.3	8	A39308	glycine reductase
71	2	33.3	8	A37521	R-phycocerythrin ga
72	2	33.3	8	S68802	nitrate reductase
73	2	33.3	8	PL0182	paramyosin - north
74	2	33.3	8	A46306	spasmogenic toxin
75	2	33.3	8	J80316	leucokinin VI - Ma
76	2	33.3	8	PT0298	Ig heavy chain CRD
77	2	33.3	8	A42057	fibroblast growth
78	2	33.3	8	PN0043	phosphatidylethano
79	2	33.3	8	I49404	prealbumin - weste
80	2	33.3	8	A35180	neutral proteinase
81	2	33.3	8	PC4372	telomeric and tetr
82	2	33.3	8	B47594	aspartate kinase (
83	2	33.3	8	T13818	cytochrome oxidase
84	2	33.3	9	D24180	fibronogen beta ch
85	2	33.3	9	D58503	translation elonga
86	2	33.3	9	S02384	probable membrane
87	2	33.3	9	C36730	hufU protein - Kle
88	2	33.3	9	P80253	glycine cleavage s
89	2	33.3	9	C57444	neuropeptide Grb-A
90	2	33.3	9	A41978	calliFERamide 1 -
91	2	33.3	9	S10920	venom protein HR-3
92	2	33.3	9	A60427	macrophage cytotox
93	2	33.3	9	S78426	52.5K protein - sp
94	2	33.3	9	G85802	hypothetical prote
95	2	33.3	10	XAVI6B	angiotensin-conver
96	2	33.3	10	1 ECLQ3M	tachykinin III - m
97	2	33.3	10	1 GNR0L2	leucosulfakinin-II
98	2	33.3	10	2 C26997	unspecific monooxy
99	2	33.3	10	2 S33844	alpha-2-macroglobu
100	2	33.3	10	2 A46491	C3 homolog HK - in

## ALIGNMENTS

## RESULT 1

F33098  
 214K exoantigen (version 3) - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C>Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: F33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: F33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <NIC>

Query Match 66.7%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02; Mismatches 0; Indels 0; Gaps 0;  
 Matches 4; Conservative 0;

QY 1 PQSV 4  
 ||||  
 Db 4 PQSV 7

## RESULT 2

PT0560  
 T-cell receptor beta chain V-D-J region (126-1CE) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0560  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0560  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-6 <FE>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 ||||  
 Db 2 SVL 4

## RESULT 3

I57650  
 hemoglobin alpha chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C>Date: 02-Jul-1996 #sequence\_revision 31-Jul-1997 #text\_change 20-Apr-2000  
 C:Accession: I57650  
 R:Whitelaw, E.; Hogben, P.; Hanscombe, O.; Proudfoot, N.J.  
 Mol. Cell. Biol. 9, 241-251, 1989  
 A:Title: Transcriptional promiscuity of the human alpha-globin gene.  
 A:Reference number: I57650; MUID:89181576; PMID:2538719  
 A:Accession: I57650  
 A>Status: translated  
 A:Molecule type: DNA  
 A:Residues: 1-9 <WHI>  
 A:Cross-references: GB:M23454; NID:G340922; PID:AAA52629.1; PID:G553329  
 A>Note: engineered sequence; this sequence was not determined in this report  
 C:Genetics:  
 A:Gene: GDB:HBA1  
 A:Cross-references: GDB:119293  
 A:Map position: 16p13.3-16p13.3

Query Match 50.0%; Score 3; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 ||||  
 Db 2 VLS 4

## RESULT 4

A42324  
 cytochrome P450c27/25 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Feb-1996  
 C:Accession: A42324  
 R:Shayiq, R.M.; Avadhani, N.G.  
 J. Biol. Chem. 267, 2421-2428, 1992  
 A:Title: Sequence complementarity between the 5'-terminal regions of mRNAs for rat m1  
 ap.  
 A:Reference number: A42324; MUID:92129322; PMID:1733943  
 A:Accession: A42324  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-12 <SHA>  
 A>Note: sequence extracted from NCBI backbone (NCBIN:78404, NCBIP:78410)

Query Match 50.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 ||||  
 Db 3 VLS 5

## RESULT 5

S69095  
 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein - Sulfolobus acid  
 N:Alternate names: Rieske iron-sulfur protein  
 C:Species: Sulfolobus acidocaldarius  
 C>Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 03-Jun-2002  
 C:Accession: S69095  
 R:Schmidt, C.L.; Anemuller, S.; Teixeira, M.; Schaefer, G.  
 FEBS Lett. 359, 239-243, 1995  
 A:Title: Purification and characterization of the Rieske iron-sulfur protein from the  
 A:Reference number: S69095; MUID:95172243; PMID:7867807  
 A:Accession: S69095  
 A:Molecule type: protein  
 A:Residues: 1-12 <SCH>  
 C:Keywords: oxidoreductase

Query Match 50.0%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 ||||  
 Db 2 SVL 4

## RESULT 6

S47361  
 T-cell antigen receptor VJ junction beta chain - human  
 C:Species: Homo sapiens (man)  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C:Accession: S47361  
 R:Lehner, P.J.  
 submitted to the EMBL Data Library, August 1994  
 A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by  
 A:Reference number: S47355  
 A:Accession: S47361  
 A>Status: preliminary  
 A:Molecule type: mRNA



A;Residues: 1-13 <LEH>  
 A;Cross-references: EMBL:Z35685; NID:G527459; PIDN:CAA84754.1; PID:G527460  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 2 SVL 4

## RESULT 7

B56864  
 dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C;Accession: B56864  
 R;Plakidou-Dymock, S.; McGivan, J.D.  
 Biochim. Biophys. Acta 1145, 105-112, 1993  
 A;Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border membrane vesicles  
 A;Reference number: A56864; MUID:93136203; PMID:8093665  
 A;Accession: B56864  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-13 <PLA>  
 A;Experimental source: renal brush-border membrane vesicles  
 C;Keywords: dipeptidylpeptide hydrolase

Query Match 50.0%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 7 VLS 9

## RESULT 8

QWAPP  
 polistes mastoparan - paper wasp (Polistes jadvigae)  
 C;Species: Polistes jadvigae  
 C;Date: 24-Sep-1981 #sequence\_revision 24-Sep-1981 #text\_change 08-Dec-1995  
 C;Accession: A01780  
 R;Hirai, Y.; Ueno, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
 Biomed. Res. 1, 185-187, 1980  
 A;Title: A new mast cell degranulating peptide, polistes mastoparan, in the venom of Polistes mastoparan  
 A;Reference number: A01780  
 A;Accession: A01780  
 A;Molecule type: protein  
 A;Residues: 1-14 <HIR>  
 A;Comment: This cytoactive peptide from wasp venom induces mast cell degranulation.  
 C;Superfamily: mastoparan  
 C;Keywords: amidated carboxyl end  
 F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 50.0%; Score 3; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 12 SVL 14

## RESULT 9

S11074  
 alcohol dehydrogenase (EC 1.1.1.1) - Baltic cod (fragments)  
 C;Species: Gadus morhua callarias (Baltic cod)  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 31-Jan-1997  
 C;Accession: S11074  
 R;Egestad, B.; Estenius, M.; Danielsson, O.; Persson, B.; Cederlund, E.; Kaiser, R.; Hol

FBBS Lett. 269, 194-196, 1990  
 A;Title: Fast atom bombardment mass spectrometry and chemical analysis in determination of the structure of the active site of alcohol dehydrogenase from Baltic cod  
 A;Reference number: S11074; MUID:90353571; PMID:2387402  
 A;Accession: S11074  
 A;Molecule type: protein  
 A;Residues: 1-5;6-14 <EGH>  
 C;Keywords: acetylated amino end; alcohol metabolism; NAD; oxidoreductase  
 F;1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 50.0%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 10 VLS 12

## RESULT 10

PN0117  
 hemoglobin alpha chain - red fox (fragment)  
 C;Species: Vulpes vulpes (red fox)  
 C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 19-May-2000  
 C;Accession: PN0117  
 R;Sukhomlinov, B.F.; Konoshenko, S.V.  
 Mol. Biol. (Mosk.) 5, 415-418, 1971  
 A;Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.  
 A;Reference number: PN0117  
 A;Accession: PN0117  
 A;Molecule type: protein  
 A;Residues: 1-15 <SUK>  
 C;Superfamily: globin; globin homology  
 C;Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 1 VLS 3

## RESULT 11

S62620  
 protein disulfide-isomerase (EC 5.3.4.1) - castor bean (fragment)  
 C;Species: Ricinus communis (castor bean)  
 C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 17-Mar-1999  
 C;Accession: S62620  
 R;Coughlan, S.J.; Hastings, C.; Winfrey Jr., R.J.  
 Eur. J. Biochem. 235, 215-224, 1996  
 A;Title: Molecular characterisation of plant endoplasmic reticulum: identification of protein disulfide-isomerase from castor bean  
 A;Reference number: S62620; MUID:96202938; PMID:8631332  
 A;Accession: S62620  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-15 <COU>  
 C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 9 SVL 11

## RESULT 12

PA0075  
 fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (I)  
 N;Alternate names: aldolase; fructose-1,6-biophosphate triosephosphate-lase  
 C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0075; PA0077  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
 A;Reference number: PA0051  
 A;Accession: PA0075  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>  
 A;Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3  
 A;Accession: PA0077  
 A;Molecule type: protein  
 A;Residues: 1-15 <CH2>  
 A;Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.4  
 C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 5 VLS 7

RESULT 13  
 PA0102  
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (*Fusarium sporotrichioides*) (4  
 C;Species: *Fusarium sporotrichioides*  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C;Accession: PA0102  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A;Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichioides*  
 A;Reference number: PA0051  
 A;Accession: PA0102  
 A;Molecule type: protein  
 A;Residues: 1-15 <CHO>  
 C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 5 VLS 7

RESULT 14  
 S71300  
 ICL3 protein - *Paramecium tetraurelia* (fragment)  
 C;Species: *Paramecium tetraurelia*  
 C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
 C;Accession: S71300  
 R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
 Eur. J. Biochem. 238, 121-128, 1996  
 A;Title: Characterization of centrin genes in *Paramecium*.  
 A;Reference number: S71298; MUID:96248429; PMID:8665928  
 A;Accession: S71300  
 A;Molecule type: protein  
 A;Residues: 1-15 <MAD>  
 A;Experimental source: strain d4-2  
 C;Genetics:  
 A;Genetic code: SGC5

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3  
 |||  
 Db 2 PQS 4

## RESULT 15

C84035  
 hypothetical protein BH3083 [imported] - *Bacillus halodurans* (strain C-125)  
 C;Species: *Bacillus halodurans*  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C;Accession: C84035  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* a  
 A;Reference number: A83650; MUID:20512582; PMID:11058132  
 A;Accession: C84035  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-15 <STO>  
 A;Cross-references: GB:AP001517; GB:BA000004; NID:g10175500; PIDN:BA806802.1; GSPDB:G  
 A;Experimental source: strain C-125  
 C;Genetics:  
 C;Gene: BH3083

Query Match 50.0%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 10 VLS 12

## RESULT 16

S11290  
 matrix protein M1 - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)  
 C;Species: influenza A virus  
 C;Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 18-Jun-1993  
 C;Accession: S11290  
 R;Robertson, J.S.  
 Nucleic Acids Res. 6, 3745-3757, 1979  
 A;Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influe  
 A;Reference number: S11286; MUID:80034428; PMID:493121  
 A;Accession: S11290  
 A;Molecule type: Genomic RNA  
 A;Residues: 1-16 <ROB>  
 A;Cross-references: EMBL:J02112  
 C;Genetics:  
 A;Map position: segment 7  
 C;Superfamily: influenza virus matrix protein M1

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 11 VLS 13

## RESULT 17

A44352  
 candidapepsin (EC 3.4.23.24), white-opaque switching regulated - yeast (*Candida albic*  
 C;Species: *Candida albicans*  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Nov-1996  
 C;Accession: A44352  
 R;Morrow, B.; Srikantha, T.; Soll, D.R.  
 Mol. Cell. Biol. 12, 2997-3005, 1992  
 A;Title: Transcription of the gene for a pepsinogen, PEPI, is regulated by white-opaq  
 A;Reference number: A44352; MUID:92318916; PMID:1620110  
 A;Accession: A44352  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <MOR>  
 C;Keywords: aspartic proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 8 SVL 10

RESULT 18  
 C61414  
 chymotrypsin (BC 3.4.21.1) - slider turtle (fragment)  
 C;Species: Pseudemys scripta (slider)  
 C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 07-May-1999  
 C;Accession: C61414  
 R;Bhargava, A.K.; Barnard, E.A.  
 J. Mol. Evol. 2, 187-198, 1973  
 A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determined  
 A;Reference number: A61414; MUID:76146602; PMID:4807189  
 A;Accession: C61414  
 A;Status: Preliminary  
 A;Molecule type: protein  
 A;Residues: 1-16 <BHA>  
 C;Keywords: hydrolase; protein digestion; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6  
 |||  
 Db 9 VLS 11

RESULT 19  
 G24687  
 T-cell receptor beta-1 chain J-B1.4 segment - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
 C;Accession: G24687  
 R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A;Title: Organization and sequences of the diversity, joining, and constant region genes  
 A;Reference number: A94081; MUID:86094276; PMID:3866244  
 A;Accession: G24687  
 A;Molecule type: DNA  
 A;Residues: 1-16 <TOY>  
 A;Cross-references: GB:M14158; NID:G338844; PIDN:AAA60671.1; PID:G553683  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 14 SVL 16

RESULT 20  
 C28587  
 T-cell receptor beta-2 chain J-B2.4 segment - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
 C;Accession: C28587  
 R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
 A;Title: Organization and sequences of the diversity, joining, and constant region genes  
 A;Reference number: A94081; MUID:86094276; PMID:3866244  
 A;Accession: C28587  
 A;Molecule type: DNA  
 A;Residues: 1-16 <TOY>  
 A;Cross-references: GB:M14159; NID:G338852; PIDN:AAA60678.1; PID:G553689

C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 14 SVL 16

RESULT 21  
 G53284  
 T-cell receptor beta 2 chain J region, Jbeta2.4 - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C;Accession: G53284  
 R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
 Mol. Immunol. 28, 881-888, 1991  
 A;Title: Evolutionarily conserved organization and sequences of germline diversity and  
 A;Reference number: A53284; MUID:91342695; PMID:1678859  
 A;Accession: G53284  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-16 <HAR>  
 A;Cross-references: GB:S60737; NID:G233916; PIDN:AAB19523.1; PID:G233923  
 A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60745)  
 C;Keywords: T-cell receptor

Query Match 50.0%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 14 SVL 16

RESULT 22  
 A34835  
 ribosomal protein L34 - Pseudomonas aeruginosa (fragment)  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 23-Jun-1993  
 C;Accession: A34835  
 R;Yee, T.W.; Smith, D.W.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990  
 A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from  
 A;Reference number: A34835; MUID:90160310; PMID:2106132  
 A;Accession: A34835  
 A;Molecule type: DNA  
 A;Residues: 1-17 <YEE>  
 A;Cross-references: GB:M30125  
 C;Genetics:  
 A;Gene: rpmH  
 C;Superfamily: Escherichia coli ribosomal protein L34  
 C;Keywords: protein biosynthesis; ribosome

Query Match 50.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6  
 |||  
 Db 11 VLS 13

RESULT 23  
 B44873  
 caldesmon - rabbit (fragment)  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 04-Mar-2000  
 C;Accession: B44873  
 R;Ikabe, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991  
 A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protein  
 A;Reference number: A44873; MUID:91378498; PMID:1898046  
 A;Accession: B44873  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-17 <IRE>  
 A;Experimental source: skeletal myosin  
 A;Note: sequence extracted from NCBI backbone (NCBIP:63202)  
 C;Superfamily: caldesmon

Query Match 50.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
 |||  
 Db 6 QSV 8

RESULT 24  
 B61414  
 Chymotrypsin (EC 3.4.21.1) - painted turtle (fragment)  
 C;Species: Chrysemys picta (painted turtle)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 07-May-1999  
 C;Accession: B61414  
 R;Bhargava, A.K.; Barnard, E.A.  
 J. Mol. Evol. 2, 187-198, 1973  
 A;Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence deter  
 A;Reference number: A61414; MUID:76146602; PMID:4807189  
 A;Accession: B61414  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-17 <BRA>  
 C;Keywords: hydrolase; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 9 VLS 11

RESULT 25  
 S74195  
 epoxide hydrolase (EC 3.3.2.3), microsomal - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 17-Mar-1999  
 C;Accession: S74195  
 R;Araya, Z.; Hellman, U.; Hansson, R.  
 Eur. J. Biochem. 231, 855-861, 1995  
 A;Title: Characterisation of taurochenodeoxycholic acid 6-alpha-hydroxylase from pig liv  
 A;Reference number: S66455; MUID:95377322; PMID:7649186  
 A;Accession: S74195  
 A;Molecule type: protein  
 A;Residues: 1-18 <ARA>  
 A;Experimental source: liver  
 C;Superfamily: epoxide hydrolase  
 C;Keywords: ether hydrolase

Query Match 50.0%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 8 SVL 10

RESULT 26  
 S54848

succinyl-CoA synthetase (EC 6.2.1.1-) alpha subunit - Pseudomonas aeruginosa (fragment  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 17-Jul-1998  
 A;Accession: S54848  
 R;Liao, X.; Lightfoot, J.; Charlebois, I.; Ouellet, C.; Morency, M.J.; Dewar, K.; Sie  
 submitted to the EMBL Data Library, January 1995  
 A;Description: Physical mapping of 44 loci including accA, aimE, ampC, ampR, arcA, ar  
 prP, pbpB, pbpC, pheS, phoA, phoB, phoS, ponA, proS, pyoSI, qin, rpoB, rpoH, rpsB, so  
 A;Reference number: S54841  
 A;Accession: S54848  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-19 <LFA>  
 A;Cross-references: EMBL:X84052  
 C;Genetics:  
 A;Gene: sucD  
 C;Superfamily: succinate-CoA ligase (ADP-forming) alpha chain  
 C;Keywords: acid-thiol ligase; ATP; phosphohistidine; phosphoprotein; tricarboxylic a

Query Match 50.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 2 SVL 4

RESULT 27  
 B53145  
 high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragme  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 18-Jul-2001  
 C;Accession: B53145  
 R;Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.  
 J. Biol. Chem. 269, 3921-3924, 1994  
 A;Title: Subunit composition of the high conductance calcium-activated potassium chan  
 A;Reference number: A53145; MUID:94140798; PMID:7508434  
 A;Accession: B53145  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <KNA>  
 A;Note: sequence extracted from NCBI backbone (NCBIP:144547)  
 C;Superfamily: fruit fly calcium-activated potassium channel slo

Query Match 50.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 11 SVL 13

RESULT 28  
 S20274  
 guanine oxidoreductase - Rhodococcus sp.  
 C;Species: Rhodococcus sp.  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
 C;Accession: S20274  
 R;Peschke, B.; Lingens, F.  
 Biol. Chem. Hoppe-Seyler 372, 1081-1088, 1991  
 A;Title: Microbial metabolism of guanine and related compounds. XII. Isolation and  
 ase from Pseudomonas putida 86.  
 A;Reference number: S20274; MUID:92162192; PMID:1789933  
 A;Accession: S20274  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <PES>

Query Match 50.0%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 17 SVL 19

## RESULT 29

S46205  
comosain (EC 3.4.22.-) - pineapple (fragment)  
C:Species: Ananas comosus (pineapple)  
C:Date: 16-Feb-1995 #sequence\_revision 01-Nov-1996 #text\_change 07-May-1999  
C:Accession: S46205  
R:Napper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, E.  
Biochem. J. 301, 727-735, 1994  
A:Title: Purification and characterization of multiple forms of the pineapple-stem-deriv  
A:Reference number: S46204; MUID:94330946; PMID:8053898  
A:Accession: S46205  
A:Molecule type: protein  
A:Residues: 1-20 <NAP>  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3  
|||  
Db 2 PQS 4

## RESULT 30

S46204  
ananain (EC 3.4.22.31) - pineapple (fragment)  
C:Species: Ananas comosus (pineapple)  
C:Date: 16-Feb-1995 #sequence\_revision 01-Nov-1996 #text\_change 07-May-1999  
C:Accession: S46204  
R:Napper, A.D.; Bennett, S.P.; Borowski, M.; Holdridge, M.B.; Leonard, M.J.C.; Rogers, E.  
Biochem. J. 301, 727-735, 1994  
A:Title: Purification and characterization of multiple forms of the pineapple-stem-deriv  
A:Reference number: S46204; MUID:94330946; PMID:8053898  
A:Accession: S46204  
A:Molecule type: protein  
A:Residues: 1-20 <NAP>  
C:Superfamily: papain  
C:Keywords: cysteine proteinase; hydrolase

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3  
|||  
Db 2 PQS 4

## RESULT 31

C49164  
chromogranin-B - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997.  
C:Accession: C49164  
R:Nielsen, E.; Welinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th  
A:Reference number: A49164; MUID:92063871; PMID:1954895  
A:Accession: C49164  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <NIE>  
A>Note: sequence extracted from NCBI backbone (NCBIP:66369)  
C:Superfamily: chromogranin B precursor

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3  
|||  
Db 2 PQS 4

## RESULT 32

B46174  
RNA-binding protein TIAR - human (fragment)  
N:Alternate names: cytotoxic granule-associated RNA-binding protein; TIA-1 related pr  
C:Species: Homo sapiens (man)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 02-Jul-1998  
C:Accession: B46174  
R:Kawakami, A.; Tian, Q.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992  
A:Title: Identification and functional characterization of a TIA-1-related nucleolysir  
A:Reference number: A46174; MUID:92409580; PMID:1326761  
A:Accession: B46174  
A>Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-20 <KAW>  
A>Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIP:114068)  
C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprot

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 16 SVL 18

## RESULT 33

S18582  
hypothetical protein K (pufQ 3' region) - Rhodobacter sphaeroides  
C:Species: Rhodobacter sphaeroides  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 03-May-1994  
C:Accession: S18582; S32855  
R:Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Olsen, J.D.  
Mol. Microbiol. 5, 2649-2661, 1991  
A:Title: DNA sequencing and complementation/deletion analysis of the bcbA-puf operon  
A:Reference number: S18580; MUID:92140030; PMID:1779756  
A:Accession: S18582  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-20 <HUN>  
A:Cross-references: EMBL:X68795

Query Match 50.0%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 14 SVL 16

## RESULT 34

T50757  
pufK protein [imported] - Rhodobacter sphaeroides  
C:Species: Rhodobacter sphaeroides  
C:Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 21-Jul-2000  
C:Accession: T50757  
R:Choudhary, M.; Kaplan, S.  
Nucleic Acids Res. 28, 862-867, 2000  
A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides  
A:Reference number: 225222; MUID:20115911; PMID:10648776  
A:Accession: T50757  
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-20 <CHO>  
 A:Cross-references: EMBL:AF195122; PIDN:AAF24301.1  
 A:Experimental source: strain 2.4.1  
 C:Genetics:  
 A:Gene: pufK

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 |||  
 Db 14 SVL 16

## RESULT 35

JU0330 hypothetical protein, 2.4K (lytA 5' region) - Streptococcus pneumoniae

C:Species: Streptococcus pneumoniae  
 C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 24-Feb-1995  
 C:Accession: JU0330

R:Diaz, E.; Garcia, J.L.  
 Gene 90, 157-162, 1990.

A:Title: Characterization of the transcription unit encoding the major pneumococcal auto

A:Reference number: JU0329; MUID:90337339; PMID:1974230

A:Accession: JU0330

A:Molecule type: DNA

A:Residues: 1-20 <DNA>

A:Experimental source: strain M31

C:Genetics:

A:Start codon: GTG

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 5 VLS 7

## RESULT 36

A61414

Chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)

C:Species: Chelydra serpentina (snapping turtle)

C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 07-May-1999

C:Accession: A61414

R:Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2, 187-198, 1973

A:Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence determ

A:Reference number: A61414; MUID:76146602; PMID:4807189

A:Accession: A61414

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 <BHA>

C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 9 VLS 11

## RESULT 37

A99091

hypothetical protein spr1755 [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001

C:Accession: A99091

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.  
 y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.  
 Y, P.; Sun, P.M.; Winkler, M.E.  
 J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.)

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: A99091

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-20 <KUR>

A:Cross-references: GB:AE007317; PIDN:RAL00558.1; PID:gi5459436; GSPDB:GN00174

C:Genetics:

A:Gene: spr1755

Query Match 50.0%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 5 VLS 7

## RESULT 38

I40505

hypothetical protein 3 (4 aa) - Bacillus stearothermophilus

C:Species: Bacillus stearothermophilus

C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 15-Oct-1999

C:Accession: I40505

R:Waye, M.M.; Winter, G.

Bur. J. Biochem. 158, 505-510, 1986

A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA s

A:Reference number: I40503; MUID:86274732; PMID:3525162

A:Accession: I40505

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references: EMBL:X04193; NID:G40233; PIDN:CAA27783.1; PID:G580944

Query Match 33.3%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 ||  
 Db 2 LS 3

## RESULT 39

S17255

ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae

C:Species: Saccharomyces cerevisiae

A:Variety: strain 07173

C:Date: 23-Apr-1993 #sequence\_revision 14-Sep-1994 #text\_change 09-May-1997

C:Accession: S17255

R:Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, FBS Lett. 284, 51-56, 1991

A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit fr

A:Reference number: S17255; MUID:91285106; PMID:2060626

A:Accession: S17255

A:Molecule type: protein

A:Residues: 1-4 <GRO>

C:Comment: A coding region for this protein could not be identified in the genome of

C:Genetics:

A:Genome: nuclear

C:Keywords: mitochondrion; protein biosynthesis; ribosome

## Query Match

Best Local Similarity 33.3%; Score 2; DB 2; Length 4;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4

```

Db      1 SV 2
||
Query Match      33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 40
T30569
hypothetical protein - Emericella nidulans
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
C;Accession: T30569
R;Morrice, J.; MacKenzie, D.A.; Parr, A.J.; Archer, D.B.
Curr. Genet. 34, 379-385, 1998
A;Title: Isolation and characterization of the acetyl-CoA carboxylase gene from Aspergillus
A;Reference number: Z20869; MUID:99087906; PMID:9871120
A;Accession: T30569
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-4 <WOR>
A;Cross-references: EMBL:Y15996; NID:el285512; PID:el218041; PIDN:CAA75927.1

Query Match      33.3%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SV 4
||
Db      3 SV 4

RESULT 41
A60521
glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N;Alternate names: glycogen phosphorylase b
C;Species: Liza ramada
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C;Accession: A60521
R;Bonamusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle
A;Reference number: A60521; MUID:90227907; PMID:2109669
A;Accession: A60521
A;Molecule type: protein
A;Residues: 1-5 <BON>
C;Superfamily: phosphorylase
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experimental

Query Match      33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SV 4
||
Db      3 SV 4

RESULT 42
T14908
hypothetical protein - parsley
C;Species: Petroselinum crispum (parsley)
C;Date: 20-Sep-1993 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C;Accession: T14908
R;Kircher, S.; Ledger, S.; Hayaishi, H.; Weisshaar, B.; Schafer, E.; Frohnmeyer, H.
Mol. Gen. Genet. 257, 595-605, 1998
A;Title: CPRF4a, a novel plant bZIP protein of the CPRF family: comparative analysis of
A;Reference number: Z18261; MUID:98265918; PMID:9604882
A;Accession: T14908
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5 <KIR>
A;Cross-references: EMBL:Y10809; NID:G3336901; PIDN:CAA71767.1; PID:G3336902
A;Experimental source: Hamburger Schnitt

Query Match      33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SV 4
||
Db      3 SV 4

RESULT 43
S55237
zinc-binding protein ZBP14 - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C;Accession: S55237
R;Robinson, K.; Jones, D.; Howell, S.; Soneji, Y.; Martin, S.; Aitken, A.
Biochem. J. 307, 267-272, 1995
A;Title: Expression and characterization of maize ZBP14, a member of a new family of
A;Reference number: S55237; MUID:95234046; PMID:7717986
A;Accession: S55237
A;Molecule type: protein
A;Residues: 1-5 <ROB>

Query Match      33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VL 5
||
Db      4 VL 5

RESULT 44
A60803
neuropeptide - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60803
R;Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A;Title: Isolation of <Glu-Ser-Lu-Arg-Tip-NH-2, a novel neuropeptide from sea anemones
A;Reference number: A60803; MUID:88222764; PMID:2897223
A;Accession: A60803
A;Molecule type: protein
A;Residues: 1-5 <GRA>
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: amidated carboxyl end (Tip) #status experimental

Query Match      33.3%; Score 2; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 QS 3
||
Db      1 QS 2

RESULT 45
PT0278
Ig heavy chain CRD3 region (clone 4-88) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0278
A;Molecule type: DNA
A;Residues: 1-5 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

```

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
 ||  
 Db 4 VL 5

RESULT 46  
 S69237  
 surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)  
 C;Species: Staphylothermus marinus  
 C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 17-Mar-1999  
 C;Accession: S69237  
 R;Peters, J.; Nitsch, M.; Kuehlmoorgen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh  
 J. Mol. Biol. 245, 385-401, 1995  
 A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua  
 A;Reference number: S69237; MUID:95139068; PMID:7837271  
 A;Accession: S69237  
 A;Molecule type: protein  
 A;Residues: 1-5 <PET>  
 A;Experimental source: strain F1, DSM 3639  
 C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 33.3%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 ||  
 Db 4 LS 5

RESULT 47  
 A58728  
 serrawettin W2 - Serratia marcescens  
 C;Species: Serratia marcescens  
 C;Date: 10-Feb-1998 #sequence\_revision 12-Feb-1998 #text\_change 12-Feb-1998  
 C;Accession: A58728  
 R;Matsuyama, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.  
 J. Bacteriol. 174, 1769-1776, 1992  
 A;Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and  
 A;Reference number: A58728; MUID:92193260; PMID:1548227  
 A;Accession: A58728  
 A;Status: unencoded polypeptide  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>  
 A;Experimental source: strain NS 25  
 C;Comment: A surfactant lipopeptide promoting flagellum-independent surface translocatio  
 C;Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencode  
 F;1/Modified site: D-leucine (Ileu) #status experimental  
 F;4/Modified site: D-phenylalanine (Phe) #status experimental  
 F;1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status expe

Query Match 33.3%; Score 2; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 ||  
 Db 1 LS 2

RESULT 48  
 A35890  
 RNA-directed DNA polymerase (EC 2.7.7.49) 66K chain - human immunodeficiency virus type  
 C;Species: human immunodeficiency virus type 1, HIV-1  
 C;Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 31-Dec-1993  
 C;Accession: A35890  
 R;Bathurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.; Pichuanes, S.; C  
 Biochem. Biophys. Res. Commun. 171, 589-595, 1990

A;Title: Characterization of the human immunodeficiency virus type-1 reverse transcri  
 A;Reference number: A35890; MUID:90386627; PMID:1698361  
 A;Accession: A35890  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-6 <BAT>  
 C;Keywords: nucleotidyltransferase

Query Match 33.3%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
 ||  
 Db 5 VL 6

RESULT 49  
 B34835  
 dnaA protein - Pseudomonas aeruginosa (fragment)  
 C;Species: Pseudomonas aeruginosa  
 C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 08-Oct-1999  
 C;Accession: B34835  
 R;Yee, T.W.; Smith, D.W.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990  
 A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from  
 A;Reference number: A34835; MUID:90160310; PMID:2106132  
 A;Accession: B34835  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-6 <YEE>  
 A;Cross-references: GB:M30125; NID:gl51419; PIDN:AAA25916.1; PID:gl51421  
 C;Keywords: DNA binding

Query Match 33.3%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
 ||  
 Db 2 SV 3

RESULT 50  
 A37765  
 hypothetical protein (csmA 5' region) - Chloroflexus aurantiacus (fragment)  
 C;Species: Chloroflexus aurantiacus  
 C;Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
 C;Accession: A37765  
 R;Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
 J. Bacteriol. 172, 4497-4504, 1990  
 A;Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantia  
 A;Reference number: A37765; MUID:90330558; PMID:2376566  
 A;Accession: A37765  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-6 <THE>  
 A;Cross-references: GB:M33964

Query Match 33.3%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2  
 ||  
 Db 1 PQ 2

RESULT 51  
 S29637  
 jacalin beta-II chain - Artocarpus champeden (fragment)  
 C;Species: Artocarpus champeden  
 C;Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998



C;Accession: S29637  
R;Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
Biochim. Biophys. Acta 1156, 219-222, 1993  
A;Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
A;Reference number: S29635; MUID:93152601; PMID:8427879  
A;Accession: S29637  
A;Molecule type: protein  
A;Residues: 1-6 <NGO>  
A;Experimental source: seed  
C;Complex: heterotetramer; two alpha and two beta chains  
A;Function:  
A;Description: seed storage protein  
A;Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine  
C;Keywords: heterotetramer; lectin; seed; storage protein

Query Match 33.3%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
||  
3 QS 4

Db

RESULT 52  
A49792  
acylaminoacyl-peptidase (EC 3.4.19.1) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 07-May-1999  
C;Accession: A49792  
R;Krishna, R.G.; Chin, C.C.Q.; Wold, F.  
Anal. Biochem. 199, 45-50, 1991  
A;Title: N-terminal sequence analysis of N(alpha)-acetylated proteins after unblocking w  
A;Reference number: A49792; MUID:92222120; PMID:1807161  
A;Accession: A49792  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <KRI>  
A;Keywords: acetylated amino end; hydrolase; omega peptidase  
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
5 VL 6

Db

RESULT 53  
B26206  
alpha-1,4-glucan-protein synthase (UDP-forming) (EC 2.4.1.112) - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 30-Oct-1992 #sequence\_revision 30-Oct-1992 #text\_change 13-Sep-1996  
C;Accession: B26206; A26206  
R;Iarner, J.; Sanger, F.  
J. Mol. Biol. 11, 491-500, 1965  
A;Title: The amino acid sequence of the phosphorylation site of muscle uridine diphospho  
A;Reference number: A26206  
A;Accession: B26206  
A;Molecule type: protein  
A;Residues: 1-6 <LAR>  
A;Experimental source: muscle  
A;Note: Lys-1 was also found  
C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
F;4/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
1 SV 2

Db

RESULT 54  
I59142  
platelet-derived growth factor B chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I59142  
R;Pech, M.; Gazit, A.; Arnstein, P.; Aaronson, S.A.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2693-2697, 1989  
A;Title: Generation of fibrosarcomas in vivo by a retrovirus that expressed the normal  
A;Reference number: I59142; MUID:89202393; PMID:2649890  
A;Accession: I59142  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:M26180; NID:G516624; PIDN:AAA39905.1; PID:G516625

Query Match 33.3%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
5 VL 6

Db

RESULT 55  
JN0859  
peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito  
C;Species: Sarda orientalis (striped bonito)  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C;Accession: JN0859  
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory  
A;Reference number: JN0859; MUID:94080036; PMID:7764272  
A;Accession: JN0859  
A;Molecule type: protein  
A;Residues: 1-7 <MAT>  
A;Experimental source: intestine  
C;Comment: The carboxyl-terminus is essential for the protein's expression of angioter  
C;Superfamily: bradykinin-potentiating peptide  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
1 SV 2

Db

RESULT 56  
PQ0663  
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)  
C;Species: porcine epidemic diarrhea virus  
C;Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 08-Oct-1999  
C;Accession: PQ0663  
R;Bridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.  
J. Gen. Virol. 74, 1795-1804, 1993  
A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epide  
issile gastroenteritis virus.  
A;Reference number: JQ2191; MUID:93389433; PMID:8397280  
A;Accession: PQ0663  
A;Molecule type: mRNA  
A;Residues: 1-7 <BRI>  
A;Cross-references: GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:G584083  
C;Comment: This virus is coronavirus related to human coronavirus 229E.  
C;Keywords: membrane protein

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
Db 3 VL 4

RESULT 57  
PT0087  
ribulose-bisphosphate carboxylase (EC 4.1.1.39) large chain - Arabidopsis thaliana (frag  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 24-Nov-1999  
C;Accession: PT0087  
R;Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.  
submitted to JIPID, December 1995  
A;Description: Two dimensional electrophoresis of plant proteins and standardization of  
A;Reference number: PN0173  
A;Accession: PT0087  
A;Molecule type: protein  
A;Residues: 1-7 <TSU>  
A;Experimental source: leaf  
C;Keywords: acetylated amino end; carbon-carbon lyase; carboxy-lyase  
F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2  
||  
Db 2 PQ 3

RESULT 58  
PN0150  
omega-gliadin 1' - Aegilops longissima (fragment)  
C;Species: Aegilops longissima  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C;Accession: PN0150  
R;Odintsova, T.I.; Egorov, T.A.  
Biochimia 55, 509-516, 1990  
A;Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of  
A;Reference number: PN0146; MUID:90283493; PMID:2354218  
A;Accession: PN0150  
A;Molecule type: protein  
A;Residues: 1-7 <ODI>  
A;Experimental source: strain K-907

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
||  
Db 4 LS 5

RESULT 59  
S70335  
endosperm protein, 40K - rye (fragment)  
C;Species: Secale cereale (rye)  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C;Accession: S70335  
R;Rocher, A.; Calero, M.; Soriano, F.; Mender, E.  
Biochim. Biophys. Acta 1295, 13-22, 1996  
A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.  
A;Reference number: S70327; MUID:96283789; PMID:8679669  
A;Accession: S70335  
A;Status: preliminary  
A;Molecule type: protein

A;Residues: 1-7 <ROC>

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
||  
Db 5 QS 6

RESULT 60  
S71299  
ICL2 protein - Paramecium tetraurelia (fragment)  
C;Species: Paramecium tetraurelia  
C;Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-Dec-1999  
C;Accession: S71299  
R;Madeddu, L.; Klotz, C.; le Caer, J.P.; Beisson, J.  
Eur. J. Biochem. 238, 121-128, 1996  
A;Title: Characterization of centrin genes in Paramecium.  
A;Reference number: S71298; MUID:96248429; PMID:8665928  
A;Accession: S71299  
A;Molecule type: protein  
A;Residues: 1-7 <Mad>  
A;Experimental source: strain d4-2  
C;Genetics:  
A;Genetic code: SGCS

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2  
||  
Db 5 PQ 6

RESULT 61  
S33244  
neuromodulatory peptide Wamide-1 - giant African snail  
C;Species: Achatina fulica (giant African snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C;Accession: S33244  
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323, 104-108, 1993  
A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of  
A;Reference number: S33244; MUID:93265912; PMID:8495720  
A;Accession: S33244  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
Db 5 SV 6

RESULT 62  
S33245  
neuromodulatory peptide Wamide-2 - giant African snail  
C;Species: Achatina fulica (giant African snail)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C;Accession: S33245  
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323, 104-108, 1993  
A;Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of  
A;Reference number: S33244; MUID:93265912; PMID:8495720  
A;Accession: S33245  
A;Status: preliminary  
A;Molecule type: protein

A:Molecule type: protein  
A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
5 SV 6

Db

## RESULT 63

S33246

neuromodulatory peptide wamide-3 - giant African snail

C:Species: Achatina fulica (giant African snail)

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C:Accession: S33246

R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A>Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of b

A:Reference number: S33244; MUID:93265912; PMID:8495720

A:Accession: S33246

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <MIN>

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
5 SV 6

Db

## RESULT 64

PT0246

Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0246

R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and f

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0246

A:Molecule type: DNA

A:Residues: 1-7 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotrimer; immunoglobulin

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
3 VL 4

Db

## RESULT 65

E30608

Ig kappa chain V-III region (Gag) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996

C:Accession: E30608

R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc

J. Immunol. 142, 3158-3163, 1989

A>Title: Structural and idiotypic characterization of the L chains of human IgM autoanti

A:Reference number: A30601; MUID:89215279; PMID:2496160

A:Accession: E30608

A>Status: preliminary

A:Residues: 1-7 <MIN>

A:Keywords: heterotrimer; immunoglobulin

A:Reference number: A94074; MUID:86067985; PMID:3865193

A:Accession: E30608

A>Status: preliminary

A:Residues: 1-7 <MIN>

A:Molecule type: protein  
A:Residues: 1-7 <GON>  
C:Keywords: heterotrimer; immunoglobulin

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
||  
6 QS 7

Db

## RESULT 66

I48086

DNA topoisomerase II alpha - Chinese hamster (fragment)

C:Species: Cricetulus griseus (Chinese hamster)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: I48086

R:Ng, S.W.; Eder, J.P.; Schnipper, L.E.; Chan, V.T.W.

J. Biol. Chem. 270, 25850-25858, 1995

A>Title: Molecular cloning and characterization of the promoter for the Chinese hamste

A:Reference number: I48086; MUID:96029684; PMID:7592770

A:Accession: I48086

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 <RES>

A:Cross-references: EMBL:U34196; NID:gl041231; PIDN:AAC52315.1; PID:gl041232

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
||  
3 LS 4

Db

## RESULT 67

S29735

polysphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreic

C:Species: Propionibacterium freudenreichii subsp. shermanii

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 03-Jun-2002

C:Accession: S29735

R:Phillips, N.F.B.; Horn, P.J.; Wood, H.G.

Arch. Biochem. Biophys. 300, 309-319, 1993

A>Title: The polysphosphate- and ATP-dependent glucokinase from Propionibacterium sherr

A:Reference number: S29735; MUID:9314332; PMID:8380966

A:Accession: S29735

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-7 <PHI>

C:Keywords: phosphotransferase

Query Match 33.3%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
3 VL 4

Db

## RESULT 68

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A>Title: Isolation, sequencing, synthesis, and pharmacological characterization of twc

A:Reference number: A94074; MUID:86067985; PMID:3865193

A:Accession: B24749

A>Status: preliminary

A:Residues: 1-7 <MIN>

A:Keywords: heterotrimer; immunoglobulin

A:Reference number: A94074; MUID:86067985; PMID:3865193

A:Accession: B24749

A>Status: preliminary

A:Residues: 1-7 <MIN>

A:Keywords: heterotrimer; immunoglobulin

A:Accession: B24749  
A:Molecule type: protein  
A:Residues: 1-8 <YAN>  
C:Superfamily: unassigned animal peptides  
C:Keywords: neuropeptide

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2  
||  
5 PQ 6

## RESULT 69

PC4131  
hypothetical protein 8 [imported] - Pseudomonas aeruginosa (fragment)

C:Species: Pseudomonas aeruginosa  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PC4131  
R:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.

Gene 167, 87-91, 1995  
A:Title: Sequencing and characterization of the downstream region of the genes encoding y for biosynthesis of heme dl.

A:Reference number: JC4552; MUID:96144254; PMID:8566617

A:Accession: PC4131

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <KAW>

A:Cross-references: DDBJ:D50473; NID:g1217594

A>Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
||  
4 LS 5

## RESULT 70

A39308

glycine reductase [EC 1.4.99.-] sulphydryl protein C, alpha chain - Clostridium sticklandii

C:Species: Clostridium sticklandii

C:Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 15-Aug-1997

C:Accession: A39308

R:Stadtman, T.C.; Davis, J.N.

J. Biol. Chem. 266, 22147-22153, 1991

A:Title: Glycine reductase protein C. Properties and characterization of its role in the

A:Reference number: A39308; MUID:92042141; PMID:1939235

A:Accession: A39308

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <STA>

C:Function:

A:Description: glycine reductase complex catalyzes the reductive deamination of glycine

C:Keywords: ATP; oxidoreductase

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
||  
4 VL 5

## RESULT 71

A37521

R-phycoerythrin gamma-E chain - red alga (Gastroclonium coulteri) (fragment)

C:Species: Gastroclonium coulteri

C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: A37521; J22565  
R:Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A:Reference number: A22565; MUID:85182601; PMID:3886644

A:Accession: A37521

A:Molecule type: protein

A:Residues: 1-8 <KLO>

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
||  
1 LS 2

## RESULT 72

S68802

nitrate reductase (NADH) inhibitor - spinach (fragment)

C:Species: Spinacia oleracea (spinach)

C:Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998

C:Accession: S68802

R:Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.

FEBS Lett. 387, 127-131, 1996

A:Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spin.

A:Reference number: S68802; MUID:96244508; PMID:8674533

A:Accession: S68802

A:Molecule type: protein

A:Residues: 1-8 <BAC>

A:Experimental source: leaves; strain cv. Bloomsdale

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
||  
3 LS 4

## RESULT 73

PL0162

paramyosin - northern quahog (fragment)

C:Species: Mercenaria mercenaria (northern quahog)

C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 11-May-2000

C:Accession: PL0162

R:Watabe, S.; Tsuchiya, T.; Hartschorne, D.J.

Comp. Biochem. Physiol. B 94, 813-821, 1989

A:Title: Phosphorylation of paramyosin.

A:Reference number: PL0162; MUID:90107385; PMID:2532591

A:Accession: PL0162

A:Molecule type: protein

A:Residues: 1-8 <WAR>

A:Experimental source: white adductor muscle

A>Note: the sequence is the phosphorylated tryptic peptide

C:Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-  
on the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated

C:Keywords: muscle; phosphoprotein

F:5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
||  
5 SV 6

## RESULT 74

A46306  
 spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)  
 C/Species: Phoneutria nigriventer  
 C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
 C/Accession: A46306  
 R/Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.  
 Toxicon 31, 377-384, 1993  
 A/Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
 A/Reference number: A46306; PMID:93276438; PMID:8503129  
 A/Accession: A46306  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-8 <MAR>

Query Match 33.3%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
 ||  
 Db 6 QS 7

RESULT 75  
 JS0316  
 Leucokinin VI - Madeira cockroach  
 C/Species: Leucophaea maderae (Madeira cockroach)  
 C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C/Accession: JS0316  
 R/Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A/Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
 A/Reference number: JS0315  
 A/Accession: JS0316  
 A/Molecule type: protein  
 A/Residues: 1-8 <HOL>  
 C/Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
 C/Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid  
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.3%; Score 2; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
 ||  
 Db 1 QS 2

Search completed: November 25, 2003, 19:36:10  
 Job time : 4.11628 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.12791 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6  
Sequence: 1 PQSVLS 6

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	50.0	10	1 LPK2 LOEMI	P41488 locusta mig
2	3	50.0	11	1 ESI_RAT	P56571 rattus norv
3	3	50.0	13	1 TEME_RANTE	P56917 rana tempor
4	3	50.0	13	1 TEME_RANTE	P56921 rana tempor
5	3	50.0	14	1 MAST_POLJA	P01517 polistes ja
6	3	50.0	15	1 ACT_PINPS	P81085 pinus pinas
7	3	50.0	16	1 H5_COTJA	P18638 coturnix co
8	3	50.0	19	1 AL22 HORSE	P81217 equus cabal
9	3	50.0	20	1 FRE3_LITIN	P56249 litoria inf
10	3	50.0	20	1 MAX8_BOMMX	P83087 bombina max
11	3	50.0	20	1 MI17_BOVIN	P35451 bos taurus
12	3	50.0	20	1 PUPK_RHOSH	Q53121 rhodobacter
13	2	33.3	4	1 RM01_YEAST	P36515 saccharomyc
14	2	33.3	6	1 ACPH_RABIT	P25154 oryctolagus
15	2	33.3	7	1 UH11_RAT	P56576 rattus norv
16	2	33.3	7	1 WNA1_ACHFU	P35919 achatina fu
17	2	33.3	7	1 WNA2_ACHFU	P35920 achatina fu
18	2	33.3	7	1 WNA3_ACHFU	P35921 achatina fu
19	2	33.3	8	1 CAD1_ENTFA	P13268 enterococcu
20	2	33.3	8	1 COM2_CONPU	P58785 conus purpu
21	2	33.3	8	1 CPD1_ENTFA	P13269 enterococcu
22	2	33.3	8	1 LCK6_LEUMA	P19988 leucophaea
23	2	33.3	8	1 NPBE_BOVIN	P15507 bos taurus
24	2	33.3	8	1 UH09_RAT	P56575 rattus norv
25	2	33.3	9	1 AL10_CARMA	P81813 carcinus ma
26	2	33.3	9	1 BS43_SERPL	P83375 serratia pl
27	2	33.3	9	1 FAR1_CALVO	P41856 calliphora
28	2	33.3	9	1 FIBB_ERYPA	P19346 erythrocebu
29	2	33.3	9	1 HUTU_KLEAE	P12381 klebsiella
30	2	33.3	9	1 OXYT_BUFRE	P42995 bufo regula
31	2	33.3	9	1 OXYT_RAJCL	P42994 raja clavai
32	2	33.3	10	1 BPP2_BOTIN	P30422 bothrops in
33	2	33.3	10	1 BPP2_BOTJA	P01022 bothrops ja

RESULT 1

#### ALIGNMENTS

34	2	33.3	10	1 ESI_LACCA	P81758 lactobacill
35	2	33.3	10	1 FAR6_PANRE	P82660 panagrellus
36	2	33.3	10	1 GON1_CLUPA	P81749 clupea pall
37	2	33.3	10	1 GSO9_BACSU	P80243 bacillus su
38	2	33.3	10	1 LSK2_LEUMA	P90339 leucophaea
39	2	33.3	10	1 MALE_KLEPN	Q05564 klebsiella
40	2	33.3	10	1 RRPL_PHODV	P39346 phocine dis
41	2	33.3	10	1 TKL2_LOEMI	P16224 locusta mig
42	2	33.3	10	1 TKL3_LOEMI	P30249 locusta mig
43	2	33.3	10	1 TKU1_UREUN	P40751 urechis uni
44	2	33.3	10	1 UPA2_HUMAN	P30088 homo sapien
45	2	33.3	10	1 UPA5_HUMAN	P30091 homo sapien
46	2	33.3	11	1 BPP3_BOTIN	P30423 bothrops in
47	2	33.3	11	1 BPP4_BOTIN	P30424 bothrops in
48	2	33.3	11	1 CEP1_ACHFU	P22790 achatina fu
49	2	33.3	11	1 FAR9_CALVO	P41864 calliphora
50	2	33.3	11	1 POOC_PSEFL	P55173 pseudomonas
51	2	33.3	11	1 RANC_RANPI	P08951 rana pipien
52	2	33.3	11	1 T2P1_PROVU	P31031 proteus vul
53	2	33.3	11	1 TKNA_CHICK	P19850 gallus gall
54	2	33.3	11	1 TKNA_GADMO	P28498 gadus morhu
55	2	33.3	11	1 TKNA_HORSE	P01290 equus cabal
56	2	33.3	12	1 FIF1_SARBU	P83349 sarcophaga
57	2	33.3	12	1 FRE1_LITIN	P82021 litoria inf
58	2	33.3	12	1 HCY1_CARMA	P81176 carcinus ma
59	2	33.3	12	1 PKA4_PERFU	P83690 periplaneta
60	2	33.3	12	1 TM2A_METWA	P80652 methanosarc
61	2	33.3	12	1 V25K_WSSV	P82004 white spot
62	2	33.3	13	1 BOWL_PSEGU	P42991 pseudophryn
63	2	33.3	13	1 CHEP_PARID	P43718 parapolybia
64	2	33.3	13	1 CRBL_VESMA	P17232 vespa manda
65	2	33.3	13	1 FIBB_RABIT	P14478 oryctolagus
66	2	33.3	13	1 HPAL_RANES	P32415 rana esculie
67	2	33.3	13	1 IDHC_PIG	P20304 sus scrofa
68	2	33.3	13	1 LMA1_LOEMI	P38496 locusta mig
69	2	33.3	13	1 NEUT_RANTE	P41536 rana tempor
70	2	33.3	13	1 PEDI_HYDAT	P80578 hydra atten
71	2	33.3	13	1 SAZA_ONCMY	P82238 oncorhynch
72	2	33.3	13	1 SAZB_ONCMY	P82239 oncorhynch
73	2	33.3	13	1 TEME_RANTE	P56920 rana tempor
74	2	33.3	13	1 UN12_CLOPA	P81353 clostridium
75	2	33.3	13	1 VG16_BACSU	P80867 bacillus su
76	2	33.3	14	1 CXIA_CONSE	P58623 conus betul
77	2	33.3	14	1 HCYA_MEGCR	Q10583 megathura c
78	2	33.3	14	1 KLP5_SCARA	P58396 scaptocosa
79	2	33.3	14	1 LPW_CITFR	P03056 citrobacter
80	2	33.3	14	1 LPW_ECOLI	P03053 escherichia
81	2	33.3	14	1 MAST_VESPA	P21654 vespa basal
82	2	33.3	14	1 MAST_VESOR	P17238 vespa orien
83	2	33.3	14	1 NEJ2_FASHE	P80526 fasciola he
84	2	33.3	14	1 PSAG_CUCSA	P42049 cucumis sat
85	2	33.3	14	1 UC34_MAIZE	P80640 zea mays (m
86	2	33.3	14	1 UN07_CLOPA	P81352 clostridium
87	2	33.3	15	1 APP3_MALPA	P83137 malva parvi
88	2	33.3	15	1 ATP2_PINPS	P81663 pinus pinas
89	2	33.3	15	1 CDN4_LITCE	P80076 litoria cae
90	2	33.3	15	1 DCMW_PSECH	P19917 pseudomonas
91	2	33.3	15	1 IRBP_CRISP	P12665 cricetidae
92	2	33.3	15	1 LEC1_PSOSC	P22582 psophocarpu
93	2	33.3	15	1 LEC2_PSOSC	P22585 psophocarpu
94	2	33.3	15	1 LEC3_PSOSC	P22583 psophocarpu
95	2	33.3	15	1 LFL_TRETH	P21234 thermus the
96	2	33.3	15	1 MCA2_RHOOP	P56870 rhodococcus
97	2	33.3	15	1 NIS1_ANAVA	Q44507 anabaena va
98	2	33.3	15	1 PH3_FRUSE	P29265 prunus sero
99	2	33.3	15	1 PRP_MYCBO	P80149 mycobacteri
100	2	33.3	15	1 RKGG_CARCR	P21586 caretta car

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LPK2_LOCM1
ID LPK2_LOCM1 STANDARD; PRT; 10 AA.
AC P41488;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Locustapyrokinin 2 (LOM-PK-2) (FXPRU-amide).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=94094539; PubMed=7903606;
RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustapyrokinin II from
RT Locusta migratoria, another member of the FXPRU-amide peptide
RT family.";
RL Comp. Biochem. Physiol. 106C:103-109(1993).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY (MYOTROPIC
CC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR Interbro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
DB 1 QSV 3

RESULT 2
ID ESI_RAT STANDARD; PRT; 11 AA.
AC P56571;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ESI protein, mitochondrial (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RA Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT P2) IS: 8.9, ITS MW IS: 25 kDa.
CC -1- SIMILARITY: BELONGS TO THE ESI FAMILY.
KW Mitochondrion.
FT NON TER 11
SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 1 QSV 3

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Db 7 VLS 9

RESULT 3
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56917;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin A.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA SImmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1398 MW; 2653612B9DECD408 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 8 VLS 10

RESULT 4
ID TEMA_RANTE STANDARD; PRT; 13 AA.
AC P56921;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin F.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA SImmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND
CC GRAM-POSITIVE BACTERIA.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 13;

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Best Local Similarity 100.0%; Pred. No. 8.1e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 VLS 6
Db 8 VLS 10

RESULT 5
MAST POLJA
ID MAST POLJA STANDARD; PRT; 14 AA.
AC P01517;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Polistes mastoparan.
OS Polistes jadvigae (Paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxID=7457;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Hirai Y., Yashihara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide, polistes mastoparan, in the
RL Biomed. Res. 1:185-187(1980).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
that couple to phospholipase C.
CC PIR; A01780; QMWAPP
DR Mast cell degranulation; Amidation.
KW MOD RES 14 14 AMIDATION.
FT MOD RES 14 14
SQ SEQUENCE 14 AA; 1636 MW; 26472A53BF4778D8 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 8.6e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 3 SVL 5
Db 12 SVL 14

RESULT 6
ACT PINPS
ID - ACT PINPS STANDARD; PRT; 15 AA.
AC P81065;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Actin (Water stress responsive protein 5) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344231;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED

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CC IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED
CC IN ALL EUKARYOTIC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- SIMILARITY: Belongs to the actin family.
DR InterPro: IPR004001; Actin.
DR InterPro: IPR004000; Actin_like.
DR Pfam: PF00022; actin; 1.
DR PROSITE: PS00406; ACTINS_1; PARTIAL.
DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
DR PROSITE: PS00432; ACTINS_2; PARTIAL.
KW Structural protein.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1574 MW; 4712F0146D5B4DE3 CRC64;

Query Match 50.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.2e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 VLS 6
Db 7 VLS 9

RESULT 7
H5_COTJA
ID - H5_COTJA STANDARD; PRT; 16 AA.
AC P18638;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Histone H5 (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae;
OC Coturnix.
OX NCBI_TaxID=93934;
RN [1]
RP SEQUENCE.
RX MEDLINE=76277939; PubMed=962913;
RA Seligy V., Roy C., Dove M., Yaguchi M.;
RT "Species variability of N-terminal sequence of avian erythrocyte-
specific histone H5.";
RL Biochem. Biophys. Res. Commun. 71:196-202(1976).
CC -!- FUNCTION: HISTONE H5 PERFORMS THE SAME FUNCTION AS H1, BEING
NECESSARY FOR THE CONDENSATION OF NUCLEOSOME CHAINS INTO HIGHER
ORDER STRUCTURES, AND REPLACES HISTONE H1 IN CERTAIN CELLS.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: ERYTHROID CELLS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
KW Chromosomal protein; Nuclear protein; DNA-binding; DNA condensation.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1665 MW; DB528219B3074D3C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

QY 4 VLS 6
Db 5 VLS 7

RESULT 8
AL22_HORSE
ID AL22_HORSE STANDARD; PRT; 19 AA.
AC P81217;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dander allergen Equ c 2.0102 (Fragment).
OX Equus caballus (Horse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin;  
 RX MEDLINE=98237590; PubMed=9578478;  
 RA Bulone V., Krogstad-Johnsen T., Smetad-Paulsen B.;  
 RT "Separation of horse dander allergen proteins by two-dimensional  
 electrophoresis -- molecular characterisation and identification of  
 RT Equ c 2.0101 and Equ c 2.0102 as lipocalin proteins.";  
 RL Eur. J. Biochem. 253:202-211(1998).  
 RN [2]  
 RP MASS SPECTROMETRY.  
 RC TISSUE=Hair dandruff;  
 RX MEDLINE=21257838; PubMed=11358533;  
 RA Goubran Botros H., Poncet P., Rabillon J., Fontaine T., Laval J.-M.,  
 RA David B.;  
 RT "Biochemical characterization and surfactant properties of horse  
 RT allergens.";  
 RL Eur. J. Biochem. 268:3126-3136(2001).  
 CC -I- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -I- MASS SPECTROMETRY: MW=16000; METHOD=Electrospray.  
 CC -I- MISCELLANEOUS: Allergen of horse dander.  
 CC -I- SIMILARITY: Belongs to the lipocalin family.  
 CC -I- CAUTION: C 2.0101 AND C 2.0102 MIGHT BE TWO VARIANTS OF THE  
 CC SAME PROTEIN.  
 DR InterPro: IPR000566; Lipocalin\_cytFABP.  
 DR PROSITE: PS00213; LIPOCALIN; PARTIAL.  
 DR Transport; Lipocalin; Allergen.  
 KW NON TER 19  
 FT NON TER 19  
 SQ SEQUENCE 19 AA; 2195 MW; A8EB6FAFC9322C26 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQS 3  
 DB 4 PQS 6  
 RESULT 9  
 PRE3 LITIN STANDARD; PRT; 20 AA.  
 ID PRE3 LITIN STANDARD; PRT; 20 AA.  
 AC P56249;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Frenatin 3.  
 OS Litoria infrafrenata (Giant tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=61195;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97368637; PubMed=9225251;  
 RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
 RT "The structures of the frenatin peptides from the skin secretion of  
 RT the giant tree frog Litoria infrafrenata.";  
 RL J. Pept. Sci. 2:117-124(1996).  
 CC -I- FUNCTION: Wide spectrum antimicrobial peptide.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
 CC glands.  
 KW Amphibian defense peptide; Antibiotic.  
 SQ SEQUENCE 20 AA; 1956 MW; 7E4ABE30EA17B20C CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 DB 4 SVL 6  
 RESULT 10  
 MAX8 BOMMX STANDARD; PRT; 20 AA.  
 ID MAX8 BOMMX STANDARD; PRT; 20 AA.  
 AC P83087;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Maximin 8.  
 OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.  
 OX NCBI\_TaxID=161274;  
 RN [1]  
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., McClean S., Orr D.F., Boursion A.J., Rao P.F., Shaw C.;  
 RT "Isolation and structural characterisation of antimicrobial peptides  
 RT from the venom of the Chinese large-webbed bell toad (Bombina  
 maxima).";  
 RL Submitted (JUN-2001) to the SWISS-PROT data bank.  
 CC -I- FUNCTION: Has antimicrobial activity.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Skin.  
 CC -I- SIMILARITY: BELONGS TO THE BOMBININ FAMILY.  
 KW Amphibian defense peptide; Antibiotic.  
 SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6BE2F949 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VLS 6  
 DB 5 VLS 7  
 RESULT 11  
 MIL17 BOVIN STANDARD; PRT; 20 AA.  
 ID MIL17 BOVIN STANDARD; PRT; 20 AA.  
 AC P35451;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE 17 kDa milk glycoprotein (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Milk;  
 RX MEDLINE=93308294; PubMed=8320368;  
 RA Soerensen E.S., Petersen T.E.;  
 RT "Purification and characterization of three proteins isolated from  
 RT the proteose peptone fraction of bovine milk.";  
 RL J. Dairy Res. 60:189-197(1993).  
 CC -I- PTM: N-GLYCOSYLATED.  
 CC -I- SIMILARITY: TO CAMEL WHEY PROTEIN.  
 KW Glycoprotein; Milk.  
 FT NON TER 1  
 FT NON TER 20  
 SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;  
 Query Match 50.0%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 POS 3
DB      5 POS 7

RESULT 12
PUFK_RHOSH
ID PUFK_RHOSH STANDARD; PRT; 20 AA.
AC Q53121; O08033;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Transcriptional regulatory protein pufk.
GN PUFK.
OS Rhodobacter sphaeroides (Rhodospseudomonas sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]_TaxID=1063;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=96349111; PubMed=8760918;
RA Gong L., Kaplan S.;
RT "Translational control of puf operon expression in Rhodobacter
RT sphaeroides 2.4.1.";
RL Microbiology 142:2057-2069(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RA McGlynn P.;
RT "R.sphaeroides genes bchC, bchX, bchY, bchZ and pufQ.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158;
RX MEDLINE=20115911; PubMed=10648776;
RA Choudhary M., Kaplan S.;
RT "DNA sequence analysis of the photosynthesis region of Rhodobacter
RT sphaeroides 2.4.1.";
RL Nucleic Acids Res. 28:862-867(2000).
CC -!- FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF PUFK.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S82643; AAB46798.1; -.
DR EMBL; AJ010302; CAB38751.1; -.
DR EMBL; AF195122; AAF24301.1; -.
DR PIR; T50757; T50757.
KW Transcription regulation.
SQ SEQUENCE 20 AA; 2262 MW; 764DBD64B9DD990C CRC64;

Query Match 50.0%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVL 5
DB      14 SVL 16

RESULT 13
RM01_YEAST
ID RM01_YEAST STANDARD; PRT; 4 AA.
AC P365T5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN MRPL1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626;
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,
RA Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal
RT subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
DR PIR; S17255; S17255.
DR SGD; L0002681; MRPL1.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SV 4
DB      1 SV 2

RESULT 14
ACPH_RABIT
ID ACPH_RABIT STANDARD; PRT; 6 AA.
AC P25154;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)
DE (APH) (Acylaminoacyl-peptidase) (Fragment).
GN APHE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX TISSUE=Muscle;
RX MEDLINE=92222120; PubMed=1807161;
RA Krishna R.G., Chin C.C.O., Wold F.;
RT "N-terminal sequence analysis of N alpha-acetylated proteins after
RT unblocking with N-acylaminoacyl-peptide hydrolase.";
RL Anal. Biochem. 199:45-50(1991).
CC -!- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
DR PIR; A49792; A49792.
DR MEROPS; S09.004; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NON_TER 6 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 VL 5  
Db 5 VL 6

## RESULT 15

UHL1\_RAT STANDARD; PRT; 7 AA.  
ID UHL1\_RAT  
AC P56576;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart;  
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
RA Jungblut P.R.;  
RL Submitted (SRP-1998) to the SWISS-PROT data bank.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 8.5, 2 ITS MW IS: 42 KDa.  
ET UNSURE 2 7  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3  
Db 1 QS 2

## RESULT 16

WWA1\_ACHFV STANDARD; PRT; 7 AA.  
ID WWA1\_ACHFV  
AC P35919;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WWamide-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "WWamide-1", -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica."  
RL FEBS Lett. 323:104-108(1993).  
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS  
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.  
DR PIR; S33245; S33245.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
Db 5 SV 6

## RESULT 17

WWA2\_ACHFV STANDARD; PRT; 7 AA.  
ID WWA2\_ACHFV  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WWamide-2.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "WWamide-1", -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica."  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33246; S33246.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
Db 5 SV 6

## RESULT 18

WWA3\_ACHFV STANDARD; PRT; 7 AA.  
ID WWA3\_ACHFV  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE WWamide-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "WWamide-1", -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica."  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33244; S33244.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
Db 5 SV 6

## RESULT 19

CAD1\_ENTFA STANDARD; PRT; 8 AA.  
ID CAD1\_ENTFA  
AC P13268;

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CAD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that  
 induces plasmid transfer in Streptococcus faecalis.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PAD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 VL 5  
 Db 5 VL 6  
 RESULT 20  
 COW2\_CONPU STANDARD; PRT; 8 AA.  
 AC P58785;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=41690;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN=Clipperton Island; TISSUE=Venom;  
 RX MEDLINE=99388839; PubMed=10461743;  
 RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 RA Oliveira B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 dynamics in the contryphan family.";  
 RL J. Pept. Res. 54:93-99(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Hydroxylation; D-amino acid.  
 FT DISULFID 2 8  
 FT MOD\_RES 4 4 D-LEUCINE.  
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 VL 5  
 Db 3 VL 4  
 RESULT 21  
 CPD1\_ENTFA STANDARD; PRT; 8 AA.  
 ID\_CPD1\_ENTFA  
 AC P13269;

DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CPD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85040388; PubMed=6436978;  
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B.;  
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";  
 RL Science 226:849-850(1984).  
 CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC BACTERIOICIN PLASMID PPD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 LS 6  
 Db 6 LS 7  
 RESULT 22  
 LCK6\_LEUMA STANDARD; PRT; 8 AA.  
 AC P19988;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucokinin VI (I-VI).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RX MEDLINE=87052651; PubMed=2877794;  
 RA Holman G.M., Cook B.J., Nachman R.J.;  
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:  
 myotropic peptides of Leucophaea maderae.";  
 RL Comp. Biochem. Physiol. 88C:27-30(1987).  
 CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
 CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
 CC -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND  
 CC HELIOTHIS ZEA ADIPOKINETIC HORMONE.  
 DR PIR; JS0316; JS0316.  
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 QS 3  
 Db 1 QS 2  
 RESULT 23  
 NPB\_BOVIN STANDARD; PRT; 8 AA.  
 ID\_NPB\_BOVIN  
 AC P15507;  
 DT 01-APR-1990 (Rel. 14, Created)

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DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=86067985; PubMed=3865193;
RX Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine."
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -|- FUNCTION: MODULATES THE ACTION OF MORPHINE.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
DB 5 PQ 6

RESULT 24
UH09 RAT
ID UH09 RAT STANDARD; PRT; 8 AA.
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QS 3
DB 5 QS 6

RESULT 25
AL10 CARMA
ID AL10 CARMA STANDARD; PRT; 9 AA.
AC P81613;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Carcinostatatin 10.
OS Carcinus maenas (Common shore crab) (Green crab).

DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -|- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -|- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 963 MW; 372D79DCB4776C7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2
DB 2 PQ 3

RESULT 26
BS43 SERPL
ID BS43 SERPL STANDARD; PRT; 9 AA.
AC P83375;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS Serratia plymuthica.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22933561; PubMed=12406768;
RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
RA Van Beeumen J., Thonart P.;
RT "Characterization of serracin P, a phage-tail-like bacteriocin, and
RT its activity against Erwinia amylovora the fire blight pathogen."
RL Appl. Environ. Microbiol. 68:5704-5710(2002).
CC -|- FUNCTION: Major component of a prophage tail sheath (Probable).
CC -|- FUNCTION: Antibacterial activity against Gram-negative bacterium
CC E. amylovora.
DR InterPro; IPR006498; Tail tube.
DR Pfam; PF04985; Phage tube; 1.
KW Antibiotic; Bacteriocin.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871E1FB CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5
DB 8 VL 9

RESULT 27
FAR1 CALVO
ID FAR1 CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RV SEQUENCE.
RC TISSUE=Thoracic ganglion;
RA MEDLINE=9219611; PubMed=1549595;
RX Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db 2 PQ 3

RESULT 28
FIBB_EYPA
ID_FIBB_EYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocyte patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RV SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RA "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen.C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9

SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VL 5
Db 4 VL 5

RESULT 29
HUTU_KLEAE
ID_HUTU_KLEAE STANDARD; PRT; 9 AA.
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (Fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RV SEQUENCE FROM N.A.
RX MEDLINE=88198018; PubMed=2834335;
RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
RA "Bidirectional promoter in the hut(P) region of the histidine
RT utilization (hut) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
RN [2]
RV SEQUENCE FROM N.A.
RX MEDLINE=90368611; PubMed=2203754;
RA Schwacha A., Bender R.A.;
RA "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5481(1990).
CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
CC yl)propanoate = urocanate + H(2)O. (By similarity).
CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -!- PATHWAY: Histidine degradation; second step.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; M19665; AAA25078.1; -.
DR EMBL; M34604; AAA25076.1; -.
DR HAMAP; MF 00577; -.
DR InterPro; IPR000193; Urocanase.
DR PROSITE; PS01233; UROCANASE; PARTIAL.
KW Histidine metabolism; Lyase; NAD.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QS 3
Db 3 QS 4

RESULT 30

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OXYT BUFRE STANDARD; PRT; 9 AA.  
 ID OXYT BUFRE STANDARD; PRT; 9 AA.  
 AC P4295;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Seritocin ([Ser5,Ile8]-oxytocin).  
 OS Bufo regularis (leopard toad).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;  
 OC Bufo.  
 NCBI\_TaxID=8390;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pituitary neurointermediate lobe;  
 RX MEDLINE=96059313; PubMed=7591488;  
 RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;  
 RT "A new neurohypophyseal peptide, seritocin ([Ser5,Ile8]-oxytocin),  
 RT identified in a dryness-resistant African toad, Bufo regularis.";  
 RL Int. J. Pept. Protein Res. 45:482-487(1995).  
 CC -!- FUNCTION: Devoid of oxytocic activity.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;  
  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QS 3  
 Db 4 QS 5  
  
 RESULT 31  
 OXYT RAJCL STANDARD; PRT; 9 AA.  
 ID OXYT RAJCL STANDARD; PRT; 9 AA.  
 AC P4295A;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Glutitocin.  
 OS Raja clavata (Thornback ray).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Squalia; Hymnosquales; Pristiogaster; Batoidae;  
 OC Rajiformes; Rajidae; Raja.  
 NCBI\_TaxID=7781;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=66123415; PubMed=5880565;  
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
 RT "Phylogeny of neurohypophyseal peptides: isolation of a new hormone,  
 RT glutitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,  
 RT the ray (Raja clavata)." ;  
 RL Biochim. Biophys. Acta 107:393-396(1965).  
 CC -!- FUNCTION: ANTIDIURETIC HORMONE.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB45B04B CRC64;  
  
 Query Match 33.3%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QS 3  
 Db 4 QS 5  
  
 RESULT 32  
 BPP2 BOTIN STANDARD; PRT; 10 AA.  
 ID BPP2 BOTIN STANDARD; PRT; 10 AA.  
 AC P30422;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; B37196; B37196  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1213 MW; 30C3546C761F773 CRC64;  
  
 Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQ 2  
 Db 6 PQ 7  
  
 RESULT 33  
 BPP2 BOTJA STANDARD; PRT; 10 AA.  
 ID BPP2 BOTJA STANDARD; PRT; 10 AA.  
 AC P01022;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme  
 DE inhibitor V-6-II).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=72118526; PubMed=4334402;  
 RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,  
 RA Kocoy O.;  
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops  
 RT jararaca. Isolation, elucidation of structure, and synthesis.";  
 RL Biochemistry 10:4033-4039(1971).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.

CC It acts as an indirect hypotensive agent.  
 DR PIR: A01255; XAVI6B.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1232 MW; 30C53546C741773 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQ 2  
 ||  
 Db 6 PQ 7

RESULT 34  
 ESL\_LACCA STANDARD; PRT; 10 AA.  
 AC P81758;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DE Putative esterase/lipase (EC 3.1.1.-) (Fragment).  
 OS Lactobacillus casei.  
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
 OC Lactobacillus.  
 OX NCBI\_TaxID=1582;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=IFPL731;  
 RA Lopez de Felipe F.;  
 RL Submitted (MAR-1999) to the SWISS-PROT data bank.  
 KW Hydrolase; Serine esterase.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1070 MW; 1C6132D732CAB1A0 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
 ||  
 Db 6 VL 7

RESULT 35  
 FAR6\_PANRE STANDARD; PRT; 10 AA.  
 AC P82660;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of FMRFamide-related  
 RT peptides (Farpe) from free-living nematode, Panagrellus redivivus."  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQ 2  
 ||  
 Db 4 PQ 5

RESULT 36  
 GONI\_CLUPEA STANDARD; PRT; 10 AA.  
 AC P81749;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I) (LH-RH)  
 DE (Luliberin I).  
 GN GNRH1.  
 OS Clupea pallasii (Pacific herring).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;  
 OC Clupea.  
 OX NCBI\_TaxID=30724;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Brain, and Pituitary;  
 RX MEDLINE=20114351; PubMed=10650929;  
 RA Carlsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,  
 RA Chang J.P., Rivier J.E., Sherwood N.M.;  
 RT "Primary structure and function of three gonadotropin-releasing  
 RT hormones, including a novel form, from an ancient teleost, herring."  
 RL Endocrinology 141:505-512(2000).  
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the GNRH family.  
 DR InterPro; IPR002012; GNRH.  
 DR Pfam; PF00446; GNRH; 1.  
 DR PROSITE; PS00473; GNRH; 1.  
 KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1105 MW; 284B20B72871F5A3 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 ||  
 Db 7 LS 8

RESULT 37  
 GS09\_BACSU STANDARD; PRT; 10 AA.  
 AC P80243;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE General stress protein 9 (GSP9) (Fragment).  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=168 / IS58;  
 RX MEDLINE=94282319; PubMed=8012595;  
 RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,  
 RA Schmid R., Mach H., Hecker M.;  
 RT "Analysis of the induction of general stress proteins of Bacillus  
 RT subtilis."  
 RL Microbiology 140:741-752(1994).  
 CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE  
 CC LIMITATION AND OXYGEN LIMITATION.





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CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA}(N)
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/annouce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D10371; BAA01208.1; -.
CC Transferase; RNA-directed RNA polymerase.
CC NON_TER 10 10
CC SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;
CC
CC Query Match 33.3%; Score 2; DB 1; Length 10;
CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 3 SV 4
CC Db 3 SV 4
CC
CC RESULT 41
CC TKL2 LOCMI
CC ID TKL2 LOCMI STANDARD; PRT; 10 AA.
CC AC P16224;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Locustatachykinin II (TK-II).
CC OS Locusta migratoria (Migratory locust).
CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
CC OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
CC OC Acridoidea; Acrididae; Oedipodinae; Locusta.
CC OX NCBI_TaxID=7004;
CC [1]
CC RN SEQUENCE.
CC RP TISSUE=Brain;
CC RX MEDLINE=90184489; PubMed=2311766;
CC RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
CC RT "Locustatachykinin I and II, two novel insect neuropeptides with
CC RT homology to peptides of the vertebrate tachykinin family.";
CC RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
CC KW Tachykinin; Neuropeptide; Amidation.
CC FT MOD_RES 10 10
CC SEQUENCE 10 AA; 1066 MW; 5D52CD6B59C865B7 CRC64;
CC
CC Query Match 33.3%; Score 2; DB 1; Length 10;
CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 5 LS 6
CC Db 3 LS 4
CC
CC RESULT 42
CC TKL3 LOCMI
CC ID TKL3 LOCMI STANDARD; PRT; 10 AA.
CC AC P30249;
CC DT 01-APR-1993 (Rel. 25, Created)
CC DT 01-APR-1993 (Rel. 25, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Locustatachykinin III (TK-III).
CC OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
OX [1]
RN SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=91219696; PubMed=2132575;
RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,
RA de Loof A.;
RT "Locustatachykinin III and IV: two additional insect neuropeptides
RT with homology to peptides of the vertebrate tachykinin family.";
RL Regul. Pept. 31:199-212(1990).
CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE
CC OVIDUCT AND FOREGUT.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
CC PIR; A60073; ECLQ3M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
FT SEQUENCE 10 AA; 1065 MW; C452CD6B59C87DC6 CRC64;
CC
CC Query Match 33.3%; Score 2; DB 1; Length 10;
CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 PQ 2
CC Db 2 PQ 3
CC
CC RESULT 43
CC TKUL UREUN
CC ID TKUL UREUN STANDARD; PRT; 10 AA.
CC AC P40751;
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)
CC DE Urechistachykinin I.
CC OS Urechis unicinctus.
CC OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
CC OX NCBI_TaxID=6432;
CC [1]
CC RN SEQUENCE, AND SYNTHESIS.
CC RP TISSUE=ventral nerve cord;
CC RX MEDLINE=93236558; PubMed=8476410;
CC RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneoka Y.;
CC RT "Two novel tachykinin-related neuropeptides in the echiuroid worm,
CC RT Urechis unicinctus.";
CC RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -!- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
CC KW Tachykinin; Neuropeptide; Amidation.
CC FT MOD_RES 10 10
CC SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;
CC
CC Query Match 33.3%; Score 2; DB 1; Length 10;
CC Best Local Similarity 100.0%; Pred. No. 7.5e+03;
CC Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 QS 3
CC Db 3 QS 4
CC
CC RESULT 44
CC UPA2 HUMAN
CC ID UPA2 HUMAN STANDARD; PRT; 10 AA.
CC AC P30088;
CC DT 01-APR-1993 (Rel. 25, Created)
CC DT 01-APR-1993 (Rel. 25, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 10) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.4, ITS MW IS: 49 KDa.  
DR SWISS-2DPAGE; P30088; HUMAN.  
FT NON TER 1  
FT UNSURE 6  
FT NON TER 10  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1079 MW; 51AC54AAB77775B7 CRC64;  
Query Match 33.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 LS 6  
Db 3 LS 4

RESULT 45  
UPAS\_HUMAN  
ID UPAS\_HUMAN STANDARD; PRT; 10 AA.  
AC P30091;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 4.85, ITS MW IS: 40 KDa.  
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF  
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT  
CC PROTEIN.  
DR SWISS-2DPAGE; P30091; HUMAN.  
FT NON TER 1  
FT VARIANT 9  
FT VARIANT 9  
FT NON TER 10  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;  
Query Match 33.3%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.5e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 VL 5  
Db 6 VL 7

RESULT 46  
BPP3\_BOTIN  
ID BPP3\_BOTIN STANDARD; PRT; 11 AA.  
AC P30423;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; C37196; C37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
FT MOD RES 1  
SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;  
Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 PQ 2  
Db 7 PQ 8

RESULT 47  
BPP4\_BOTIN  
ID BPP4\_BOTIN STANDARD; PRT; 11 AA.  
AC P30424;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting  
DE enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8723;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
RT peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
CC angiotensin-converting enzyme and enhances the action of  
CC bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; D37196; D37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1  
FT MOD RES 1  
SQ SEQUENCE 11 AA; 1143 MW; 20BBF13C7741777 CRC64;  
Query Match 33.3%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

Qy 1 PQ 2  
Db 7 PQ 8

RESULT 48  
CEP1\_ACHFV STANDARD; PRT; 11 AA.  
AC P22790;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-DEC-1992 (Rel. 24, Last annotation update)  
DE Cardio-excitatory peptide-1 (ACEP-1).  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Ferussac; TISSUE=Heart atrium;  
RX MEDLINE=90211261; PubMed=2322251;  
RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;  
RT "A novel cardio-excitatory peptide isolated from the atria of the  
RT African giant snail, Achatina fulica";  
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).  
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO  
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL  
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE  
CC MOVEMENT OF ACHATINA.  
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.  
DR PIR; A34662; A34662.  
KW Hormone; Amidation.  
FT MOD RES 11  
SQ SEQUENCE 11 AA; 1305 MW; 826D5B9C7741365 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

Qy 2 QS 3  
Db 3 QS 4

RESULT 49  
FAR9\_CALVO STANDARD; PRT; 11 AA.  
AC F41864;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE CalliPMPamide 9.  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=thoracic ganglion;  
RX MEDLINE=92196111; PubMed=1549595;  
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
RA Rehfeld J.F., Thorpe A.;  
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
RT neuropeptides (designated calliPMPamides) from the blowfly  
RT Calliphora vomitoria";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).  
CC -1- SIMILARITY: BELONGS TO THE FARP (FARFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; I41978; I41978.

KW Neuropeptide; Amidation.  
FT MOD RES 11  
SQ SEQUENCE 11 AA; 1359 MW; 8160CB46CAA44321 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

Qy 3 SV 4  
Db 1 SV 2

RESULT 50  
PQQC\_PSEFL STANDARD; PRT; 11 AA.  
AC P55173;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DB Coenzyme PQQ synthesis protein C (Fragment).  
GN PQQC.  
OS Pseudomonas fluorescens.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=294;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHAO;  
RX MEDLINE=96064397; PubMed=8526497;  
RA Schnider U., Keel C., Defago G., Haas D.;  
RT "TnS-directed cloning of pqq genes from Pseudomonas fluorescens CHAO:  
RT mutational inactivation of the genes results in overproduction of the  
RT antibiotic pyoluteorin";  
RL Appl. Environ. Microbiol. 61:3856-3864(1995).  
CC -1- FUNCTION: REQUIRED FOR COENZYME PYROLO-QUINOLINE-QUINONE (PQQ)  
CC BIOSYNTHESIS.  
CC -1- SIMILARITY: TO OTHER BACTERIAL PQQC.  
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DR EMBL; X87299; CAA60734.1; -.  
DR PIR; S58244; S58244.  
KW PQQ.  
FT NON TER 11  
SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0;

Qy 5 LS 6  
Db 6 LS 7

RESULT 51  
RANC\_RANPI STANDARD; PRT; 11 AA.  
AC P08951;  
DT 01-NOV-1988 (Rel. 09, Created)  
DT 01-NOV-1988 (Rel. 09, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Ranatensin-C.  
OS Rana pipiens (Northern leopard frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.

OX NCBI\_TaxID=8404;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=84131099; PubMed=6141890;  
 RA Nakajima T.;  
 RL Unpublished results, cited by:  
 RL Erspamer V., Erspamer G.F., Mazzanti G., Eudean R.;  
 RL Comp. Biochem. Physiol. 77C:99-108(1984).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY;  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PFO2044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation.  
 FT MOD\_RES 11 11  
 FT SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;  
 SQ  
 Query Match 33.3%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQ 2  
 DB 3 PQ 4  
 RESULT 52  
 T2P1\_PROVU  
 ID T2P1\_PROVU STANDARD; PRT; 11 AA.  
 AC P31031;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)  
 DE (R.PvuI) (Fragment).  
 GN PVUIR.  
 OS Proteus vulgaris.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Proteus.  
 OX NCBI\_TaxID=585;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 13315;  
 RX MEDLINE=93087186; PubMed=1454536;  
 RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;  
 RT "Cloning and characterization of genes for the PvuI restriction and  
 RT modification system";  
 RT Nucleic Acids Res. 20:5743-5747(1992).  
 CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND  
 CC CLEAVES AFTER T-4.  
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give  
 CC specific double-stranded fragments with terminal 5'-phosphates.  
 CC  
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 CC  
 CC -----  
 CC EMBL; L04163; AAA25660.1; -.  
 DR PIR; S35490; S35490.  
 DR REBASE; 1541; PvuI.  
 KW Restriction system; Hydrolase; Nuclease; Endonuclease.  
 FT NON\_TER 1 1  
 FT SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;  
 SQ  
 Query Match 33.3%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SV 4  
 DB 2 SV 3  
 RESULT 53  
 TKNA\_CHICK  
 ID TKNA\_CHICK STANDARD; PRT; 11 AA.  
 AC P19850;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Intestine;  
 RX MEDLINE=88204263; PubMed=2452461;  
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;  
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";  
 RL Regul. Pept. 20:171-180(1988).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
 CC MUSCLES.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
 DR PIR; JN0023; JN0023.  
 DR InterPro; IPR002040; Tachykinin.  
 DR Pfam; PFO2202; Tachykinin; 1.  
 DR PROSITE; PS00267; TACHYKININ; 1.  
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
 FT MOD\_RES 11 11  
 FT SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;  
 SQ  
 Query Match 33.3%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQ 2  
 DB 4 PQ 5  
 RESULT 54  
 TKNA\_GADMO  
 ID TKNA\_GADMO STANDARD; PRT; 11 AA.  
 AC P28498;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Substance P.  
 OS Gadus morhua (Atlantic cod).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.  
 OX NCBI\_TaxID=8049;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Brain;  
 RX MEDLINE=92298992; PubMed=1376687;  
 RA Jensen J., Conlon J.M.;  
 RT "Substance-P-related and neurokinin-A-related peptides from the brain  
 RT of the cod and trout.";  
 RL Eur. J. Biochem. 206:659-664(1992).  
 CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND

CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
CC MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; S23306; S23306.  
DR InterPro; IPR003580; Protachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 PQ 2  
4 PQ 5  
Db  
  
RESULT 55  
TKNA\_HORSE  
ID TKNA\_HORSE STANDARD; PRT; 11 AA.  
AC P01290;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Substance P.  
GN TAC1 OR NK1A OR TAC2 OR NKA.  
OS Equus caballus (Horse); and  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796, 10141;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Horse;  
RA Studer R.O., Trzeciak A., Lergier W.;  
RT "Isolation and amino-acid sequence of substance P from horse  
intestine."  
RL Helv. Chim. Acta 56:860-866(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C. porcellus;  
RX MEDLINE=90044685; PubMed=2478925;  
RA Murphy R.;  
RT "Primary amino acid sequence of guinea-pig substance P.";  
RL Neuropeptides 14:105-110(1989).  
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,  
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND  
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH  
MUSCLES.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.  
DR PIR; A01558; SPHO.  
DR PIR; A60654; A60654.  
DR InterPro; IPR003580; Protachykinin.  
DR InterPro; IPR002040; Tachykinin.  
DR Pfam; PF02202; Tachykinin; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00267; TACHYKININ; 1.  
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.  
FT MOD RES 11 11  
SQ SEQUENCE 11 AA; 1349 MW; 3E75FE3C9D6C6C7 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 8.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 PQ 2

Db 4 PQ 5  
  
RESULT 56  
FIF1\_SARBU  
ID FIF1\_SARBU STANDARD; PRT; 12 AA.  
AC P83349;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neb-FIRFamide 1.  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AMIDATION, AND FUNCTION.  
RC TISSUE=CNS;  
RX MEDLINE=22342733; PubMed=12438685;  
RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,  
RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L;  
RT "Identification in Drosophila melanogaster of the invertebrate G  
protein-coupled FMRFamide receptor.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).  
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular  
junctions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1389 MW; 2DC45519C14AB5A7 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 PQ 2  
3 PQ 4  
Db  
  
RESULT 57  
FRE1\_LITIN  
ID FRE1\_LITIN STANDARD; PRT; 12 AA.  
AC P82021;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Frenatin 1.  
OS Litoria infrafrænata (Giant tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=61195;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97368637; PubMed=9225251;  
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "The structures of the frenatin peptides from the skin secretion of  
the giant tree frog Litoria infrafrænata.";  
RL J. Pept. Sci. 11:117-124(1996).  
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
glands.  
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB  
Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD RES 12 12  
SQ SEQUENCE 12 AA; 1141 MW; C622550BC365B72D CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 DB 6 LS 7

RESULT 58  
 HCY1 CARMA  
 ID HCY1 CARMA STANDARD; PRT; 12 AA.  
 AC P83176;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hemocyanin subunit 1 (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=90151075; PubMed=2620501;  
 RA Neuteboom B., Sierdsema S.J., Beintema J.J.;  
 RT "The relationship of crustacean terminal sequences and immunological  
 RT characterization of hemocyanin subunits."  
 RL Comp. Biochem. Physiol. 94B:587-592(1989).  
 CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers  
 CC occurring freely dissolved in the hemolymph of many mollusks and  
 CC arthropods.  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: Hemolymph.  
 CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN  
 CC SUBFAMILY.  
 CC  
 DR PIR; C60529; C60529.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0016970; F:Hemocyanin; IDA.  
 DR GO; GO:0015671; P:oxygen transport; TAS.  
 KW Transport; Oxygen transport; Copper; Hemolymph.  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1237 MW; 89936FE6E2B5A2D5 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SV 4  
 DB 5 SV 6

RESULT 59  
 PPK4 PERFU  
 ID PPK4 PERFU STANDARD; PRT; 12 AA.  
 AC P82630;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-4 (PPK-PK-4) (YXPRL-amide).  
 OS Periplaneta fuliginosa (Smokybrown cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 OC Blattidae; Periplaneta.  
 OX NCBI\_TaxID=36977;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;

RT "Tagma-specific distribution of EXPRLamides in the nervous system of  
 RT the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -!- MASS SPECTROMETRY: MW=1437.9; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR INTERPRO; IPR001484; Pyrokinin.  
 DR PROSITE; PS00539; PYROKININ; FALSE NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD\_RES 12  
 FT MOD\_RES 12  
 FT MOD\_RES 12  
 SQ SEQUENCE 12 AA; 1439 MW; F9B53049FF42CRA1 CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LS 6  
 DB 3 LS 4

RESULT 60  
 TM2A METWA  
 ID TM2A METWA STANDARD; PRT; 12 AA.  
 AC P80652;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
 DE (EC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M  
 DE methyltransferase 28 kDa subunit) (Fragment).  
 DE Methanosarcina mazei (Methanosarcina frisia).  
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.  
 OX NCBI\_TaxID=2209;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
 RX MEDLINE=96370840; PubMed=8774736;  
 RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
 RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
 RT coenzyme M methyltransferase from Methanosarcina mazei Go1  
 RT reconstituted in ether lipid liposomes.";  
 RL Eur. J. Biochem. 239:857-864(1996).  
 CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
 CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
 CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
 CC TETRAHYDROMETHANOPTERIN.  
 CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
 CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
 CC (methylthio)ethanesulfonate.  
 CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
 FT NON\_TER 12  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1321 MW; 6DE4A5766232D76B CRC64;

Query Match 33.3%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VL 5  
 DB 7 VL 8

RESULT 61  
 V25K WSSV  
 ID V25K WSSV STANDARD; PRT; 12 AA.  
 AC P82004;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 25 kDa structural polyprotein (Fragment).  
 OS White spot syndrome virus (WSSV).  
 OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae.  
 OX NCBI\_TaxID=92652;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=South Carolina;  
 RX MEDLINE=20214217; PubMed=10752552;  
 RA Wang Q., Poulos B.T., Lightner D.V.;  
 RT "Protein analysis of geographic isolates of shrimp white spot syndrome virus."  
 RL Arch. Virol. 145:263-274(2000).  
 RC 1- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1283 MW; C5409AD9ECB731A9 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 8.8e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LS 6  
 Db 3 LS 4  
 RESULT 62  
 BOWL\_PSEGU STANDARD; PRT; 13 AA.  
 AC P42931;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Bombesin-like peptide L (PG-L).  
 OS Pseudophryne guentheri (Guenther's toadlet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;  
 OC Myobatrachinae; Pseudophryne.  
 OX NCBI\_TaxID=30349;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=90287814; PubMed=2356157;  
 RA Simmaco M., Severini C., de Biase D., Barra D., Boses F.,  
 RA Roberts J.D., Melchiorri P., Erpamer V.;  
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of  
 RT the Australian frog Pseudophryne guentheri."  
 RL Peptides 11:299-304(1990).  
 CC 1- SUBCELLULAR LOCATION: Secreted.  
 CC 1- TISSUE SPECIFICITY: Skin.  
 CC 1- SIMILARITY: BELONGS TO THE BOMBESIN/NEUROMEDIN B/RANATENSIN  
 CC FAMILY.  
 DR PIR; A60409;  
 DR InterPro; IPR000874; Bombesin.  
 DR Pfam; PF02044; Bombesin; 1.  
 DR PROSITE; PS00257; BOMBESIN; 1.  
 KW Amphibian defense peptide; Bombesin family; Amidation;  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1372 MW; D6DE0D24BD98C366 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 PQ 2  
 Db 5 PQ 6

RESULT 63  
 CHEP\_PARID

ID CHEP\_PARID STANDARD; PRT; 13 AA.  
 AC P42718;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Chemotactic peptide.  
 OS Parapolybia indica.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Polistinae; Parapolybia.  
 OX NCBI\_TaxID=31921;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Toki T., Yasuhara T., Nakajima T.;  
 RT "Isolation and sequential analysis of peptides on the venom sac of  
 RT Parapolybia indica."  
 RL Eisei Dobutsu 39:105-111(1988).  
 KW Chemotaxis; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1298 MW; 5C950CE8E39D5873 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LS 6  
 Db 12 LS 13  
 RESULT 64  
 CRBL\_VESMA STANDARD; PRT; 13 AA.  
 ID CRBL\_VESMA  
 AC P17232;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Vespid chemotactic peptide M (VESCP-M).  
 OS Vespa mandarinia (Hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OX NCBI\_TaxID=7446;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Nakajima T., Fukuda K., Tsukamoto Y., Mori M., Kitada C.,  
 RA Fujino M.;  
 RL (In) Muneata E. (eds.);  
 RL Peptide chemistry 1983, pp.185-190, Protein Research Foundation,  
 RL Osaka (1984).  
 CC 1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis  
 CC of neutrophils.  
 KW Mast cell degranulation; Chemotaxis; Amidation.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1384 MW; 2650402B9DF92338 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LS 6  
 Db 9 LS 10  
 RESULT 65  
 FIBB\_RABIT STANDARD; PRT; 13 AA.  
 ID FIBB\_RABIT  
 AC P14478;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)



28-FEB-2003 (Rel. 41, Last annotation update)  
Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.  
RA Blomback B., Blomback M., Grondahl N.J.;  
RT "Studies on fibrinopeptides from mammals."  
RL Acta Chem. Scand. 19:1789-1791(1965).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
CC INTERPRO: IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma; Sulfation.  
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.  
FT MOD RES 4 4 SULFATION.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
DB 8 VL 9  
  
RESULT 66  
HPAL\_RANGES STANDARD; PRT; 13 AA.  
AC P32415;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Hemolytic protein A1 (Fragment).  
OS Rana esculenta (Edible frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OX NCBI\_TaxID=8401;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=90198965; PubMed=2317508;  
RA Simmaco M., de Biase D., Severini C., Aita M., Brspamer G.F.,  
RA Barra D., Bossa F.;  
RT "Purification and characterization of bioactive peptides from skin  
RT extracts of Rana esculenta."  
RL Biochim. Biophys. Acta 1033:318-323(1990).  
CC -!- FUNCTION: Shows hemolytic activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
DR PIR; S09018.  
KW Amphibian defense peptide; Amidation; Hemolysis.  
FT MOD RES 13 13 AMIDATION.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LS 6

Db 9 LS 10  
  
RESULT 67  
IDHC\_FIG STANDARD; PRT; 13 AA.  
ID IDHC\_FIG  
AC P20304;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1.1.42)  
DE (Oxalosuccinate decarboxylase) (IDH) (NADP+-specific IDH) (IDP)  
DE (Fragment).  
GN IDH1.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87308293; PubMed=2887570;  
RA Bailey J.M., Colman R.F.;  
RT "Isolation of the glutamyl peptide labeled by the nucleotide analogue  
RT 2-(4-bromo-2,3-dioxobutylthio)-1,N(6)-ethenoadenosine  
RT 2',5'-biphosphate in the active site of NADP+-specific isocitrate  
RT dehydrogenase."  
RL J. Biol. Chem. 262:12620-12626(1987).  
RN [2]  
RP SEQUENCE.  
RX MEDLINE=87308292; PubMed=3624273;  
RA Ehrlich R.S., Colman R.F.;  
RT "Characterization of an active site peptide modified by the substrate  
RT analogue 3-bromo-2-ketoglutarate on a single chain of dimeric NADP+-  
RT dependent isocitrate dehydrogenase."  
RL J. Biol. Chem. 262:12614-12619(1987).  
CC -!- CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)  
CC + NADPH.  
CC -!- SUBUNIT: Homodimer.  
DR InterPro; IPR001804; Isohd.  
DR PROSITE; PS00470; IDH IMDH; PARTIAL.  
KW Oxidoreductase; NADP; Tricarboxylic acid cycle.  
FT NON TER 1 1  
FT ACT SITE 5 5 POTENTIAL.  
FT NON TER 13 13  
SQ SEQUENCE 13 AA; 1353 MW; 1B640F0E9F7C71E0 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LS 6  
DB 9 LS 10  
  
RESULT 68  
LMA1\_LOCFMI STANDARD; PRT; 13 AA.  
ID LMA1\_LOCFMI  
AC P38496;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Lom-AG-mycotropin I (Accessory gland myotropin I).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Male accessory gland;  
RX MEDLINE=91271087; PubMed=2052501;

RA Paenen L., Tips A., Schoofs L., Proost P., van Damme J., de Loof A.;  
 RT "Low-AG-myotropin: a novel myotropic peptide from the male accessory  
 glands of *Locusta migratoria*.";  
 RL Peptides 12:7-10(1991).  
 CC -!- FUNCTION: THE EXACT PHYSIOLOGICAL FUNCTION IS STILL UNKNOWN. THIS  
 MYOTROPIC PEPTIDE IS ACTIVE ON THE OVIDUCT AND, TO A LESSER  
 CC EXTENT, ON THE HINDGUT. TRANSFERRED FROM THE MALE TO THE FEMALE  
 CC DURING COPULATION.  
 CC -!- TISSUE SPECIFICITY: MALE ACCESSORY GLANDS.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 13 13  
 SQ SEQUENCE 13 AA; 1368 MW; DE1ACAF482EB72D CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 LS 6  
 DB 7 LS 8  
 RESULT 69  
 NEUT\_RANTE STANDARD; PRT; 13 AA.  
 ID P41536;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Neurotensin (NT).  
 OS Rana temporaria (European common frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92245104; PubMed=1574601;  
 RA Shaw C., McKay D.M., Halton D.W., Thim L., Buchanan K.D.;  
 RT "Isolation and primary structure of an amphibian neurotensin.";  
 RL Regul. Pept. 38:23-31(1992).  
 CC -!- FUNCTION: Smooth muscle-contracting peptide.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: IDENTIFIED IN BRAIN, INTESTINE, AND RECTUM,  
 CC BUT NOT IN STOMACH OR SKIN.  
 CC -!- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.  
 DR PIR; A61067; A61067.  
 KW Vasoactive; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 13 AA; 1569 MW; 56A53D69EF410DD3 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QS 3  
 DB 1 QS 2  
 RESULT 70  
 PEDI\_HYDAT STANDARD; PRT; 13 AA.  
 ID P80578;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Pedin.  
 OS Hydra attenuata (Hydra) (*Hydra vulgaris*).  
 CC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;  
 CC Hydridae; Hydra.  
 OX NCBI\_TaxID=6087;  
 RN [1]  
 RP SEQUENCE.

EX MEDLINE=96232307; PubMed=8674432;  
 RA Hofmeister S.A.H.;  
 RT "Isolation and characterization of two new morphogenetically active  
 RL peptides from *Hydra vulgaris*.";  
 RL Development 122:1941-1948(1996).  
 CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT  
 CC DEVELOPMENT.  
 KW Morphogen.  
 SQ SEQUENCE 13 AA; 1512 MW; 6F526683F37632CB CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VL 5  
 DB 7 VL 8  
 RESULT 71  
 SAZA\_ONCMY STANDARD; PRT; 13 AA.  
 ID P82238;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Salmocidin 2A (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Serum;  
 RA Henry M.A., Secombes C.J.;  
 RT "Purification and partial characterization of antibacterial peptides  
 from rainbow trout, *Oncorhynchus mykiss*.";  
 RL Submitted (DSC-1999) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Plasma serum.  
 KW Antibiotic.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;  
 Query Match 33.3%; Score 2; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VL 5  
 DB 4 VL 5  
 RESULT 72  
 SA2B\_ONCMY STANDARD; PRT; 13 AA.  
 ID P82239;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Salmocidin 2B (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Serum;  
 RA Henry M.A., Secombes C.J.;  
 RT "Purification and partial characterization of antibacterial peptides

RT from rainbow trout, Oncorhynchus mykiss.";  
RL Submitted (DEC-1999) to the SWISS-PROT data bank.  
CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Plasma serum.  
KW Antibiotic.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1400 MW; 5FPB792AEABE5873 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
DB 4 VL 5  
  
RESULT 73  
TENE\_RANTE STANDARD; PRT; 13 AA.  
AC P56920;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Temporin E.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
OC NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022710;  
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
RT temporaria.";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
CC bacteria.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
DB 1 VL 2

RESULT 74  
UN12 CLOPA STANDARD; PRT; 13 AA.  
AC P81331;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein CP 12 from 2D-page (Fragment).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OC NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=98291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC -!- PROTEIN IS: 5.8, ITS MW IS: 42.7 kDa.  
FT VARIANT 4 4 L -> V.  
FT VARIANT 5 5 Q -> I.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1465 MW; 70AA9E98455D405B CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
DB 3 VL 4  
  
RESULT 75  
VG16 BACSU STANDARD; PRT; 13 AA.  
ID VG16\_BACSU  
AC P80867;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vegetative protein 16 (VEG16) (Fragment).  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OC NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=168 / IS58;  
RX MEDLINE=97443988; PubMed=9298659;  
RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,  
RA Hecker M.;  
RT "First steps from a two-dimensional protein index towards a response-  
RT regulation map for Bacillus subtilis.";  
RL Electrophoresis 18:1451-1463(1997).  
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1372 MW; 20FB27BDC9ECA2D7 CRC64;  
  
Query Match 33.3%; Score 2; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.4e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SV 4  
DB 8 SV 9

Search completed: November 25, 2003, 19:28:24  
Job time : 3.19934 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 11.2674 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 POSVLS 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	66.7	15	15	Q97090 human immun
2	4	66.7	15	15	Q80362 human immun
3	4	66.7	15	15	Q97098 human immun
4	4	66.7	15	15	Q79359 human immun
5	4	66.7	15	15	Q97092 human immun
6	4	66.7	15	15	Q97094 human immun
7	4	66.7	18	15	O12692 simian-huma
8	4	66.7	20	3	Q9UR76 candida alb
9	3	50.0	8	4	Q9HCQ0 homo sapien
10	3	50.0	8	12	Q83349 murine coro
11	3	50.0	8	12	Q89498 murine hepa
12	3	50.0	8	13	P87488 oncorhynchu
13	3	50.0	9	4	Q9UCS8 homo sapien
14	3	50.0	9	6	Q8HZY2 canis famil
15	3	50.0	11	7	Q29831 homo sapien
16	3	50.0	12	4	Q9NTR7 homo sapien

17	3	50.0	12	6	Q9TQY4	Q9TQY4 bos taurus
18	3	50.0	12	6	Q9MZS4	Q9MZS4 canis famil
19	3	50.0	13	2	Q8RS9G	Q8RS9G uncultured
20	3	50.0	13	5	Q9U5J2	Q9U5J2 trypanosoma
21	3	50.0	13	12	Q9WVG5	Q9WVG5 sigma virus
22	3	50.0	14	4	P78359	P78359 homo sapien
23	3	50.0	14	11	Q9RIU3	Q9RIU3 rattus norv
24	3	50.0	15	7	Q9TNQ3	Q9TNQ3 homo sapien
25	3	50.0	15	11	Q05694	Q05694 mus musculu
26	3	50.0	15	16	Q9K8C3	Q9K8C3 bacillus ha
27	3	50.0	16	2	Q45663	Q45663 bacillus su
28	3	50.0	16	2	Q9B5C1	Q9B5C1 nitrosomona
29	3	50.0	16	2	P82597	P82597 bacillus sp
30	3	50.0	16	7	O77922	O77922 oreochromis
31	3	50.0	16	8	Q9T2Q6	Q9T2Q6 solanum tub
32	3	50.0	16	12	Q88250	Q88250 sendai viru
33	3	50.0	16	12	Q88249	Q88249 sendai viru
34	3	50.0	16	12	Q86966	Q86966 murine hepa
35	3	50.0	16	12	Q99154	Q99154 sendai viru
36	3	50.0	17	2	Q9R560	Q9R560 bacillus su
37	3	50.0	17	2	Q93UW3	Q93UW3 agrobacteri
38	3	50.0	17	5	Q9TWC6	Q9TWC6 dirofilaria
39	3	50.0	17	6	Q9TRW1	Q9TRW1 oryctolagus
40	3	50.0	17	10	Q9S8Y3	Q9S8Y3 lupinus arb
41	3	50.0	17	12	Q84098	Q84098 influenza vi
42	3	50.0	18	2	Q8L2T5	Q8L2T5 neisseria m
43	3	50.0	18	4	Q9POM3	Q9POM3 homo sapien
44	3	50.0	18	4	Q9UCF4	Q9UCF4 homo sapien
45	3	50.0	18	4	Q8N303	Q8N303 homo sapien
46	3	50.0	18	6	Q97773	Q97773 cercopithe
47	3	50.0	18	6	P79214	P79214 oryctolagus
48	3	50.0	18	6	Q9TR57	Q9TR57 sus scrofa
49	3	50.0	18	8	Q8HBE6	Q8HBE6 tectona gra
50	3	50.0	18	10	Q9S8I7	Q9S8I7 oryza sativ
51	3	50.0	18	10	Q9S8I8	Q9S8I8 oryza sativ
52	3	50.0	18	11	Q9WTP8	Q9WTP8 rattus norv
53	3	50.0	19	2	Q9RLU4	Q9RLU4 lactococcus
54	3	50.0	19	2	Q9R5M3	Q9R5M3 rhodococcus
55	3	50.0	19	4	Q9NP11	Q9NP11 homo sapien
56	3	50.0	19	11	Q62637	Q62637 rattus norv
57	3	50.0	19	12	Q69345	Q69345 human herpe
58	3	50.0	19	15	Q9ORF8	Q9ORF8 human immun
59	3	50.0	19	15	Q905G8	Q905G8 human immun
60	3	50.0	20	4	Q9NZ27	Q9NZ27 homo sapien
61	3	50.0	20	4	Q9NZ28	Q9NZ28 homo sapien
62	3	50.0	20	10	Q9S7J0	Q9S7J0 ananas como
63	3	50.0	20	10	Q41475	Q41475 solanum tub
64	3	50.0	20	10	Q9S965	Q9S965 ananas como
65	3	50.0	20	10	Q9S8M1	Q9S8M1 ananas como
66	3	50.0	20	10	Q9FPF8	Q9FPF8 arabidopsis
67	3	50.0	20	11	Q9QVH2	Q9QVH2 rattus sp.
68	3	50.0	20	16	Q8CYA3	Q8CYA3 streptococ
69	3	33.3	4	11	Q08433	Q08433 rattus sp.
70	2	33.3	7	8	Q9S945	Q9S945 saccharomyc
71	2	33.3	7	10	Q9C5B3	Q9C5B3 arabidopsis
72	2	33.3	7	13	Q8UJ20	Q8UJ20 gallus gall
73	2	33.3	7	13	O42564	O42564 fugu rubrip
74	2	33.3	7	15	Q8TE81	Q8TE81 human immun
75	2	33.3	8	2	Q45615	Q45615 bacillus su
76	2	33.3	8	2	Q9X3K1	Q9X3K1 prochloroco
77	2	33.3	8	2	Q56140	Q56140 streptococ
78	2	33.3	8	2	Q56246	Q56246 thermophili
79	2	33.3	8	2	Q56429	Q56429 thermus the
80	2	33.3	8	2	Q93SP2	Q93SP2 pseudomonas
81	2	33.3	8	2	Q45889	Q45889 clostridium
82	2	33.3	8	2	Q9R4M3	Q9R4M3 enterococcu
83	2	33.3	8	3	P87225	P87225 saccharomyc
84	2	33.3	8	3	Q9URB9	Q9URB9 saccharomyc
85	2	33.3	8	4	Q9UHK1	Q9UHK1 homo sapien
86	2	33.3	8	4	Q9Y4X6	Q9Y4X6 homo sapien
87	2	33.3	8	4	Q9H4D3	Q9H4D3 homo sapien
88	2	33.3	8	4	Q8I0B8	Q8I0B8 homo sapien
89	2	33.3	8	5	O02032	O02032 lytechinus

90 2 33.3 8 8 019957 019957 gossypium h  
 91 2 33.3 8 8 092Y3 092Y3 begonia for  
 92 2 33.3 8 8 019961 019961 gossypium d  
 93 2 33.3 8 8 019958 019958 gossypium b  
 94 2 33.3 8 8 094V82 094V82 varanus yuw  
 95 2 33.3 8 8 094Y2 094Y2 asterina pe  
 96 2 33.3 8 8 019960 019960 gossypium m  
 97 2 33.3 8 8 092TMN4 092TMN4 begonia for  
 98 2 33.3 8 8 094VB2 094VB2 varanus sal  
 99 2 33.3 8 8 092Y2 092Y2 begonia tai  
 100 2 33.3 8 8 019959 019959 gossypium t

## ALIGNMENTS

RESULT 1  
 Q97090  
 ID Q97090 PRELIMINARY; PRT; 15 AA.  
 AC Q97090;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag polyprotein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LAI;  
 RX MEDLINE=98184535; PubMed=9525623;  
 RA Wei Q., Fultz P.N.;  
 RT "Extensive diversification of human immunodeficiency virus type 1  
 RT subtype B strains during dual infection of a chimpanzee that  
 RT progressed to AIDS.";  
 RL J. Virol. 72:3005-3017(1998).  
 DR EMBL; U56889; AAC59299.1; -;  
 DR InterPro; IPR000071; Retrovir\_p17.  
 DR Pfam; PF00540; Gag\_p17; 1.  
 KW AIDS; Core protein; Polyprotein.  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1577 MW; 5AC228686229C18E CRC64;  
 Query Match 66.7%; Score 4; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 6 SVLS 9

RESULT 2  
 Q80362  
 ID Q80362 PRELIMINARY; PRT; 15 AA.  
 AC Q80362;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag protein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UG266;  
 RX MEDLINE=93371703; PubMed=8363755;  
 RA Louwagie J.J., McCutchan F., Brennan T., Peeters M., Brennan T.,  
 RA Sanders-Buell E., Eddy G., van der Groen G., Franssen K.,  
 RA Gershy-Damet M., Deleys R., Burke D.;  
 RT "Phylogenetic analysis of gag genes from seventy international HIV-1  
 RT isolates provides evidence for multiple genotypes.";

RT isolates provides evidence for multiple genotypes.";  
 RL AIDS 7:769-780(1993).  
 DR EMBL; L11798; AAA45087.1; -;  
 FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1533 MW; 43123AEAF229C18E CRC64;  
 Query Match 66.7%; Score 4; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 6 SVLS 9

RESULT 3  
 Q97098  
 ID Q97098 PRELIMINARY; PRT; 15 AA.  
 AC Q97098;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag polyprotein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=LAI;  
 RX MEDLINE=98184535; PubMed=9525623;  
 RA Wei Q., Fultz P.N.;  
 RT "Extensive diversification of human immunodeficiency virus type 1  
 RT subtype B strains during dual infection of a chimpanzee that  
 RT progressed to AIDS.";  
 RL J. Virol. 72:3005-3017(1998).  
 DR EMBL; U56897; AAC59307.1; -;  
 DR InterPro; IPR000071; Retrovir\_p17.  
 DR Pfam; PF00540; Gag\_p17; 1.  
 KW AIDS; Core protein; Polyprotein.  
 FT NON\_TER 1  
 SQ SEQUENCE 15 AA; 1487 MW; 5AC22868622AA49A CRC64;  
 Query Match 66.7%; Score 4; DB 15; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 6 SVLS 9

RESULT 4  
 Q79359  
 ID Q79359 PRELIMINARY; PRT; 15 AA.  
 AC Q79359;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Gag protein (Gag polyprotein) (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K7;  
 RX MEDLINE=93371703; PubMed=8363755;  
 RA Louwagie J.J., McCutchan F., Brennan T., Peeters M., Brennan T.,  
 RA Sanders-Buell E., Eddy G., van der Groen G., Franssen K.,  
 RA Gershy-Damet M., Deleys R., Burke D.;  
 RT "Phylogenetic analysis of gag genes from seventy international HIV-1  
 RT isolates provides evidence for multiple genotypes.";

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RL AIDS 7:769-780(1993).
DR EMBL; L11772; AAA44692.2; -.
DR InterPro; IPR000071; Retrovir_p17.
DR Pfam; PF00540; Gag_p17; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1500 MW; 5AC22874122AA9A CRC64;

Query Match 66.7%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 6 SVLS 9

RESULT 5
Q97092 ID Q97092 PRELIMINARY; PRT; 15 AA.
AC Q97092;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=LAI;
RX MEDLINE=98184535; PubMed=9525623;
RA Wei Q., Fultz P.N.;
RT "Extensive diversification of human immunodeficiency virus type 1
RT subtype B strains during dual infection of a chimpanzee that
RT progressed to AIDS.";
RL J. Virol. 72:3005-3017(1998).
DR EMBL; U56891; AAC59301.1; -.
KW Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1616 MW; 5AC228686227909A CRC64;

Query Match 66.7%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 6 SVLS 9

RESULT 6
Q97094 ID Q97094 PRELIMINARY; PRT; 15 AA.
AC Q97094;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]_TaxID=11676;
RP SEQUENCE FROM N.A.
RC STRAIN=LAI;
RX MEDLINE=98184535; PubMed=9525623;
RA Wei Q., Fultz P.N.;
RT "Extensive diversification of human immunodeficiency virus type 1
RT subtype B strains during dual infection of a chimpanzee that
RT progressed to AIDS.";
RL J. Virol. 72:3005-3017(1998).

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DR EMBL; U56893; AAC59303.1; -.
DR InterPro; IPR000071; Retrovir_p17.
DR Pfam; PF00540; Gag_p17; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1604 MW; 5AC228686236D18E CRC64;

Query Match 66.7%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 6 SVLS 9

RESULT 7
O12692 ID O12692 PRELIMINARY; PRT; 18 AA.
AC O12692;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag polyprotein (Fragment).
GN GAG.
OS Simian-Human immunodeficiency virus.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=57667;
RN [1]_TaxID=57667;
RP SEQUENCE FROM N.A.
RC STRAIN=SHIVku1;
RX MEDLINE=97312452; PubMed=9168993;
RA Stephens E.B., Mukherjee S., Sahni M., Zhuge W., Raghavan R.,
RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.Q.,
RA Narayan O.;
RT "A cell-free stock of simian-human immunodeficiency virus that causes
RT AIDS in pig-tailed macaques has a limited number of amino acid
RT substitutions in both SIVmac and HIV-1 regions of the genome and has
RT offered cytotropism.";
RL Virology 231:313-321(1997).
DR EMBL; U89249; AAC57878.1; -.
DR InterPro; IPR000071; Retrovir_p17.
DR Pfam; PF00540; Gag_p17; 1.
KW AIDS; Core protein; Polyprotein.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1961 MW; E0647725D22E62EB CRC64;

Query Match 66.7%; Score 4; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 6 SVLS 9

RESULT 8
Q9UR76 ID Q9UR76 PRELIMINARY; PRT; 20 AA.
AC Q9UR76;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE N-acetylglucosaminidase A (Fragment).
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]_TaxID=5476;
RP SEQUENCE
RX MEDLINE=94356217; PubMed=8075797;
RA Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;
RT "Purification and characterization of two forms of N-

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RT acetylglucosaminidase from Candida albicans showing widely different
RL micro chain glycosylation."
RL Microbiology 140:1543-1553(1994).
SQ SEQUENCE 20 AA; 2178 MW; DA602087EDDB4D47 CRC64;

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POSV 4
Db 9 POSV 12
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RESULT 9
Q9HCQ0 PRELIMINARY; PRT; 8 AA.
AC Q9HCQ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).
GN HSPDE10A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453115; PubMed=1098054;
RA Fujishige K., Kotera J., Yuasa K., Omori K.;
RT "The human phosphodiesterase PDE10A gene. Genomic organization and
RL evolutionary relatedness with other PDEs containing GAF domains.";
DR EMBL; AB041779; BAB16368.1; -.
FT NON TER
FT SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
Db 3 POS 5
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RESULT 10
Q83349 PRELIMINARY; PRT; 8 AA.
AC Q83349;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 0.8 kDa protein.
OS Murine coronavirus MHV (strain A59).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11142;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A59;
RX MEDLINE=89299451; PubMed=2545027;
RA Pachuk C.J., Bredenbeek P.J., Zoltick P.W., Spaan W.J., Weiss S.R.;
RT "Molecular cloning of the gene encoding the putative polymerase of
RT mouse hepatitis coronavirus, strain A59.";
RL Virology 171:141-148(1989).
DR EMBL; M27198; AAA74010.1; -.
KW Hypothetical protein.
SQ SEQUENCE 8 AA; 787 MW; ECB732C7287DC766 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
Db 3 POS 5
|||
|||

RESULT 11
Q89498 PRELIMINARY; PRT; 8 AA.
AC Q89498;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CORONAVIRUS proviral defective INTERFERING PARTICLE (DLSSSE) OBTAINED
DE AFTER SERIAL PASSAGE 17, with 2 recombination SITES and ORFS (DLSSSE).
OS Murine hepatitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8920822; PubMed=2845661;
RA Makino S., Shieh C.K., Soe L.H., Baker S.C., Lai M.M.;
RT "Primary structure and translation of a defective interfering RNA of
RL murine coronavirus.";
DR EMBL; M23258; AAA91862.1; -.
FT NON TER
FT SEQUENCE 8 AA; 815 MW; ECB732C72862D766 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 6 VLS 8
|||
|||

RESULT 12
P87488 PRELIMINARY; PRT; 8 AA.
AC P87488;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Growth hormone 2 (Fragment).
GN GH-2-A OR GH-2-B.
OS Oncorhynchus kisutch (Coho salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8019;
RN [1]
RP SEQUENCE OF 41-48 FROM N.A.
RX MEDLINE=94173883; PubMed=8127856;
RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
RT "One of two growth hormone genes in coho salmon is sex-linked.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1628-1631(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
RL Proc. Natl. Acad. Sci. U.S.A. 91:0-0(0).
DR EMBL; U04930; AAD13472.1; -.
DR EMBL; U04931; AAD13476.1; -.

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FT NON_TER      1      1
FT NON_TER      8      8
SQ SEQUENCE      8 AA; 902 MW; 92233732D5A5B326 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 13; Length 8;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVL 5
Db      4 SVL 6

RESULT 13
Q9UCS8      PRELIMINARY;      PRT;      9 AA.
ID Q9UCS8;
AC Q9UCS8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Apolipoprotein A-I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE.
RX MEDLINE=92075698; PubMed=1742316;
RA Enholm C., Bozas S.E., Tenkanen H., Kirsbaum L., Metso J.,
RA Murphy B., Walker I.D.;
RT "The apolipoprotein A-I binding protein of placenta and the SP-40,40
RT apolipoprotein A-I."
RT apolipoprotein A-I."
RL Biochim. Biophys. Acta 1086:255-260(1991).
FT NON_TER      1
FT NON_TER      1
FT NON_TER      9
SQ SEQUENCE      9 AA; 981 MW; 7FE37775A6C7776B CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 POS 3
Db      4 POS 6

RESULT 14
Q8HZY2      PRELIMINARY;      PRT;      9 AA.
ID Q8HZY2;
AC Q8HZY2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Leptin (Fragment).
GN LEP.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_TaxID=9615;
RP SEQUENCE FROM N.A.
RA Kanaku N., Toda M.;
RT "PCR cloning of the dog leptin gene."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB097078; BAC41247.1; -.
FT NON_TER      1
FT NON_TER      1
FT NON_TER      9
SQ SEQUENCE      9 AA; 945 MW; 808A2D5A6C1A1F5 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 6; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 QSV 4
Db      5 QSV 7

RESULT 15
Q29831      PRELIMINARY;      PRT;      11 AA.
ID Q29831;
AC Q29831;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gene fragment encoding human histocompatibility antigen HLA-DR alpha
DE (exon 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83169718; PubMed=6403940;
RA Das H.K., Biro P.A., Cohen S.N., Erlich H.A., von Gabain A.,
RA Lawrence S.K., Lemaux P.G., McDevitt H.O., Peterlin B.M., Schulz M.F.,
RA Sood A.K., Weissman S.M.;
RT "Use of synthetic oligonucleotide probes complementary to genes for
RT human HLA-DR alpha and beta as extension primers for the isolation of
RT 5' specific clones."
RL Proc. Natl. Acad. Sci. U.S.A. 80:1531-1535(1983).
DR EMBL; V00525; CAA23784.1; -.
SQ SEQUENCE      11 AA; 1230 MW; 9378714E0865B1EA CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 7; Length 11;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VLS 6
Db      9 VLS 11

RESULT 16
Q9NTR7      PRELIMINARY;      PRT;      12 AA.
ID Q9NTR7;
AC Q9NTR7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE DJ78N10.1 (Eyes absent (Drosophila) homolog 4) (Fragment).
GN EY44.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Dunn M.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121959; CAB32069.1; -.
FT NON_TER      12
FT NON_TER      12
SQ SEQUENCE      12 AA; 1394 MW; C15EA7952D472AB6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 3; DB 4; Length 12;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 QSV 4
Db      10 QSV 12

RESULT 17
Q9TQY4

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ID Q9TQY4 PRELIMINARY; PRT; 12 AA.  
AC Q9TQY4;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Glycoprotein H-B N-TERMINAL, GPI-B N-TERMINAL-KEX2/subtilisin-related protease (Fragment).  
DE Bos taurus (Bovine).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91340701; PubMed=1874725;  
RA Christie D.L., Batchelor D.C., Palmer D.J.;  
RT "Identification of kex2-related proteases in chromaffin granules by partial amino acid sequence analysis.";  
RL J. Biol. Chem. 266:15679-15683(1991).  
FT NON\_TER 1  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1303 MW; 9F2FF9E2782DC5BA CRC64;  
  
Query Match 50.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVL 5  
Db |||  
1 SVL 3  
  
RESULT 18  
Q9MZS4 PRELIMINARY; PRT; 12 AA.  
ID Q9MZS4  
AC Q9MZS4;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Growth hormone (Fragment).  
GN GH.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lantinga-van Leeuwen I.S., Mol J.A.;  
RT "Cloning and characterization of the 5'-flanking region of the canine growth hormone gene.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF166119; AAF89582.1; -.  
FT NON\_TER 12  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1229 MW; 2B587268EBCB45417 CRC64;  
  
Query Match 50.0%; Score 3; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVL 5  
Db |||  
8 SVL 10  
  
RESULT 19  
Q8RSG9 PRELIMINARY; PRT; 13 AA.  
ID Q8RSG9  
AC Q8RSG9;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Hypothetical 1.4 kDa protein.  
OS uncultured bacterium.

OG Plasmid pB4.  
OC Bacteria; environmental samples.  
OX NCBI\_TaxID=77133;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tauch A.;  
RT "The IncP beta plasmid pB4 encodes a tripartite antibiotic efflux system of the RND-MFP-OEP type conferring erythromycin and roxithromycin resistance in Pseudomonas sp. B13.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ431260; CAD24397.1; -.  
KW Hypothetical protein; Plasmid.  
SQ SEQUENCE 13 AA; 1359 MW; D1535C038748A33D CRC64;  
  
Query Match 50.0%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVL 5  
Db |||  
2 SVL 4  
  
RESULT 20  
Q9U5J2 PRELIMINARY; PRT; 13 AA.  
ID Q9U5J2  
AC Q9U5J2;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE GPI-phospholipase C (Fragment).  
GN GPI-PLC.  
OS Trypanosoma brucei.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
OX NCBI\_TaxID=5691;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ILTari;  
RA Webb H.D., Gaud A.F., Carrington M.;  
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally related genes or to genes showing the same developmentally regulated expression.";  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ250727; CAB60093.1; -.  
DR InterPro; IPR003633; Varsurfglyc\_PPLC.  
DR Pfam; PF03490; Varsurf\_PPLC; 1.  
FT NON\_TER 13  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1541 MW; 535AA96B464CA373 CRC64;  
  
Query Match 50.0%; Score 3; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 POS 3  
Db |||  
9 POS 11  
  
RESULT 21  
Q9WMG5 PRELIMINARY; PRT; 13 AA.  
ID Q9WMG5  
AC Q9WMG5;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
DE 3 protein (Fragment).  
GN GENE 3.  
OS Sigma virus.  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Rhabdoviridae; unclassified Rhabdoviridae.  
OX NCBI\_TaxID=11301;  
RN [1]  
RP SEQUENCE FROM N.A.

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RX MEDLINE=93212481; PubMed=8384742;
RA Teninges D., Bras F., Dezelee S.;
RT "Genome organization of the sigma rhabdovirus: six genes and a gene
overlap.";
RL Virology 193:1018-1023(1993).
DR EMBL; S57850; AAD40700.1; -.
FT NON TER
SQ SEQUENCE 13 AA; 1456 MW; 9AF4F3FDE75E32D5 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 12; Length 13;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
Db 6 SVL 8

RESULT 22
P78359
ID P78359 PRELIMINARY; PRT; 14 AA.
AC P78359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NF-kappa-B transcription factor p65 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pye S., Nelles L., Huylebroeck D.;
RT "5' cDNA sequence RelA isolated from Human umbilical vein endothelial
cells.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88316; AAB48487.1; -.
FT NON TER
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 4; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
Db 10 POS 12

RESULT 23
Q9RLU3
ID Q9RLU3 PRELIMINARY; PRT; 14 AA.
AC Q9RLU3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE R-ras GTPase activating protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Iwashita S.;
RT "5'-flanking region of R-ras GTPase activating protein.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB021982; BAA81903.1; -.
FT NON TER
SQ SEQUENCE 14 AA; 1594 MW; 3C91E28A0C8E3E28 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 11; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 12 VLS 14

RESULT 24
Q9TNO3
ID Q9TNO3 PRELIMINARY; PRT; 15 AA.
AC Q9TNO3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Class II HLA DR5 ligand.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=94164692; PubMed=8119729;
RA Falk K., Rotzschke O., Stevanovic S., Jung G., Rammensee H.G.;
RT "Pool sequencing of natural HLA-DR, DQ, and DP ligands reveals
detailed peptide motifs, constraints of processing, and general
rules.";
RL Immunogenetics 39:230-242(1994).
KW MHC.
SQ SEQUENCE 15 AA; 1738 MW; 5C8F3CE934481042 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 7; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 13 VLS 15

RESULT 25
Q05694
ID Q05694 PRELIMINARY; PRT; 15 AA.
AC Q05694;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proline-rich protein (Fragment).
GN MP6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RA Roberts S.G.E., Layfield R., McDonald C.J.;
RT "The mouse proline-rich protein MP6 promoter binds isoprenaline-
inducible paroid nuclear proteins via a highly conserved NFKB/rel-
like site.";
RL Nucleic Acids Res. 19:5205-5211(1991).
DR EMBL; X61126; CAA43438.1; -.
FT NON TER
SQ SEQUENCE 15 AA; 1557 MW; C0FF9514A8F70EE4 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 11; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 12 VLS 14

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
Cytochrome C554 (Fragment).  
Nitrosomonas europaea.  
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
Nitrosomonadaceae; Nitrosomonas.  
NCBI\_TaxID=915;  
[1]  
SEQUENCE  
MEDLINE=93224468; PubMed=8385668;  
McTavish H., LaQuier F., Arciero D., Logan M., Mundfrom G.,  
Fuchs J.A., Hooper A.B.;  
"Multiple copies of genes coding for electron transport proteins in  
the bacterium Nitrosomonas europaea.";  
J. Bacteriol. 175:2445-2447(1993).  
HSSP; P02185; 111M.  
SEQUENCE 16 AA; 1895 MW; 8A4F5D240FB0B3F9 CRC64;  
Query Match 50.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VLS 6  
Db 1 VLS 3

RESULT 29  
P82597 PRELIMINARY; PRT; 16 AA.  
AC P82597;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
DE Thermotable monoacylglycerol lipase (MGLP) (24 kDa) (EC 3.1.1.23)  
(Fragment).  
OS Bacillus sp.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1409;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=H-257;  
RX MEDLINE=20198254; PubMed=10731713;  
RA Imamura S., Kitaara S.;  
RT "Purification and characterization of a monoacylglycerol lipase from  
the moderately thermophilic Bacillus sp. H-257.";  
J. Biochem. 127:419-425(2000).  
CC -!- FUNCTION: HYDROLYZES MONOACYLGLYCEROLS, WITH THE HIGHEST ACTIVITY  
OCCURRING WITH 1-MONOLAURYLGLYCEROL.  
CC -!- ENZYME REGULATION: NOT INHIBITED BY CHOLATE, BUT SLIGHTLY  
INHIBITED BY TRITON X-100 AND DEOXYCHOLATE.  
CC -!- SUBUNIT: MONOMER.  
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 4.66. OPTIMUM  
TEMPERATURE IS 75 DEGREES CELSIUS AND MAXIMUM ACTIVITY AT PH 6-8.  
CC -!- MISCELLANEOUS: THIS LIPASE IS NOT SECRETED EXTRACELLULARLY AS  
OTHER BACTERIAL LIPASES.  
KW Hydrolase.  
FT NON\_TER 16 16  
SQ SEQUENCE 16 AA; 1787 MW; 900CF59289521D8F CRC64;  
Query Match 50.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VLS 6  
Db 6 VLS 8

RESULT 30  
O77922 PRELIMINARY; PRT; 16 AA.  
ID O77922  
AC O77922;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

01-MAY-2000 (TrEMBLrel. 13, Created)  
01-OCT-2000 (TrEMBLrel. 15, Created)  
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
Hypothetical protein BH3083.  
GN BH3083  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=86665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125 / JCM 9153;  
RX MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,  
Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,  
Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
halodurans and genomic sequence comparison with Bacillus subtilis.";  
Nucleic Acids Res. 28:4317-4331(2000).  
RL EMBL; AF001517; BAB0802.1; --  
DR Hypothetical protein; Complete proteome.  
SQ SEQUENCE 15 AA; 1816 MW; 9044F141BD577A58 CRC64;  
Query Match 50.0%; Score 3; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VLS 6  
Db 10 VLS 12

RESULT 27  
Q45663 PRELIMINARY; PRT; 16 AA.  
AC Q45663;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE SacB levanucrase.  
OS Bacillus subtilis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1423;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Marburg;  
RX MEDLINE=85295507; PubMed=2993818;  
RA Steinmetz M., Le Coq D., Aymerich S., Gonzy-Treboul G., Gay P.;  
RT "The DNA sequence of the gene for the secreted Bacillus subtilis  
enzyme levanucrase and its genetic control sites.";  
Mol. Gen. Genet. 200:220-228(1985).  
RL EMBL; X02730; CAA26512.1; --  
SQ SEQUENCE 16 AA; 1840 MW; E8CF83DC73713DA9 CRC64;  
Query Match 50.0%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QSV 4  
Db 5 QSV 7

RESULT 28  
Q9R5C1 PRELIMINARY; PRT; 16 AA.  
ID Q9R5C1  
AC Q9R5C1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

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DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 16 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
RX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050035; AAC41374.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1893 MW; A56619E46BAB5P2D CRC64;

Query Match 50.0%; Score 3; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
DB 6 VLS 8

RESULT 31
Q9T2Q6 PRELIMINARY; PRT; 16 AA.
AC Q9T2Q6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Cytochrome-C reductase 11 kDa subunit (EC 1.10.2.2) (Fragment).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE.
RX MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 16 AA; 1904 MW; AFC237AE7549E2B5 CRC64;

Query Match 50.0%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
DB 7 SVL 9

RESULT 32
Q88250 PRELIMINARY; PRT; 16 AA.
AC Q88250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F protein (Fragment)..
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11191;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60152; AAA47808.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1648 MW; 049B529F01B29066 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
DB 6 PQS 8

RESULT 33
Q88249 PRELIMINARY; PRT; 16 AA.
AC Q88249;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F protein (Fragment).
OS Sendai virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX NCBI_TaxID=11191;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91012818; PubMed=2170692;
RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;
RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,
RT TCs, which is sensitive to trypsin and chymotrypsin.";
RL J. Virol. 64:5660-5664(1990).
DR EMBL; M60154; AAA47807.1; -.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1649 MW; 049B529F01B298C4 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQS 3
DB 6 PQS 8

RESULT 34
Q86966 PRELIMINARY; PRT; 16 AA.
AC Q86966;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P28 (Fragment).
OS ORF 1A.
OS Murine hepatitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11138;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96078996; PubMed=7494259;
RA Chen W., Baric R.S.;
RT "Function of a 5'-end genomic RNA mutation that evolves during
RT persistent mouse hepatitis virus infection in vitro.";

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RL J. Virol. 69:7529-7540(1995).  
 DR EMBL; S80452; AAB35657.1; -.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1567 MW; 8B1ABEE0EB72E00CF CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VLS 6  
 ||||  
 Db 14 VLS 16

## RESULT 35

Q99154  
 ID Q99154 PRELIMINARY; PRT; 16 AA.  
 AC Q99154;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
 DE F protein (fragment).  
 OS Sendai virus.  
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
 OC Paramyxoviridae; Paramyxovirinae; Respirivirus.  
 OX NCBI\_TaxID=11191;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91012818; PubMed=2170692;  
 RA Itoh M., Ming T.D., Hayashi T., Mochizuki Y., Homma M.;  
 RT "Pneumopathogenicity of a Sendai virus protease-activation mutant,  
 RT TCs, which is sensitive to trypsin and chymotrypsin.";  
 RL J. Virol. 64:5660-5664(1990).  
 DR EMBL; M60153; AAA47806.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1606 MW; 739B529F01B298D0 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3  
 ||||  
 Db 6 POS 8

## RESULT 36

Q9R560  
 ID Q9R560 PRELIMINARY; PRT; 17 AA.  
 AC Q9R560;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
 DE Menaguiol oxidase (Fragment).  
 OS Bacillus subtilis  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93356600; PubMed=8394685;  
 RA Lamma E., Schagger H., Kroger A.;  
 RT "The menaguiol oxidase of Bacillus subtilis W23.";  
 RL Arch. Microbiol. 159:574-578(1993).  
 SQ SEQUENCE 17 AA; 1750 MW; 87A251230A5831C3 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 ||||  
 Db 5 SVL 7

## RESULT 37

Q93UW3  
 ID Q93UW3 PRELIMINARY; PRT; 17 AA.  
 AC Q93UW3;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE RepA protein (fragment).  
 GN REPA.  
 GN Agrobacterium tumefaciens.  
 OS Agrobacterium tumefaciens.  
 OG Plasmid pRiA4b.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Rhizobiaceae; Rhizobium.  
 OX NCBI\_TaxID=356;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A4;  
 RA Liang Y., Aoyama T., Oka A.;  
 RT "Organization of the conjugal transfer genes of the hairy-root-  
 RT inducing plasmid A4.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB050904; BAB47270.1; -.  
 KW Plasmid.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1655 MW; 4455CAD15C1A5520 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
 ||||  
 Db 4 SVL 6

## RESULT 38

Q9TWC6  
 ID Q9TWC6 PRELIMINARY; PRT; 17 AA.  
 AC Q9TWC6;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)  
 DE 22L kDa excretory-secretory protein (fragment).  
 OS Dirofilaria immitis (Canine heartworm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
 OC Onchocercidae; Dirofilaria.  
 OX NCBI\_TaxID=6287;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96258562; PubMed=8992320;  
 RA Frank G.R., Grievie R.B.;  
 RT "Purification and characterization of three larval excretory-secretory  
 RT proteins of Dirofilaria immitis.";  
 RL Mol. Biochem. Parasitol. 75:221-229(1996).  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 2048 MW; 478557C5392B4B7 CRC64;

Query Match 50.0%; Score 3; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3  
 ||||  
 Db 2 POS 4

## RESULT 39

Q9TRW1  
 ID Q9TRW1 PRELIMINARY; PRT; 17 AA.  
 AC Q9TRW1;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CALDESNON-PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
  by protein kinase C.";
RL Arch. Biochem. Biophys. 288:538-542 (1991).
DR InterPro; IPR006018; Caldesmon_LSP.
DR Pfam; PF02029; Caldesmon; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 1889 MW; 77EACD3EB02F95F6 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
Db 6 QSV 8

RESULT 40
Q9S8Y3
ID Q9S8Y3 PRELIMINARY; PRT; 17 AA.
AC Q9S8Y3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE L-asparaginase isoform A (EC 3.5.1.1) (Fragment).
OS Lupinus arboreus (Tree lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
OX NCBI_TaxID=3972;
RN [1]
RP SEQUENCE.
RX MEDLINE=92344803; PubMed=1368361;
RA Lough T.J., Chang K.S., Carne A., Monk B.C., Reynolds P.H.,
RA Farnden K.J.;
RA Phytochemistry 31:1519-1527 (1992).
RL Phytochemistry 17 AA; 1703 MW; 9AEDD9691F7F0807 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
Db 8 SVL 10

RESULT 41
Q84098
ID Q84098 PRELIMINARY; PRT; 17 AA.
AC Q84098;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza A/pw/rostock/34 (H7N1), matrix protein (Seg 7), 3' end of
  vna (Initiator region for protein coding) (Fragment).
OS Influenzavirus A.
OS Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80034428; PubMed=493121;
RA Roberton J.S.;
RT "5' and 3' terminal nucleotide sequences of the rna genome segments of
  influenza virus.";
RL Nucleic Acids Res. 6:3745-3757 (1979).
DR EMBL; J02112; AAA43305.1; -.
DR InterPro; IPR001561; Flu_M1.
DR Pfam; PF00598; Flu_M1; 1.
KW Matrix protein.
FT NON_TER 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1795 MW; COD59B0984ED10E1 CRC64;

Query Match 50.0%; Score 3; DB 12; Length 17;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 11 VLS 13

RESULT 42
Q8L2T5
ID Q8L2T5 PRELIMINARY; PRT; 18 AA.
AC Q8L2T5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tryptophan transporter (Fragment).
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=126E;
RX STRAIN=126E;
RX MEDLINE=22051050; PubMed=12055303;
RA Zhu P., Klutch M.J., Bash M.C., Tsang R.S.W., Ng L.K., Tsai C.M.;
RT "Genetic Diversity of Three lgt Loci for Biosynthesis of
  Lipooligosaccharide (LOS) in Neisseria Species.";
RL Microbiology 148:1833-1844 (2002).
DR EMBL; AF470685; AAM33537.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1944 MW; 08DE06F3E9B8C27E CRC64;

Query Match 50.0%; Score 3; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 6 VLS 8

RESULT 43
Q9P0M3
ID Q9P0M3 PRELIMINARY; PRT; 18 AA.
AC Q9P0M3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Polymyositis/scleroderma autoantigen 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bliskovsky V., Miller M., Mock B.;
RT "Structure and localization of mouse PM-Scl genes.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AF152839; AAF73199.1; -.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2025 MW; AIF292BC77872D67 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 11 VLS 13

RESULT 44
Q9UCF4 ID Q9UCF4 PRELIMINARY; PRT; 18 AA.
AC Q9UCF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Chymotrypsinogen homolog (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93285747; PubMed=8509158;
RA Kim Y.J., Zhou Z., Hurtado J., Wood D.L., Choi A.S., Pescovitz M.D.,
RA Warfel K.A., VandaGriff J., Davis J.K., Kwon B.S.;
RT "LDM patients' sera recognize a novel 30-kD pancreatic autoantigen
RT related to chymotrypsinogen.";
RL Immunol. Invest. 22:219-227(1993).
SQ SEQUENCE 18 AA; 1826 MW; 38105D1037CA6837 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 9 VLS 11

RESULT 45
Q8N303 ID Q8N303 PRELIMINARY; PRT; 18 AA.
AC Q8N303;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029372; AA029372.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2043 MW; 3D94B543DBE8825F CRC64;

Query Match 50.0%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 3 VLS 5

RESULT 46
O97773 ID O97773 PRELIMINARY; PRT; 18 AA.
AC O97773;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Mibp protein (Fragment).
GN MIBP.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA Bliskovsky V., Zajac K.M.;
RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
RT a tissue specific alternative exon in the mibp gene.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88970; AA000667.1; -.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2069 MW; CA377C765ABEE28A CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
Db 11 POS 13

RESULT 47
P79214 ID P79214 PRELIMINARY; PRT; 18 AA.
AC P79214;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CFTR protein.
GN CFTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97254985; PubMed=9100367;
RA Vuilliamier S., Kaltenboeck B., Lecointre G., Lehn P., Denamur E.;
RT "Phylogenetic analysis of cystic fibrosis transmembrane conductance
RT regulator gene in mammalian species argues for the development of a
RT rabbit model for cystic fibrosis.";
RL Mol. Biol. Evol. 14:372-380(1997).
DR EMBL; X35931; CAA65172.1; -.
SQ SEQUENCE 18 AA; 2080 MW; 4D1CS5056C1CE1B5 CRC64;

Query Match 50.0%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 11 VLS 13

RESULT 48
Q9TR57 ID Q9TR57 PRELIMINARY; PRT; 18 AA.
AC Q9TR57;

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OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartoideae; Oryzeae; Oryza.
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=95175599; PubMed=7870812;
RA	Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT	"Molecular and physiological responses to abscisic acid and salts in
RT	roots of salt-sensitive and salt-tolerant indica rice varieties.";
RL	Plant Physiol. 107:177-186(1995).
DR	Gramene; Q9S8I7; -.
SQ	SEQUENCE 18 AA; 2094 MW; 0CD245DB237E7520 CRC64;

  

Query Match	50.0%;	Score 3;	DB 10;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 6.3e+03;		
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;			
Gaps	0;			

  

Qy	3 SVL 5
Db	12 SVL 14

  

RESULT 51	
Q9S8I8	
ID	Q9S8I8 PRELIMINARY; PRT; 18 AA.
AC	Q9S8I8;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE	40 kDa PI 8.5 ABCISSIC acid-induced protein (Fragment).
OS	Oryza sativa (Rice).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC	Ehrhartoideae; Oryzeae; Oryza.
OX	NCBI_TaxID=4530;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=95175599; PubMed=7870812;
RA	Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;
RT	"Molecular and physiological responses to abscisic acid and salts in
RT	roots of salt-sensitive and salt-tolerant indica rice varieties.";
RL	Plant Physiol. 107:177-186(1995).
DR	Gramene; Q9S8I8; -.
SQ	SEQUENCE 18 AA; 2097 MW; 146450D9A97E6D83 CRC64;

  

Query Match	50.0%;	Score 3;	DB 10;	Length 18;
Best Local Similarity	100.0%;	Pred. No. 6.3e+03;		
Matches	3;	Conservative	0;	Mismatches 0;
Indels	0;			
Gaps	0;			

  

Qy	3 SVL 5
Db	12 SVL 14

  

RESULT 52	
Q9WTP8	
ID	Q9WTP8 PRELIMINARY; PRT; 18 AA.
AC	Q9WTP8;
DT	01-NOV-1999 (TREMBLrel. 12, Created)
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE	R-ras GTPase activating protein (Fragment).
OS	R-RAS GAP.
GN	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sprague-Dawley;
RA	Iwashita S., Kobayashi M.;
RT	"NGF-mediated downregulation of R-ras GAP expression.";



RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB020479; BAA78368.1; --  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2104 MW; 6BC3355FDC91E28A CRC64;

Query Match 50.0%; Score 3; DB 11; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
Db 12 QSV 14

RESULT 53  
Q9RLU4 PRELIMINARY; PRT; 19 AA.  
ID Q9RLU4  
AC Q9RLU4  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE NisG protein (Fragment).  
GN NISG.  
OS Lactococcus lactis.  
OG Plasmid pLEB513.  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1358;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N8; TRANSPOSON=Tn5481;  
RX MEDLINE=99452384; PubMed=10524753;  
RA Immonen T., Wahlstroem G., Takala T., Saris P.E.J.;  
RT "Evidence for a mosaic structure of the Tn5481 in Lactococcus lactis N8.";  
RL DNA Seq. 9:245-261 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N8; TRANSPOSON=Tn5481;  
RX MEDLINE=99452385; PubMed=10524754;  
RA Immonen T., Saris P.E.J.;  
RT "Characterization of the nisEG operon of the nisin Z producing Lactococcus lactis subsp. lactis N8 strain.";  
RL DNA Seq. 9:263-274 (1998).  
DR EMBL: AJ000993; CAA04441.1; --  
KW Plasmid.  
FT NON\_TER 1 1  
SQ SEQUENCE 19 AA; 2139 MW; 6A429DC80BE73613 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
Db 4 VLS 6

RESULT 54  
Q9R5M3 PRELIMINARY; PRT; 19 AA.  
ID Q9R5M3  
AC Q9R5M3  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Quinolone oxidoreductase 82 kDa subunit (Fragment).  
OS Rhodococcus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Nocardiaceae.  
OX NCBI\_TaxID=1827;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92162192; PubMed=1789933;  
RA Peschke B., Lingsen F.;

RT "Microbial metabolism of quinoline and related compounds. XII. Isolation and characterization of the quinoline oxidoreductase from *Rhodococcus spec. B1* compared with the quinoline oxidoreductase from *Pseudomonas putida* 86.";  
RT Biol. Chem. Hoppe-Seyler 372:1081-1088 (1991).  
RL NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2057 MW; C21C630CDFB128E0 CRC64;

Query Match 50.0%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
Db 17 SVL 19

RESULT 55  
Q9NP11 PRELIMINARY; PRT; 19 AA.  
ID Q9NP11  
AC Q9NP11  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Pyruvate dehydrogenase E1-alpha subunit (EC 1.2.4.1) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=89132585; PubMed=2537010;  
RA Endo H., Tomura H., Kagawa Y., Ohta S.;  
RT "Defective gene in lactic acidosis: abnormal pyruvate dehydrogenase E1 alpha-subunit caused by a frame shift.";  
RL Am. J. Hum. Genet. 44:358-364 (1989).  
DR EMBL: M21447; AAA31853.2; --  
KW Oxidoreductase.  
FT NON\_TER 19 19  
SQ SEQUENCE 19 AA; 2030 MW; 02984909538D3E94 CRC64;

Query Match 50.0%; Score 3; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
Db 11 VLS 13

RESULT 56  
Q62637 PRELIMINARY; PRT; 19 AA.  
ID Q62637  
AC Q62637  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Xanthine dehydrogenase (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague Dawley;  
RX MEDLINE=94268906; PubMed=8208609;  
RA Chow C.-W., Clark M., Rinaldo J., Chalkley R.;  
RT "Identification of the Rat Xanthine Dehydrogenase/Oxidase Promoter.";  
RL Nucleic Acids Res. 22:1846-1854 (1994).  
DR EMBL: U08123; AAB60444.1; --  
FT NON\_TER 1 1  
FT VARIANT 19 19 H -> Q.

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FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2128 MW; A02841D686F50139 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 11; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
DB 8 QSV 10

RESULT 57
Q69345 PRELIMINARY; PRT; 19 AA.
AC Q69345;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 57 k protein (Fragment).
OS Human herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86232558; PubMed=3012465;
RA McGeech D.J., Davison A.J.;
RT "DNA sequence of the herpes simplex virus type 1 gene encoding
RT glycoprotein gH, and identification of homologues in the genomes of
RT varicella-zoster virus and Epstein-Barr virus.";
RL Nucleic Acids Res. 14:4281-4292(1986).
DR EMBL; X03896; CAA27535.1; -.
DR InterPro; IPR004936; Herpes_UL21.
DR Pfam; PF03252; UL21; 1.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2155 MW; D960532B4FACE79A CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 12; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4
DB 17 QSV 19

RESULT 58
Q90RF8 PRELIMINARY; PRT; 19 AA.
AC Q90RF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=97CG276;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127550; AAK84913.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2304 MW; 2727D4B66AE69237 CRC64;

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Query Match
Best Local Similarity 50.0%; Score 3; DB 15; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
DB 7 POS 9

RESULT 59
Q905G8 PRELIMINARY; PRT; 19 AA.
AC Q905G8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=97CG281;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410447; AAL10254.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2366 MW; 367E64E194069237 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 15; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
DB 7 POS 9

RESULT 60
Q9NZ27 PRELIMINARY; PRT; 20 AA.
AC Q9NZ27;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ATP7B (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220213; AAF67659.1; -.
FT NON_TER 1
FT VARIANT 3 3 H -> Q.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2365 MW; AAB07911D719FBF2 CRC64;

Query Match
Best Local Similarity 50.0%; Score 3; DB 4; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5
DB 6 SVL 8

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RESULT 61  
Q9NZ28  
ID Q9NZ28 PRELIMINARY; PRT; 20 AA.  
AC Q9NZ28  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE ATP7B (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang N., Wu Z.Y., MuRong S.X., Lin M.T.;  
RT "The characteristics of mutation of the Wilson disease gene (ATP7B)  
RT exon16 in Chinese.";  
RL Chin. J. Neurosci. 14:209-212(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220212; AAF27929.1; -;  
FT NON\_TER 1 1  
FT VARIANT 9 9 T -> I.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2344 MW; AAA2CERFBE19PBF2 CRC64;  
Query Match 50.0%; Score 3; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVL 5  
DB 6 SVL 8  
RESULT 62  
Q9S7J0  
ID Q9S7J0 PRELIMINARY; PRT; 20 AA.  
AC Q9S7J0  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Bromelain (Fragment)  
OS Ananas comosus (Pineapple)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;  
OC Bromeliaceae; Ananas.  
OX NCBI\_TaxID=4615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Harrach T., Eckert K., Schulze-Forster K., Nuck R., Grunow D.,  
RA Maurer H.R.;  
RT "Isolation and partial characterization of basic proteinases from stem  
RT bromelain.";  
RL J. Protein Chem. 14:41-52(1995).  
RN [2]  
RP SEQUENCE.  
RA MEDLINE=94330946; PubMed=8053898;  
RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,  
RA Rogers E.E., Duan Y., Laursen R.A., Reinhold B., Shames S.L.;  
RL Biochem. J. 301:727-735(1994).  
DR InterPro; IPR000668; Peptidase\_C1.  
DR Pfam; PF00112; Peptidase\_C1; 1.  
SQ SEQUENCE 20 AA; 2144 MW; 83A842BC812C3EBC CRC64;  
Query Match 50.0%; Score 3; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVL 5  
DB 6 SVL 8  
RESULT 63  
Q41475  
ID Q41475 PRELIMINARY; PRT; 20 AA.  
AC Q41475  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Potato patatin (Fragment)  
OS Solanum tuberosum (Potato)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=4113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Twell D., Ooms G.;  
RT "Structural diversity of the patatin gene family in potato cv.  
RT Desiree."; Genet. 212:325-336(1988).  
RL Mol. Gen. Genet. 212:325-336(1988).  
DR EMBL; M35434; AAA33826.1; -;  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2128 MW; 3C5B6336BCD9E8D1 CRC64;  
Query Match 50.0%; Score 3; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVL 5  
DB 6 SVL 8  
RESULT 64  
Q9S965  
ID Q9S965 PRELIMINARY; PRT; 20 AA.  
AC Q9S965  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Bromelain (Fragment)  
OS Ananas comosus (Pineapple)  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;  
OC Bromeliaceae; Ananas.  
OX NCBI\_TaxID=4615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Harrach T., Eckert K., Schulze-Forster K., Nuck R., Grunow D.,  
RA Maurer H.R.;  
RT "Isolation and partial characterization of basic proteinases from stem  
RT bromelain.";  
RL J. Protein Chem. 14:41-52(1995).  
RN [2]  
RP SEQUENCE.  
RA MEDLINE=95298192; PubMed=779262;  
RA Harrach T., Eckert K., Schulze-Forster K., Nuck R., Grunow D.,  
RA Maurer H.R.;  
RT "Isolation and partial characterization of basic proteinases from stem  
RT bromelain.";  
RL J. Protein Chem. 14:41-52(1995).  
RN [2]  
RP SEQUENCE.  
RA MEDLINE=94330946; PubMed=8053898;  
RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,  
RA Rogers E.E., Duan Y., Laursen R.A., Reinhold B., Shames S.L.;  
RL Biochem. J. 301:727-735(1994).  
DR InterPro; IPR000668; Peptidase\_C1.  
DR Pfam; PF00112; Peptidase\_C1; 1.  
SQ SEQUENCE 20 AA; 2144 MW; 83A842BC812C3EBC CRC64;  
Query Match 50.0%; Score 3; DB 10; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVL 5  
DB 6 SVL 8  
RESULT 65  
Q9NZ28  
ID Q9NZ28 PRELIMINARY; PRT; 20 AA.  
AC Q9NZ28  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE ATP7B (Fragment)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang N., Wu Z.Y., MuRong S.X., Lin M.T.;  
RT "The characteristics of mutation of the Wilson disease gene (ATP7B)  
RT exon16 in Chinese.";  
RL Chin. J. Neurosci. 14:209-212(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Fang L.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220212; AAF27929.1; -;  
FT NON\_TER 1 1  
FT VARIANT 9 9 T -> I.  
FT NON\_TER 20 20  
SQ SEQUENCE 20 AA; 2344 MW; AAA2CERFBE19PBF2 CRC64;  
Query Match 50.0%; Score 3; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVL 5  
DB 6 SVL 8

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Q9S8M1
ID Q9S8M1 PRELIMINARY; PRT; 20 AA.
AC Q9S8M1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE COMOSAIN (Fragment).
OS Ananas comosus (Pineapple).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinidae incertae sedis;
OC Bromeliaceae; Ananas.
OX NCBI_TaxID=4615;
RN [1]
RP SEQUENCE
RX MEDLINE=94330946; PubMed=8053898;
RA Napper A.D., Bennett S.P., Borowski M., Holdridge M.B., Leonard M.J.,
RA Rogers E.B., Duan Y., Laursen R.A., Reinhold B., Shames S.L.;
RL Biochem. J. 301:727-735(1994).
DR InterPro; IPR000668; Peptidase C1.
DR Pfam; PF00112; Peptidase C1; 1-
SQ SEQUENCE 20 AA; 2219 MW; 83A84A16232C3EBC CRC64;

Query Match 50.0%; Score 3; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
Db 2 POS 4

RESULT 66
Q9FPH8
ID Q9FPH8 PRELIMINARY; PRT; 20 AA.
AC Q9FPH8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE F16G20.160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
RA Ecker J.;
RT "Full length cDNA sequence of Arabidopsis thaliana.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325021; AAC40373.1; -.
SQ SEQUENCE 20 AA; 2291 MW; 5E30B3448A415CA4 CRC64;

Query Match 50.0%; Score 3; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 3 VLS 5

RESULT 67
Q9QVH2
ID Q9QVH2 PRELIMINARY; PRT; 20 AA.
AC Q9QVH2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chromogranin-B, CGB-GLUCAGONOMA peptide (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

```

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OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92063871; PubMed=1954895;
RA Nielsen E., Wellinder B.S., Madsen O.D.;
RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
RT peptides through processing at mono-, di-, or tribasic residues.";
RL Endocrinology 129:3147-3156(1991).
DR InterPro; IPR001990; Granin.
DR Pfam; PF01271; Granin; 1.
FT NON TER 1
FT NON TER 20
SQ SEQUENCE 20 AA; 2549 MW; 9AA9A230D0F151A8 CRC64;

Query Match 50.0%; Score 3; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3
Db 2 POS 4

RESULT 68
Q8CYA3
ID Q8CYA3 PRELIMINARY; PRT; 20 AA.
AC Q8CYA3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN SPF1755.
OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=171101;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21429245; PubMed=11544234;
RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burgett S.,
RA Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C.,
RA Gilmour R., Glas J.S., Khoja H., Kraft A.R., Lagace R.E.,
RA LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P.,
RA Mahren S.M., McHenry M., Mcleaster K., Mundy C.W., Niclas T.I.,
RA Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
RA Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
RA Zook C.A., Baltz R.H., Jaskunas S.R., Rostek P.R. Jr., Skatrud P.L.,
RA Glass J.I.;
RT "Genome of the bacterium Streptococcus pneumoniae strain R6.";
RL J. Bacteriol. 183:5703-5717(2001).
DR EMBL; AB008540; AAL00558.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 20 AA; 2386 MW; 22FE65701CB2D21F CRC64;

Query Match 50.0%; Score 3; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6
Db 5 VLS 7

RESULT 69
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gunn;  
RX MEDLINE=91282758; PubMed=1840486;  
RA Sato H., Aono S., Kashiwata S., Koiwai O.;  
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the  
hyperbilirubinemic Gunn rat.";  
RL Biochem. Biophys. Res. Commun. 177:1161-1164 (1991).  
DR EMBL; S38636; AAB19259.1; -.  
KW Transferase.  
FT NON\_TER 1  
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;  
  
Query Match 33.3%; Score 2; DB 11; Length 4;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
Db 2 VL 3  
  
RESULT 70  
Q95945  
ID Q95945 PRELIMINARY; PRT; 7 AA.  
AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Inside intron 5 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
nucleotide sequence of the gene coding for subunit 1 of yeast  
cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941 (1980).  
DR EMBL; V00694; CAA24066.1; -.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;  
  
Query Match 33.3%; Score 2; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 LS 6  
Db 6 LS 7  
  
RESULT 71  
Q9CSB3  
ID Q9CSB3 PRELIMINARY; PRT; 7 AA.  
AC Q9CSB3;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Hypothetical 0.7 kDa protein (Fragment).  
GN DiDi 10A-2B.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Root;  
RX MEDLINE=21171025; PubMed=11277426;  
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
RT "Arabidopsis thaliana genes expressed in the early compatible  
interaction with root-knot nematodes.";  
RL Mol. Plant Microbe Interact. 14:288-299 (2001).  
DR EMBL; AJ286350; CAB71014.2; -.  
KW Hypothetical protein.  
FT NON\_TER 1  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 719 MW; 6732C7287BB325D0 CRC64;  
  
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Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 VL 5  
Db 6 VL 7  
  
RESULT 72  
Q8JJ20  
ID Q8JJ20 PRELIMINARY; PRT; 7 AA.  
AC Q8JJ20;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Extracellular fatty acid binding protein (Fragment).  
GN EXPABP.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Wang Q., Li N., Li H.;  
RT "Cloning and sequencing of 3' UTR of EXPABP gene in chicken.";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF487519; AAL96665.1; -.  
FT NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;  
  
Query Match 33.3%; Score 2; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SV 4  
Db 3 SV 4  
  
RESULT 73  
O42564  
ID O42564 PRELIMINARY; PRT; 7 AA.  
AC O42564;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
GN SCN8A.  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
RT two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015(1997).
DR EMBL; U97673; AAB80916.1; -.
KW Ionic channel.
FT NON_TER 1
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 33.3%; Score 2; DB 13; Length 7;
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LS 6
Db 6 LS 7

RESULT 74
Q8JE81
ID Q8JE81 PRELIMINARY; PRT; 7 AA.
AC Q8JE81;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22056123; PubMed=12060770;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: A bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AAK32344.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 33.3%; Score 2; DB 15; Length 7;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db 1 PQ 2

RESULT 75
Q45615
ID Q45615 PRELIMINARY; PRT; 8 AA.
AC Q45615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GutB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94253000; PubMed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol
RT dehydrogenase gene.";

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RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL; L16626; AAA20875.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 33.3%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQ 2
Db 6 PQ 7

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Job time : 12.2674 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 15.314 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	100.0	6	22	Colostrinin derive
2	6	100.0	6	22	Colostrinin peptid
3	6	100.0	6	22	Colostrinin peptid
4	6	100.0	6	22	Ewe colostrinin pe
5	6	100.0	6	23	Colostrinin consti
6	6	100.0	6	23	Colostrinin consti
7	6	100.0	6	23	Neural cell regula
8	6	100.0	18	15	Hypotensive polype
9	4	66.7	4	16	Ubiquitin peptide

10	4	66.7	4	20	AAW92324	E2A/pbx1 immunogen
11	4	66.7	5	20	AAW92323	E2A/pbx1 immunogen
12	4	66.7	5	23	AAU75881	SREBP2 S1P proteas
13	4	66.7	6	20	AAW92315	E2A/pbx1 immunogen
14	4	66.7	6	20	AAW92302	Transport peptide
15	4	66.7	8	15	AAW82270	Plasma membrane lo
16	4	66.7	8	20	AAW96368	Plasma membrane lo
17	4	66.7	8	21	AAW15693	HIV gag myristolat
18	4	66.7	8	21	AAW22848	HIV gag plasma mem
19	4	66.7	8	22	ABP12530	HIV A02 super moti
20	4	66.7	8	22	ABP12531	HIV A02 super moti
21	4	66.7	8	22	ABP14440	HIV A03 super moti
22	4	66.7	8	22	ABP15515	HIV A03 super moti
23	4	66.7	8	22	ABP15516	HIV A24 super moti
24	4	66.7	8	22	ABP20717	HIV A24 super moti
25	4	66.7	8	22	ABP22864	HIV A11 motif gag
26	4	66.7	8	23	ABG93003	Myristoylation org
27	4	66.7	8	24	ABP56598	HIV gag amino-term
28	4	66.7	9	15	AAW73717	Antigen fragment 3
29	4	66.7	9	20	AAW55463	HLA binding plu-1
30	4	66.7	9	20	AAW92321	E2A immunogenic pe
31	4	66.7	9	22	ABP14476	HIV A03 super moti
32	4	66.7	9	22	ABP17821	HIV B58 super moti
33	4	66.7	9	22	ABP17918	HIV B58 super moti
34	4	66.7	9	22	ABP20722	HIV A03 motif gag
35	4	66.7	9	22	ABP22869	HIV A11 motif gag
36	4	66.7	9	22	ABW73123	Tumour antigen pep
37	4	66.7	9	22	ABW73124	Tumour antigen pep
38	4	66.7	9	22	ABW73125	Tumour antigen pep
39	4	66.7	9	23	ABJ09400	Hepatitis B virus
40	4	66.7	9	23	AAU90453	Chlamydia pneumoniae
41	4	66.7	10	17	AAU90649	S. acidocaldarius
42	4	66.7	10	20	AAW82304	Transport peptide
43	4	66.7	10	22	ABP11686	HIV A01 super moti
44	4	66.7	10	22	ABP12769	HIV A02 super moti
45	4	66.7	10	22	ABP12770	HIV A02 super moti
46	4	66.7	10	22	ABP12771	HIV A02 super moti
47	4	66.7	10	22	ABP15694	HIV A24 super moti
48	4	66.7	10	22	ABP17825	HIV B58 super moti
49	4	66.7	10	22	ABP17919	HIV B58 super moti
50	4	66.7	10	22	ABP20530	HIV A03 motif gag
51	4	66.7	10	22	ABP20539	HIV A03 motif gag
52	4	66.7	10	22	ABP20716	HIV A03 motif gag
53	4	66.7	10	22	ABP22863	HIV A11 motif gag
54	4	66.7	10	22	AAW95453	PRAME derived HLA-
55	4	66.7	10	22	AAW95614	Human complementar
56	4	66.7	10	22	AAW95616	Human complementar
57	4	66.7	10	22	AAW95693	Saccharomyces cere
58	4	66.7	10	24	ABJ19987	MHC binding peptid
59	4	66.7	10	24	ABJ19627	Neuronal nitric ox
60	4	66.7	11	16	AAW67271	Ubiquitin peptide
61	4	66.7	11	16	AAW67272	Ubiquitin peptide
62	4	66.7	11	21	AAW56247	Human secreted pro
63	4	66.7	11	22	ABP14552	HIV A03 super moti
64	4	66.7	11	22	ABP17201	HIV B27 super moti
65	4	66.7	11	22	ABP17202	HIV B27 super moti
66	4	66.7	11	22	ABP18788	HIV B62 super moti
67	4	66.7	12	20	AAW80388	Peptide eluted aft
68	4	66.7	12	21	AAW63328	Sterol-regulatory
69	4	66.7	12	23	ABG78536	Multiple sclerosis
70	4	66.7	13	6	AAW50642	Sequence (b) of a
71	4	66.7	13	20	AAW92320	E2A/pbx1 immunogen
72	4	66.7	13	22	AAW68083	Antitumour peptide
73	4	66.7	13	22	AAW68084	Antitumour peptide
74	4	66.7	13	22	AAW31919	Amino acid sequenc
75	4	66.7	13	22	AAW73149	Tumour antigen pep
76	4	66.7	13	22	AAW73150	Tumour antigen pep
77	4	66.7	13	22	AAW73151	Tumour antigen pep
78	4	66.7	13	23	AAU91248	Nucleic acid selec
79	4	66.7	13	23	AAU75880	SREBP2 S1P proteas
80	4	66.7	14	20	AAW36491	Fragment of human
81	4	66.7	14	20	AAW92316	E2A/pbx1 immunogen
82	4	66.7	14	20	AAW95267	Anti-progesterone

83 4 66.7 14 20 AAW95269 Anti-progesterone  
 84 4 66.7 14 21 AAY84226 Amino acid sequenc  
 85 4 66.7 14 22 AAM97129 Human peptide #404  
 86 4 66.7 14 23 ABP62326 Human immunopeptid  
 87 4 66.7 15 10 AAP90191 Antigenic peptide  
 88 4 66.7 15 14 AAR39526 Calmodulin inhibit  
 89 4 66.7 15 15 AAR48962 Truncated GAG. Sy  
 90 4 66.7 15 16 AAR80352 Protein polymeric  
 91 4 66.7 15 16 AAR80353 Protein polymeric  
 92 4 66.7 15 16 AAR80355 Protein polymeric  
 93 4 66.7 15 18 AAW25036 Ubiquitous nuclear  
 94 4 66.7 15 19 AAW49740 Glutamine donor pe  
 95 4 66.7 15 19 AAW54714 Peptide from HIV p  
 96 4 66.7 15 20 AAW95144 Phage peptide K5 b  
 97 4 66.7 15 20 AAW95125 Peptide K5 express  
 98 4 66.7 15 21 AAB07637 A human alpha-heli  
 99 4 66.7 15 22 ABP24574 HIV DR super motif  
 100 4 66.7 15 22 ABB56064 Vascular dementia-

## ALIGNMENTS

RESULT 1  
 AAB72271  
 ID AAB72271 standard; peptide; 6 AA.  
 XX AC AAB72271;  
 XX XX  
 DT 14-MAY-2001 (first entry)  
 XX XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 26.  
 XX XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX Synthetic.  
 OS XX  
 XX WO200111937-A2.  
 PN XX  
 XX XX  
 PD 22-FEB-2001.  
 XX XX  
 PF 17-AUG-2000; 2000WO-US22818.  
 XX XX  
 PR 17-AUG-1999; 99US-0149311.  
 XX XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REG-) REGEN THERAPEUTICS PLC.  
 XX XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX MPI; 2001-202804/20.  
 DR XX  
 XX XX  
 PT Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 6 AA;  
 Query Match 100.0%; Score 6; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 POSVLS 6  
 Db 1 POSVLS 6  
 |||||  
 |||||  
 RESULT 2  
 AAB72524  
 ID AAB72524 standard; Peptide; 6 AA.  
 XX AC AAB72524;  
 XX XX  
 DT 09-MAY-2001 (first entry)  
 XX XX  
 DE Colostrinin peptide #25.  
 XX XX  
 KW Dermatalogical; oxidative stress regulator; colostrinin.  
 XX Unidentified.  
 OS XX  
 XX WO200112650-A2.  
 PN XX  
 XX 22-FEB-2001.  
 PD XX  
 PF 17-AUG-2000; 2000WO-US22665.  
 XX XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX XX  
 PI Stanton GJ, Hughes TK, Boldogh I;  
 XX MPI; 2001-218342/22.  
 DR XX  
 XX XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX XX  
 PS Claim 6; Page 26; 48pp; English.  
 XX XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX XX  
 SQ Sequence 6 AA;  
 Query Match 100.0%; Score 6; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 POSVLS 6  
 Db 1 POSVLS 6  
 |||||  
 |||||  
 RESULT 3  
 AAB72556  
 ID AAB72556 standard; Peptide; 6 AA.  
 XX AC AAB72556;  
 XX XX  
 DT 09-MAY-2001 (first entry)  
 XX XX



colostrinin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -

Claim 7; Page 27; 63pp; English.

The present invention provides the sequences of a number of peptides found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

Sequence 6 AA;

Query Match 100.0%; Score 6; DB 22; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSVLS 6  
|||  
DB 1 PQSVLS 6

RESULT 5  
AAE20253  
ID AAE20253 standard; peptide; 6 AA.  
XX AC AAE20253;  
XX DT 18-JUN-2002 (first entry)  
XX DE Colostrinin constituent peptide #25.  
XX KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress; therapy; oxidative damage; skin; aging; wound healing; cell replacement; tissue; organ; cosmetic procedure; repair; regeneration; preservation; transplantation; implantation; dermatological; vulnery.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Modified-site 6 /note= "Optionally C-terminal amide"  
XX WO200213850-A1.  
XX PD 21-FEB-2002.  
XX PF 17-AUG-2000; 2000WO-US22776.  
XX PR 17-AUG-2000; 2000WO-US22776.  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2002-269151/31.  
XX  
XX Composition useful for the modulation of blood cell proliferation in a patient comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analog -  
XX  
XX Claim 6; Page 26; 51pp; English.  
XX  
XX The invention relates to a composition which comprises a blood cell regulator selected from colostrinin, its constituent peptide and/or analogue. The invention is used for modulating the oxidative stress level in a cell e.g. mammalian or human cell present in a cell culture, tissue, organ, or organism; or for treating oxidative damage to the skin of a patient e.g. animal or human; to modulate oxidative stress during/

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6  
 |||||  
 Db 1 PQSVLS 6

# RESULT 6

AA051060  
 ID AAM51060 standard; Peptide; 6 AA.

XX AC AAM51060;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (casein amino acids 174-179).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; beta-casein; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 6 /note= "optional C-terminal amidation"

XX FN WO200213849-A1.

XX PD 21-FEB-2002.

XX PE 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 CC blood cell regulator selected from colostrinin, its constituent peptide  
 CC and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 174-179. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunologic regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6  
 |||||  
 Db 1 PQSVLS 6

# RESULT 7

AA014602

ID AAO14602 standard; peptide; 6 AA.

XX AC AAO14602;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 25.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 6 /note= "Optional C-terminal amide"

XX FN WO200213851-A1.

XX PD 21-FEB-2002.

XX PE 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analog -

XX PS Claim 7; Page 21; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 6; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSVLS 6  
DB 1 PQSVLS 6

RESULT 8

AAR58332  
ID AAR58332 standard; peptide; 18 AA.

XX AC AAR58332;

XX DT 22-SEP-1994 (first entry)

XX DE Hypotensive polypeptide.

XX KW Hypotensive; antioxidative; calcium absorption; salt; food;  
XX KW pharmaceuticals; physiologically active agents.

XX OS Lactobacillus helveticus.

XX PN JP06041191-A.

XX PD 15-FEB-1994.

XX PF 03-MAR-1993; 93JP-0043047.

XX PR 04-MAR-1992; 92JP-0047340.

XX PA (CALV ) CALPIS SHOKUHIN KOGYO KK.

XX DR WPI; 1994-089332/11.

XX PT New polypeptide - used in physiologically active agents having  
XX PT e.g. hypotensive antioxidative and calcium absorption promoting  
XX PT activity

XX PS Claim 1-2; Page 8; 10pp; Japanese.

XX CC Sequences (AAR58319-341) are used in conjunction with  
XX CC physiologically active agents showing a property such as  
XX CC hypotensive activity, calcium absorption promoting activity and  
XX CC antioxidative activity. The peptides are non-toxic and can be  
XX CC used in physiologically active agents.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 6; DB 15; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQSVLS 6  
DB 2 PQSVLS 7

RESULT 9

AAR67270  
ID AAR67270 standard; peptide; 4 AA.

XX AC AAR67270;

XX DT 27-JUL-1995 (first entry)

XX DE Ubiquitin peptide extension, cRAS.

XX PA

KW Ubiquitin; peptide extension; assay; protein kinase; C-terminal;  
KW Ha-RAS protein; farnesyl-protein transferase;  
KW carboxy methyl transferase.

XX OS Synthetic.

XX PN US5366871-A.

XX PD 22-NOV-1994.

XX PF 13-NOV-1991; 91US-0791935.

XX PR 13-NOV-1991; 91US-0791935.

XX PA (UTAH ) UNIV UTAH.

XX PI Rechsteiner MC, Yoo YJ;

XX DR WPI; 1995-005826/01.

XX PT Assay for enzymes that modify peptide chains - using a substrate  
XX PT comprising a ubiquitin-peptide extension contg. a sequence  
XX PT modified by the enzyme

XX PS Disclosure; Column 7; 14pp; English.

XX CC The sequences given in AAR67262-70 represent ubiquitin-peptide  
XX CC extensions which are used in the method of the invention for  
XX CC assaying enzymes that modify peptide chains. These sequences  
XX CC represent extensions which are known to be modified in the presence  
XX CC of an enzyme being assayed for, and the reaction mixture formed is  
XX CC then analysed. This method may be used for assaying protein kinases  
XX CC or enzymes which modify the C-terminal end of Ha-RAS protein, such  
XX CC as farnesyl-protein transferase, or carboxy methyl transferase.  
XX CC These peptides are less expensive to synthesise than standard  
XX CC peptides used in these methods and they may be purified from  
XX CC bacterial extracts by simple acid extraction.

XX SQ Sequence 4 AA;

Query Match 66.7%; Score 4; DB 16; Length 4;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
DB 1 SVLS 4

RESULT 10

AAW92324

ID AAW92324 standard; peptide; 4 AA.

XX AC AAW92324;

XX DT 09-APR-1999 (first entry)

XX DE E2A/pbx1 immunogenic fusion peptide #7.

XX KW E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;  
XX KW epitope; acute lymphoblastic leukemia.

XX OS Synthetic.

XX PN US5858682-A.

XX PD 12-JAN-1999.

XX PF 02-AUG-1996; 96US-0691997.

XX PR 02-AUG-1996; 96US-0691997.

XX PA (PHAR-) PHARMINGEN.

XX PI Gruenwald S, Monell C, Sang B;  
 XX FI WPI; 1999-119870/10.  
 XX DR Monoclonal antibody specific for E2A/pbx1 fusion protein - useful  
 PT for diagnosis of acute lymphoblastic leukemia  
 PT Claim 6; Column 27-28; 21pp; English.  
 XX PS This sequence represents a peptide used in a method for constructing  
 XX CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal  
 CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This  
 CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.  
 XX SQ Sequence 4 AA;  
 Query Match 66.7%; Score 4; DB 20; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SVLS 6  
 Db 1 SVLS 4  
 RESULT 11  
 AAW92323  
 ID AAW92323 standard; peptide; 5 AA.  
 XX AC - AAW92323;  
 XX DT 09-APR-1999 (first entry)  
 XX DE E2A/pbx1 immunogenic fusion peptide #6.  
 XX KW E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;  
 KW epitope; acute lymphoblastic leukemia.  
 XX OS Synthetic.  
 XX PN US5858682-A.  
 XX PD 12-JAN-1999.  
 XX PF 02-AUG-1996; 96US-0691997.  
 XX PR 02-AUG-1996; 96US-0691997.  
 XX PA (PHAR-) PHARMINGEN.  
 XX PI Gruenwald S, Monell C, Sang B;  
 XX DR WPI; 1999-119870/10.  
 XX PT Monoclonal antibody specific for E2A/pbx1 fusion protein - useful  
 PT for diagnosis of acute lymphoblastic leukemia  
 XX PS Claim 5; Column 27-28; 21pp; English.  
 XX CC This sequence represents a peptide used in a method for constructing  
 CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal  
 CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This  
 CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.  
 XX SQ Sequence 5 AA;  
 Query Match 66.7%; Score 4; DB 20; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SVLS 6  
 Db 1 SVLS 4

Db 2 SVLS 5  
 RESULT 12  
 AAU75881  
 ID AAU75881 standard; Protein; 5 AA.  
 XX AC AAU75881;  
 XX DT 08-MAY-2002 (first entry)  
 XX DE SREBP2 SIP protease recognition sequence #2.  
 KW Amyloid precursor protein; SREBP2-lacI fusion protein;  
 KW notropic; neuroprotective; cardiant; antidiabetic; vasotropic;  
 KW proteolysis inhibition; transcription repressor; reporter gene;  
 KW transcriptional regulator; Notch-1; SREBP; neurological disease;  
 KW sterol regulatory element-binding protein; cardiac disease;  
 KW metabolic disease; Alzheimer's disease; diabetes; cardiovascular disease;  
 KW SIP protease recognition sequence.  
 XX OS Cricetulus griseus.  
 XX OS Homo sapiens.  
 XX PN US6333167-B1.  
 XX PD 25-DEC-2001.  
 XX PF 10-MAR-2000; 2000US-0522666.  
 XX PR 10-MAR-2000; 2000US-0522666.  
 XX PA (AMHP) AMERICAN HOME PROD CORP.  
 XX PI Quinet EM, Shuey DJ;  
 XX DR WPI; 2002-163178/21.  
 XX PT Screening compounds for inhibition of proteolysis, useful for  
 PT identifying agents for treating e.g. Alzheimer's disease, comprises  
 PT using cells that express a transcription repressor in the presence of a  
 PT protease -  
 XX PS Disclosure; Column 8; 48pp; English.  
 XX CC The invention relates to screening compounds for the ability to inhibit  
 CC proteolysis of a substrate by using a recombinant eukaryotic cell  
 CC that expresses: (i) a chimeric protein consisting of a transcription  
 CC repressor part and a protease recognition part; and (ii) a  
 CC reporter gene, linked to a transcriptional regulator sequence,  
 CC responsive to the transcription regulator. The method is used to identify  
 CC inhibitors of the proteolysis of membrane-associated polypeptides,  
 CC specifically amyloid precursor protein (APP), Notch-1 and sterol  
 CC regulatory element-binding proteins (SREBP). The inhibitors are  
 CC potentially useful in treatment of neurological, cardiac or metabolic  
 CC diseases, e.g. Alzheimer's disease, diabetes and cardiovascular disease.  
 CC The method is suitable for large scale screening and does not require  
 CC preliminary cloning of the target protease. The present sequence  
 CC represents an SIP protease recognition sequence as found in the  
 CC SREBP2-lacI (lac repressor) chimeric fusion protein used  
 CC to demonstrate the method of the invention.  
 XX SQ Sequence 5 AA;  
 Query Match 66.7%; Score 4; DB 23; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 SVLS 6  
 Db 2 SVLS 5



XX Claim 34; Page 42; 155pp; English.

XX New vector systems comprise a sequence adapted for intracellular delivery and expression contg. a promoter operably linked to an antibody gene encoding an antibody which binds to a specific target antigen. The antibody is esp. a single chain antibody in which the heavy and light chain variable regions are joined via a hydrophilic linker peptide. Localisation sequences are pref. included in the CC constructs. The sequence AAR48270 is the known N-terminal sequence of CC plasma membrane localised HIV gag protein and is a pref. CC localisation sequence for the novel constructs.

XX (Updated on 25-MAR-2003 to correct FN field.)

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 5 SVLS 8

RESULT 16

AAW96368

ID AAW96368 standard; Peptide; 8 AA.

XX AC AAW96368;

XX DT 19-JUL-1999 (first entry)

DE Plasma membrane localisation signal peptide.

XX Antibody; immune response; modulation; MHC; IRM; receptor;  
intrabody; major histocompatibility complex; graft rejection;  
immunomodulatory response molecule; regulation; transplantation;  
retention signal; localisation signal; golgi apparatus; ER;  
endoplasmic reticulum.

XX Synthetic.

XX WO9914353-A2.

XX PD 25-MAR-1999.

XX PF 18-SEP-1998; 98WO-US19563.

XX PR 19-SEP-1997; 97US-0059339.

XX (DAND ) DANA FARBER CANCER INST INC.

XX Marasco W, Mhashikar A;

XX WPI; 1999-229546/19.

XX Altering the regulation of the immune system

XX Disclosure; Page 29; 56pp; English.

XX Intracellular binding to a desired target by an intracellularly expressed antibody (i.e. an intrabody) can be used to knock out multiple locuses of immunomodulatory receptor molecules (IRMs), so that the expression of multiple major histocompatibility (MHC) molecules is blocked. This selective targeting of IRMs, their pathways or components, can be used to selectively regulate the immune system by controlling expression of these molecules and preventing an undesired immune response in a cell. Any component of the MHC pathway or the MHC assembly line or antigen presentation can be targeted. Intrabodies can be used to knock out the immune response in a particular tissue or portion of the body to prepare it for cell or tissue transplantation. Alternatively, an organ for

XX transplantation can be perfused with the intrabody ex vivo. The CC intrabodies can comprise whole antibodies, heavy chains, Fab' fragments, single-chain antibodies and diabodies. The intrabodies CC also comprise an intracellular localisation signal to facilitate CC interception of expressed proteins. For example, if the target was CC a cell surface receptor, the antibody would comprise a leader CC sequence and an endoplasmic reticulum (ER) or Golgi apparatus CC retention signal. This peptide is a localisation sequence for the CC plasma membrane and is found in the HIV gag protein. For CC other localisation sequences see AAW96345-W96377.

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 20; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 5 SVLS 8

RESULT 17

AAB15693

ID AAB15693 standard; Peptide; 8 AA.

XX AC AAB15693;

XX DT 08-JAN-2001 (first entry)

XX DE HIV gag myristolation sequence.

XX Human immunodeficiency virus; HIV; gag; myristolation sequence;  
single-chain antibody; stabilon; stabilising fusion peptide; vaccine;  
gene therapy; protein degradation modulation; protein stability;  
Alzheimer's disease.

XX Human immunodeficiency virus.

XX WO200042185-A1.

XX PD 20-JUL-2000.

XX PF 11-JAN-2000; 2000WO-US00558.

XX PR 11-JAN-1999; 99US-0115505.

XX (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.

XX (MCIN/) MCINNIS P A.

XX Chain DG;

XX WPI; 2000-476059/41.

XX Modulating degradability of protein or peptide useful for gene therapy  
involving antibodies, comprises altering a gene at the N terminus to  
render protein or peptide metabolically stable -

XX Disclosure; Page 51; 76pp; English.

XX The present sequence is the amino terminal myristolation sequence of  
HIV gag. It may be used to direct stabilised single-chain antibodies  
to the plasma membrane. The N-terminus of the single-chain antibody is  
linked to a stabilising fusion peptide, referred to as a stabilon, which  
increases stability of the antibody against proteolysis in vivo.  
Degradation of the antibody may be modulated by linking the stabilon to  
the antibody through a protease-sensitive linker region. The stabilon is  
removed upon induction of expression of a specific restriction protease  
by means of an inducible promoter, and this renders the antibody  
susceptible to proteolysis by the N-end rule pathway. This method for  
regulating protein stability allows removal of the antibody after it has  
bound to its target antigen. Stabilised recombinant proteins may be used  
in gene therapy for the treatment of disorders such as Alzheimer's

CC disease.  
 XX Sequence 8 AA;  
 SQ

Query Match 66.7%; Score 4; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 Db 5 SVLS 8

RESULT 18  
 AAB22848  
 ID AAB22848 standard; peptide; 8 AA.  
 XX AC AAB22848;  
 XX DT 10-JAN-2001 (first entry)  
 XX DE HIV gag plasma membrane-targeting myristoylation sequence.  
 XX KW Controlled release delivery system; drug targeting;  
 KW drug-specific antibody; intracellular half-life; gene therapy;  
 KW diabetes; autoimmune disease; inflammatory disease; infectious disease;  
 KW cancer; side effect; subcellular localisation sequence.  
 XX OS Human immunodeficiency virus.  
 XX WO200050089-A2.  
 XX PD 31-AUG-2000.  
 XX PF 25-FEB-2000; 2000WO-US04749.  
 XX PR 26-FEB-1999; 99US-0122103.  
 XX (MIND-) MINDSET BIOPHARMACEUTICALS USA INC.  
 XX Chain DG;  
 XX WPI; 2000-572044/53.  
 XX Delivering a drug, to a patient suffering from cancer or diabetes, at a  
 PT predetermined site, comprises altering a target cell to express a drug  
 PT specific antibody by gene therapy and administering the drug -  
 XX Disclosure; Page 45; 69pp; English.

CC The invention relates to a controlled release drug delivery system.  
 CC Target cells in a patient are transformed with an expression construct  
 CC encoding an antibody (particularly a single chain antibody) to the drug  
 CC to be delivered. The antibody contains a modulator of intracellular  
 CC half-life; this can either be a stabilising or destabilising residue  
 CC located in the N-terminus after the initial methionine, or a peptide  
 CC ("stabilon") containing a stabilising residue linked to the antibody  
 CC N-terminus via a protease cleavage site. On administration of the drug,  
 CC the antibody binds the drug, localising it at the target cells but  
 CC maintaining it in an inactive state. As the antibody is degraded (the  
 CC timescale for which is dependent upon the N-terminal or stabilon amino  
 CC acids), the drug is released at its site of action where it can exert  
 CC its effects. The antibody encoded by the expression construct (and  
 CC therefore the therapeutic agent) can be targeted to particular  
 CC subcellular locations (e.g., the nucleus) by including the appropriate  
 CC cellular localisation signals. The novel method may be used to deliver  
 CC therapeutic agents to patients with a variety of conditions such as  
 CC diabetes, autoimmune diseases, inflammatory diseases, infectious  
 CC diseases and especially cancer. The delivery method of the invention  
 CC causes a drug to become almost immediately localised at its site of  
 CC action in an inactive form where it accumulates. Once released by  
 CC antibody degradation, the drug is at an effective concentration only at  
 CC the target site, with very little free drug being available in the rest

CC of the body. The system of the invention therefore reduces the side  
 CC effects caused by therapeutic agents, and also provides economic benefits  
 CC as a smaller amount can be administered to the patient. Sequences  
 CC AAB22835- AAB22837 and AAB22839-B22857 represent subcellular localisation  
 CC sequences which can be incorporated into a drug-specific antibody used in  
 CC the method of the invention.  
 XX

QY Sequence 8 AA;  
 Db

Query Match 66.7%; Score 4; DB 21; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 Db 5 SVLS 8

RESULT 19  
 ABP12530  
 ID ABP12530 standard; Peptide; 8 AA.  
 XX AC ABP12530;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A02 super motif gag peptide #1.  
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif; vpr;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX OS Human immunodeficiency virus type 1.  
 XX WO200124810-A1.  
 XX PD 12-APR-2001.  
 XX PF 05-OCT-2000; 2000WO-US27766.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 125; 448pp; English.

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP125347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 1 SVLS 4

RESULT 20  
 ABP12531  
 ID ABP12531 standard; Peptide; 8 AA.  
 XX  
 AC ABP12531;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A02 super motif gag peptide #2.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PS Claim 32; Page 125; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. (I)  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 1 SVLS 4

RESULT 21  
 ABP14440  
 ID ABP14440 standard; Peptide; 8 AA.  
 XX  
 AC ABP14440;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A03 super motif gag peptide #2.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PS Claim 32; Page 164; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. (I)  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX SQ Sequence 8 AA;



Query Match 66.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 ||||  
 Db 2 SVLS 5

## RESULT 22

ABP15515  
 ID ABP15515 standard; Peptide; 8 AA.  
 XX  
 AC ABP15515;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A24 super motif gag peptide #1.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PT  
 PS Claim 32; Page 186; 448pp; English.  
 XX

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;  
 SQ

Query Match 66.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 ||||  
 Db 1 SVLS 4

## RESULT 23

ABP15516  
 ID ABP15516 standard; Peptide; 8 AA.  
 XX  
 AC ABP15516;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A24 super motif gag peptide #2.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.

OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US27766.  
 XX  
 PR 05-OCT-1999; 99US-0412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PT  
 PS Claim 32; Page 186; 448pp; English.  
 XX

CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.

XX Sequence 8 AA;  
 SQ

Query Match 66.7%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 ||||

```

Db          1 SVLS 4

RESULT 24
ABP20717
ID ABP20717 standard; Peptide; 8 AA.
XX
AC
XX
DT
XX
DE HIV A03 motif gag peptide #380.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 294; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 66.7%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 2 SVLS 5

RESULT 25
ABP22864
ID ABP22864 standard; Peptide; 8 AA.
XX
AC
XX
DT
XX
DE HIV A11 motif gag peptide #243.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 337; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 66.7%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 2 SVLS 5

RESULT 26
ABG93003
ID ABG93003 standard; Peptide; 8 AA.

```

XX AC ABG93003;  
XX DT 20-NOV-2002 (first entry)  
XX DE Myristoylation organelle localisation sequence peptide #10.  
XX KW Regulator; transcription; cell death; phenotype; molecular scaffold;  
KW gene therapy; cancer; cardiovascular disease; arrhythmia; heart failure;  
KW ischaemia; obesity; neurodegenerative disease; Alzheimer's disease;  
KW bone pathology; dermatologic disease; psoriasis; infection; AIDS;  
KW acquired immunodeficiency syndrome; cosmetic; wound healing;  
KW antibiotic transport; drug toxicity; drug resistance; immunobiology;  
KW inflammation; allergic response; human immunodeficiency virus.  
XX OS Human immunodeficiency virus type.  
XX PN WO200262822-A2.  
XX PD 15-AUG-2002.  
XX PF 04-FEB-2002; 2002WO-US02814.  
XX PR 02-FEB-2001; 2001US-265589P.  
XX PR 05-FEB-2001; 2001US-265880P.  
XX PR 27-FEB-2001; 2001US-271423P.  
XX PR 23-JAN-2001; 2001US-263226P.  
XX PR 28-MAR-2000; 2000US-192586P.  
XX PR 22-SEP-1997; 97US-935377P.  
XX (UYRP ) UNIV ROCHESTER.  
XX PI Zauderer M, Smith ES;  
XX WPI; 2002-643398/69.  
XX DR Identifying regulator polypeptides which influence target  
XX PT transcriptional regulatory regions, useful for treating cancer,  
XX PT comprises introducing host cells expressing the polypeptide into a  
XX PT library of polynucleotides -  
XX PT Disclosure; Page 38; 224pp; English.  
XX PS The invention discloses a method for identifying polynucleotides encoding  
CC a regulator polypeptide, whose expression induces activation of a target  
CC transcriptional regulatory region in a host cell. The method comprises  
CC providing a population of eukaryotic host cells capable of expressing the  
CC polypeptide, introducing into the host cell a library of polynucleotides  
CC encoding the polypeptides, permitting expression of the polypeptides and  
CC then recovering them from the host cells. The target transcriptional  
CC regulatory region is operably associated with a polynucleotide encoding a  
CC gene product, the expression of which results in host cell death or cause  
CC the host cells to exhibit a pre-determined modified phenotype and where  
CC the gene product is expressed upon activation of target transcriptional  
CC regulatory region. Each candidate regulator polypeptide comprises a  
CC candidate peptide and a molecular scaffold fused to the peptide so that  
CC the peptide is displayed on the surface of the candidate regulator  
CC polypeptide. The methods are useful in selecting and/or screening  
CC regulator molecules, such as polypeptides, which directly or indirectly  
CC induce or suppress the transcriptional activation of a target  
CC transcriptional regulatory region in a eukaryotic host cell. These  
CC regulator molecules may be used (e.g. in gene therapy) for preventing or  
CC treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases  
CC (e.g. arrhythmia, heart failure, ischaemia), obesity, neurodegenerative  
CC diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic  
CC diseases (e.g. psoriasis), infections (e.g. viral, bacterial), acquired  
CC immunodeficiency syndrome (AIDS), in cosmetic applications and in wound  
CC healing. The method is also useful in screening regulator molecules that  
CC block antibiotic transport mechanisms, in drug toxicities and drug  
CC resistance applications and in improving the performance of existing or  
CC developmental drugs. It may also be used in immunobiology, inflammation,  
CC allergic response and in biotechnology applications. The sequences  
CC presented in ABG92946-ABG93029 are examples of regulator polypeptides.

XX SQ Sequence 8 AA;  
XX Query Match 66.7%; Score 4; DB 23; Length 8;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX QY 3 SVLS 6  
XX DB 5 SVLS 8  
XX RESULT 27  
XX ID ABP56598 standard; Peptide; 8 AA.  
XX AC ABP56598;  
XX DT 24-MAR-2003 (first entry)  
XX DE HIV gag amino-terminal peptide sequence SEQ ID NO:64.  
XX KW Identification; intrabody; eukaryotic cell; immunoglobulin; selection;  
KW cardiovascular; diminished arrhythmia potential; cardiomyocyte; stroke;  
KW enhanced contractile property; heart failure; arrhythmia; embolic;  
KW sarcolemmal calcium cycling; artery; arteriole; angina; atherosclerosis;  
KW LDL metabolism; HDL metabolism; skin biology; keloid formation.  
XX OS Human immunodeficiency virus type 1.  
XX PN WO200286096-A2.  
XX PD 31-OCT-2002.  
XX PF 23-JAN-2002; 2002WO-US01677.  
XX PR 23-JAN-2001; 2001US-263225P.  
XX PR 24-JAN-2001; 2001US-263200P.  
XX PR 27-FEB-2001; 2001US-271422P.  
XX PR 15-JUN-2001; 2001US-298095P.  
XX (UYRP ) UNIV ROCHESTER MEDICAL CENT.  
XX PI Zauderer M, Wei C, Smith ES;  
XX WPI; 2003-103408/09.  
XX PT Selecting polynucleotides encoding an intracellular immunoglobulin  
XX PT which induces a modified phenotype in a eukaryotic host cell, by  
XX PT introducing library of polynucleotides encoding immunoglobulin subunit  
XX PT polypeptides -  
XX PS Disclosure; Page 45; 257pp; English.  
XX CC The present invention describes a method for selecting polynucleotides  
CC (PNS) encoding an intracellular immunoglobulin molecule or its fragment  
CC whose expression induces a modified phenotype in a eukaryotic host cell  
CC (I). The method comprises introducing into (i) a first and second library  
CC of PNS encoding, through operable association with a transcriptional  
CC control region, first and second intracellular immunoglobulin subunit  
CC polypeptides, respectively. The method is useful for selecting  
CC polynucleotides which encode an intracellular immunoglobulin molecule, or  
CC fragment. The method is useful e.g. for identifying polynucleotides which  
CC singly or collectively encode intracellular immunoglobulin molecules, or  
CC which sensitise host cells to killing by an agent. The method may also be  
CC used in cardiovascular applications; for screening for diminished  
CC arrhythmia potential in cardiomyocytes and for enhanced contractile  
CC properties of cardiomyocytes and diminish heart failure potential; for  
CC identifying intracellular immunoglobulin molecules that will regulate  
CC intracellular and sarcolemmal calcium cycling in cardiomyocytes to  
CC prevent arrhythmias or that will diminish embolic phenomena in arteries  
CC and arterioles leading to strokes and angina; in screening for decreases  
CC in atherosclerosis-producing mechanisms to find intracellular

CC immunoglobulin molecules that regulate LDL and HDL metabolism; in skin  
 CC biology applications; and in regulating or inhibiting keloid formation.  
 CC ABZ22379 to ABZ22449 and ABP56536 to ABP56618 represent sequences used in  
 CC the exemplification of the present invention.

XX SQ Sequence 8 AA;

Query Match 66.7%; Score 4; DB 24; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 5 SVLS 8

## RESULT 28

AA73717  
 ID AAR73717 standard; peptide; 9 AA.

XX AC AAR73717;

XX AC (updated)

DT 25-MAR-2003 (first entry)

DT 15-JUN-1995

XX Antigen fragment 33, from HBV (a) has binding affinity for HLA-2.1.  
 DE  
 XX  
 KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV;  
 KW HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr;  
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2;  
 KW MAGE-1; melanoma antigen-1; core antigen; surface antigen;  
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic;  
 KW diagnostic; MHC class I molecule; major histocompatibility complex;  
 KW HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;  
 KW algorithm prediction; MBP; CMV; cytomegalovirus; HSV;  
 KW herpes simplex virus; influenza A; ML.

OS Hepatitis B virus.

XX WO9420127-A1.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

PR 04-JUN-1993; 93US-0073205.

PR 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

XX Grey HM, Kast WM, Sette A, Sidney J;

XX WPI; 1994-302678/37.

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used  
 PT for treatment or prophylaxis of cancer, virus infection or  
 PT autoimmune diseases.

XX Disclosure; Page 81; 138pp; English.

XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using  
 CC motifs disclosed in the invention, these peptides were screened for  
 CC further motifs. Only peptides with binding affinity of at least 1%  
 CC (binding affinity is expressed as an IC50 value) as compared to the  
 CC standard peptide (AAR71293) in assays. This peptide from the HBV ENV(a)  
 CC molecule has a binding value of 0.0580. The peptides of the  
 CC invention can induce cytotoxic T lymphocytes which can react with  
 CC target cells. They can be used for the treatment or prophylaxis of  
 CC cancer, eg. prostate cancer or lymphoma, etc.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 9 AA;

Query Match 66.7%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSV 4  
 Db 6 PQSV 9

## RESULT 29

AA55463  
 ID AAY55463 standard; peptide; 9 AA.

XX AC AAY55463;

XX 17-JAN-2000 (first entry)

XX HLA binding plu-1 peptide.

XX Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;  
 KW breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;  
 KW therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.

OS Synthetic.

OS Homo sapiens.

XX WO9949034-A1.

XX 30-SEP-1999.

XX 19-MAR-1999; 99WO-GB00866.

XX 20-MAR-1998; 98GB-0005877.

XX (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

XX Taylor-papadimitriou J;

XX WPI; 1999-591090/50.

XX New nucleic acid encoding the cancer-associated polypeptide plu-1, for  
 PT diagnosis, treatment and prevention of cancer, especially of breast and  
 PT ovary -

XX Example 2; Fig 12; 173pp; English.

XX The invention relates to a human cancer-associated polypeptide plu-1.  
 CC The plu-1 polypeptide can be recombinantly expressed by standard  
 CC recombinant methodology. Detection of the plu-1 nucleic acid or the  
 CC polypeptide is used for the following: (i) diagnosis (including imaging)  
 CC and prognosis of, and determination of susceptibility to, cancer,  
 CC specifically ovarian or breast cancer; and (ii) treating cancer (by  
 CC inducing an immune response against cancer cells, e.g. as a vaccine, or  
 CC by antisense inhibition). Antigens derived from the polypeptide are used  
 CC to generate activated cytotoxic T lymphocytes, or dendritic cells, for  
 CC subsequent return to the patient for treatment of cancer. The polypeptide  
 CC may also be used to identify inhibitors of plu-1 activity. Fragments of  
 CC the polypeptide, and antibodies raised against plu-1, are useful as assay  
 CC and imaging agents, also therapeutically (to induce an anti-idiotypic  
 CC response or where conjugated to cytotoxic agents). The plu-1 antigen is  
 CC expressed more commonly in breast tumors than some known tumor antigens.  
 CC Sequences AAY5320-629 represent predicted peptides from the plu-1  
 CC polypeptide which may bind to the human class I alleles B27, A2, A3 and  
 CC All.

XX Sequence 9 AA;

Query Match 66.7%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5

```

Db          |||||
            4 QSVL 7

RESULT 30
AAW92321
ID  AAW92321 standard; peptide; 9 AA.
XX
XX  AC  AAW92321;
XX
XX  DT  09-APR-1999 (first entry)
XX
XX  DE  E2A immunogenic peptide.
XX
XX  KW  E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;
XX  KW  epitope; acute lymphoblastic leukemia.
XX
XX  OS  Synthetic.
XX
XX  PN  US5858682-A.
XX
XX  PD  12-JAN-1999.
XX
XX  PF  02-AUG-1996; 96US-0691397.
XX
XX  PR  02-AUG-1996; 96US-0691997.
XX
XX  PA  (PHAR-) PHARMINGEN.
XX
XX  PI  Gruenwald S, Monell C, Sang B;
XX
XX  WPI; 1999-119870/10.
XX
XX  Monoclonal antibody specific for E2A/pbx1 fusion protein - useful
XX  for diagnosis of acute lymphoblastic leukemia
XX
XX  Example 2; Column 25-26; 21pp; English.
XX
XX  This sequence represents a peptide used in a method for constructing
XX  antigenic E2A/pbx1 fusion proteins used for raising monoclonal
XX  antibodies which specifically bind with an E2A/pbx1 fusion epitope. This
XX  peptide can be used for the diagnosis of acute lymphoblastic leukemia.
XX
SQ  Sequence 9 AA;
    Query Match 66.7%; Score 4; DB 20; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db  |||||
    4 SVLS 7

RESULT 31
ABP14476
ID  ABP14476 standard; Peptide; 9 AA.
XX
XX  AC  ABP14476;
XX
XX  DT  15-JUL-2002 (first entry)
XX
XX  DE  HIV A03 super motif gag peptide #38.
XX
XX  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX  vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX  antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX  Human immunodeficiency virus type 1.
XX
XX  WO200124810-A1.
XX
XX  12-APR-2001.
XX

XX 05-OCT-2000; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US-0412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 165; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
SQ  Sequence 9 AA;
    Query Match 66.7%; Score 4; DB 22; Length 9;
    Best Local Similarity 100.0%; Pred. No. 9.3e+05;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db  |||||
    3 SVLS 6

RESULT 32
ABP17821
ID  ABP17821 standard; Peptide; 9 AA.
XX
XX  AC  ABP17821;
XX
XX  DT  15-JUL-2002 (first entry)
XX
XX  DE  HIV B58 super motif gag peptide #40.
XX
XX  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX  vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX  antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX  Human immunodeficiency virus type 1.
XX
XX  WO200124810-A1.
XX
XX  12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX
XX

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PR 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 XX WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 234; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 2 SVLS 5  
 RESULT 33  
 ABP17918  
 ID ABP17918 standard; Peptide; 9 AA.  
 AC  
 XX ABP17918;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 XX HIV B58 super motif gag peptide #137.  
 DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 FN  
 XX 12-APR-2001.  
 PD  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX  
 PF 05-OCT-1999; 99US-0412863.  
 XX  
 PR (EPIM-) EPIMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 XX WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 234; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 XX WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 PS Claim 32; Page 236; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 2 SVLS 5  
 RESULT 34  
 ABP20722  
 ID ABP20722 standard; Peptide; 9 AA.  
 AC  
 XX ABP20722;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 XX HIV A03 motif gag peptide #385.  
 DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 FN  
 XX 12-APR-2001.  
 PD  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX  
 PF 05-OCT-1999; 99US-0412863.  
 XX  
 PR (EPIM-) EPIMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX Baker DM, Celis E, Kubo RT, Grey HM;  
 XX

XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PT  
 XX Claim 32; Page 294; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 9 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 3 SVLS 6  
 RESULT 35  
 ABP22869  
 ID ABP22869 standard; Peptide; 9 AA.  
 AC  
 XX ABP22869;  
 DT 15-JUL-2002 (first entry)  
 DE HIV A11 motif gag peptide #248.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS  
 XX WO200124810-A1.  
 PN 12-APR-2001.  
 PD  
 XX 05-OCT-2000; 2000WO-US27766.  
 PF  
 XX 05-OCT-1999; 99US-0412863.  
 PR (EPIM-) EPIMUNE INC.  
 PA  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HW;  
 XX WPI; 2001-354887/37.  
 DR  
 XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 337; 448pp; English.  
 PS The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 9 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 3 SVLS 6  
 RESULT 36  
 AAB73123  
 ID AAB73123 standard; Peptide; 9 AA.  
 XX  
 AC AAB73123;  
 XX 09-MAY-2001 (first entry)  
 DT  
 XX Tumour antigen peptide #7.  
 DE  
 XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200111044-A1.  
 PN 15-FEB-2001.  
 PD  
 XX 03-AUG-2000; 2000WO-JP05220.  
 PF  
 XX 05-AUG-1999; 99JP-0222101.  
 PR (ITOH/) ITOH K.  
 PA  
 XX Itoh K;  
 PI  
 XX WPI; 2001-191541/19.  
 DR  
 XX Tumor antigen peptides which induce tumor-specific cytotoxic T-cells  
 PT and polynucleotides encoding them for treatment of cancer -  
 XX Claim 1; Page 67; 75pp; Japanese.  
 PS  
 XX The present invention relates to peptides which are partial sequences of  
 CC

```

CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer.
XX
SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
DB |||||
6 QSVL 9

RESULT 37
AAB73124
ID AAB73124 standard; Peptide; 9 AA.
XX
AC AAB73124;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #8.
XX
XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX
OS Homo sapiens.
XX
PN WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP05220.
XX
PR 05-AUG-1999; 99JP-0222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
PT and polynucleotides encoding them for treatment of cancer -
XX
PS Claim 1; Page 67; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer.
XX
SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
DB |||||
6 QSVL 9

RESULT 38
AAB73125
ID AAB73125 standard; Peptide; 9 AA.
XX
AC AAB73125;
XX
DT 09-MAY-2001 (first entry)
XX
DE Tumour antigen peptide #9.

```

```

XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.
XX Homo sapiens.
XX WO200111044-A1.
XX
PD 15-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-JP05220.
XX
PR 05-AUG-1999; 99JP-0222101.
XX
PA (ITOH/) ITOH K.
XX
PI Itoh K;
XX
WPI; 2001-191541/19.
XX
PT Tumor antigen peptides which induce tumor-specific cytotoxic T-cells
PT and polynucleotides encoding them for treatment of cancer -
XX
PS Claim 1; Page 68; 75pp; Japanese.
XX
CC The present invention relates to peptides which are partial sequences of
CC src/lck family proteins. The present sequence is one such peptide. The
CC peptides are useful for producing vaccines for the treatment of cancer,
CC including colon cancer and small-cell lung cancer.
XX
SQ Sequence 9 AA;

Query Match 66.7%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
DB |||||
6 QSVL 9

RESULT 39
ABJ09400
ID ABJ09400 standard; Peptide; 9 AA.
XX
AC ABJ09400;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus analogue #12.
XX
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
XX virucide; hepatotropic; antiinflammatory.
XX
OS Hepatitis B virus.
XX
PN WO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000WO-US24802.
XX
PR 08-SEP-2000; 2000WO-US24802.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
XX Celis E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/69.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises

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Query Match 66.7%; Score 4; DB 17; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 2 SVLS 5

## RESULT 42

AAW82304  
ID AAW82304 standard; Peptide; 10 AA.

XX AC AAW82304;

XX DT 15-MAR-1999 (first entry)  
XX DE Transport peptide fragment.

XX KW Targetting agent; gastrointestinal tract; brain; drug delivery;  
XX KW drug targetting; phage display; transport peptide.  
XX OS Synthetic.

XX PN WO9851825-AL.

XX PD 19-NOV-1998.

XX PF 15-MAY-1998; 98WO-US10079.

XX PR 15-MAY-1997; 97US-0857046.

XX PA (CYTO-) CYTOGEN CORP.

XX PA (ELAN-) ELAN CORP PLC.

XX PI Alvarez VL, O'Mahony DJ, Seveso M;

XX WPI; 1998-009778/01.

XX PT New targeting agents enabling transport of active agents through human/animal tissue, or their uptake - useful in the treatment and prevention of diseases, especially of the gastro-intestinal tract (GIT)  
XX PS Claim 7; Page 66; 83pp; English.  
CC This is a fragment of peptide 28.1 (see AAW82290), a peptide isolated from a phage display library on the basis of its ability to enhance transport of phage from the rat gastrointestinal tract (GIT) to brain. Claimed transport or uptake targeting agents can include this, or other, claimed peptide fragments (see AAW82300-10). Such transport or targeting agents permit or facilitate the transport of an active agent through a human or animal tissue such as GIT lumen, or uptake of the active agent into the human or animal tissue. The active agent is preferably a drug or drug-containing nanoparticle or microparticle. Therapeutic methods of administration, pharmaceutical compositions and formulations based on the targeting peptides are also provided.

XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 20; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5

Db 2 QSVL 5

## RESULT 43

ABP11686

ID ABP11686 standard; Peptide; 10 AA.

XX AC ABP11686;

XX DT 15-JUL-2002 (first entry)

XX DE HIV A01 super motif gag peptide #58.

XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.  
XX OS Human immunodeficiency virus type 1.

XX PN WO200124810-A1.

XX PD 12-APR-2001.

XX PF 05-OCT-2000; 2000WO-US27766.

XX PR 05-OCT-1999; 99US-0412863.

XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Celis E, Kubo RT, Grey HW;

XX WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -  
XX PS Claim 32; Page 108; 448pp; English.  
CC The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB225347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX SQ

Sequence 10 AA;

Query Match

Best Local Similarity

Matches

4; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

3 SVLS 6

Db

1 SVLS 4

RESULT 44

ABP12769

ID

ABP12769 standard; Peptide; 10 AA.

XX AC

ABP12769;

Query Match

Best Local Similarity

Matches

4; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

3 SVLS 6

Db

1 SVLS 4

RESULT 44

ABP12769

ID

ABP12769 standard; Peptide; 10 AA.

XX AC

ABP12769;

XX 15-JUL-2002 (first entry)  
 XX HIV A02 super motif gag peptide #240.  
 DE HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 KW Human immunodeficiency virus type 1.  
 XX OS WO200124810-A1.  
 XX PN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.  
 XX PR (EPIM-) EPIMUNE INC.  
 XX PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 130; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 3 SVLS 6  
 RESULT 45  
 ABP12770  
 ID ABP12770 standard; Peptide; 10 AA.  
 XX AC ABP12770;  
 XX ABP12770;  
 XX 15-JUL-2002 (first entry)  
 XX HIV A02 super motif gag peptide #242.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

DE HIV A02 super motif gag peptide #241.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX OS Human immunodeficiency virus type 1.  
 XX PN WO200124810-A1.  
 XX PD 12-APR-2001.  
 XX PF 05-OCT-2000; 2000WO-US27766.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 130; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 3 SVLS 6  
 RESULT 46  
 ABP12771  
 ID ABP12771 standard; Peptide; 10 AA.  
 XX AC ABP12771;  
 XX ABP12771;  
 XX 15-JUL-2002 (first entry)  
 XX HIV A02 super motif gag peptide #242.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;

KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 XX 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 130; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 10 AA;  
 XX Query Match 66.7%; Score 4; DB 22; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db ||||  
 1 SVLS 4  
 RESULT 47  
 ABP15694  
 ID ABP15694 standard; Peptide; 10 AA.  
 XX  
 AC ABP15694;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A24 super motif gag peptide #180.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX

OS Human immunodeficiency virus type 1.  
 XX WO200124810-A1.  
 XX 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 190; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABU25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX SQ Sequence 10 AA;  
 XX Query Match 66.7%; Score 4; DB 22; Length 10;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db ||||  
 1 SVLS 4  
 RESULT 48  
 ABP17825  
 ID ABP17825 standard; Peptide; 10 AA.  
 XX  
 AC ABP17825;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV B58 super motif gag peptide #44.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 XX

XX 12-APR-2001.  
 PD 05-OCT-2000; 2000WO-US27766.  
 PF 05-OCT-1999; 99US-0412863.  
 XX 05-OCT-1999; 99US-0412863.  
 PR (EPIM-) EPIMMUNE INC.  
 PA Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1 -  
 PT Claim 32; Page 234; 448pp; English.  
 PS The present invention describes a composition (I) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db 3 SVLS 6  
 RESULT 49  
 ABP17919  
 ID ABP17919 standard; Peptide; 10 AA.  
 XX AC ABP17919;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV B58 super motif gag peptide #138.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 XX PN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX PS The present invention describes a composition (I) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db 3 SVLS 6  
 RESULT 50  
 ABP20530  
 ID ABP20530 standard; Peptide; 10 AA.  
 XX AC ABP20530;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A03 motif gag peptide #193.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 XX PN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.  
 XX PR 05-OCT-1999; 99US-0412863.

PF 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIMMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 XX peptide groups, useful for vaccinating against HIV-1 -  
 PT Claim 32; Page 236; 448pp; English.  
 PS The present invention describes a composition (I) comprising a prepared  
 XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db 3 SVLS 6  
 RESULT 50  
 ABP20530  
 ID ABP20530 standard; Peptide; 10 AA.  
 XX AC ABP20530;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A03 motif gag peptide #193.  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 OS WO200124810-A1.  
 XX PN 12-APR-2001.  
 XX PD 05-OCT-2000; 2000WO-US27766.  
 XX PF 05-OCT-1999; 99US-0412863.

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XX PA (EPIM-) EPIMUNE INC.
XX PI
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX DR WPI; 2001-354887/37.
XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 290; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 1 SVLS 4

RESULT 51
ABP20539
ID ABP20539 standard; Peptide; 10 AA.
XX AC
XX AC ABP20539;
XX DT 15-JUL-2002 (first entry)
XX DE HIV A03 motif gag peptide #202.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

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PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
DR WPI; 2001-354887/37.
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PT peptide groups, useful for vaccinating against HIV-1 -
XX PS Claim 32; Page 290; 448pp; English.
XX CC The present invention describes a composition (I) comprising a prepared
XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to
XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC may be used for immunising subjects against HIV-1 infections. The use of
XX CC group-based vaccines has several advantages over traditional vaccines,
XX CC particularly when compared to the use of whole antigens in vaccine
XX CC compositions. There is evidence that the immune response to whole
XX CC antigens is directed largely toward variable regions of the antigen,
XX CC allowing for immune escape due to mutations. The groups for inclusion in
XX CC an group-based vaccine may be selected from conserved regions of viral or
XX CC tumour-associated antigens, which therefore reduces the likelihood of
XX CC escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC in whole antigens can be avoided with the use of group-based vaccines.
XX CC An additional advantage of an group-based vaccine approach is the ability
XX CC to combine selected groups (CTL and HTL), and further, to modify the
XX CC composition of the groups, achieving, for example, enhanced
XX CC immunogenicity. Accordingly, the immune response can be modulated, as
XX CC appropriate, for the target disease. Similar engineering of the response
XX CC is not possible with traditional approaches. ABP1501 to ABP25412
XX CC represent peptide sequences used in the exemplification of the present
XX CC invention.
XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
DB 2 SVLS 5

RESULT 52
ABP20716
ID ABP20716 standard; Peptide; 10 AA.
XX AC
XX AC ABP20716;
XX DT 15-JUL-2002 (first entry)
XX DE HIV A03 motif gag peptide #379.
XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX KW antigen; vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus type 1.
XX PN WO200124810-A1.
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000WO-US27766.
XX PR 05-OCT-1999; 99US-0412863.
XX PA (EPIM-) EPIMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

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DR WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 XX Claim 32; Page 294; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 5 SVLS 8  
 RESULT 53  
 ID ABP22863  
 XX ABP22863 standard; Peptide; 10 AA.  
 AC  
 XX ABP22863;  
 AC  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX HIV A11 motif gag peptide #242.  
 DE  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 FN WO200124810-A1.  
 PD  
 XX 12-APR-2001.  
 PD  
 XX 05-OCT-2000; 2000WO-US27766.  
 PF  
 XX 05-OCT-1999; 99US-0412863.  
 PR  
 XX (EPIM-) EPIMMUNE INC.  
 PA  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 DR  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1 -  
 XX Claim 32; Page 337; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX Sequence 10 AA;  
 SQ  
 Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db |||||  
 5 SVLS 8  
 RESULT 54  
 ID AAG99453  
 XX AAG99453 standard; Peptide; 10 AA.  
 AC  
 XX AAG99453;  
 AC  
 XX 01-OCT-2001 (first entry)  
 DT  
 XX PRAME derived HLA-A\*0201 binding peptide SEQ ID NO: 95.  
 DE  
 XX Vaccine; immune response; T cell response; epitope; proteasome;  
 KW cancer; infection.  
 KW  
 XX Unidentified.  
 OS  
 XX EP1118860-A1.  
 FN  
 XX 25-JUL-2001.  
 PD  
 XX 21-JAN-2000; 2000EP-0200242.  
 PF  
 XX 21-JAN-2000; 2000EP-0200242.  
 PR  
 XX (UYLE-) RIJKSUNIV LEIDEN.  
 PA (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.  
 XX  
 PI Ossendorp F, Offringa R, Melief CJM, Kessler JH;  
 XX WPI; 2001-427158/46.  
 DR  
 XX Selecting and/or producing a T cell epitope useful in a vaccine  
 PT comprises subjecting a precursor peptide or polypeptide to the action  
 PT of a 20S proteasome to determine the location of the C-terminus -  
 XX  
 PS Disclosure; Page 53; 102pp; English.

XX The present invention describes a method of producing T cell epitopes,  
CC involving subjecting a precursor peptide to the action of a 20S  
CC proteasome, in order to locate the C-terminus of said epitope. This can  
CC be used in the production of vaccines, which can then be used to provoke  
CC a T cell response in the treatment of diseases such as cancer and  
CC infections. The present sequence is a peptide described in the  
CC exemplification of the invention.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 3 SVLS 6  
  
RESULT 55  
AAG95614  
ID AAG95614 standard; Peptide; 10 AA.  
XX AC AAG95614;  
XX DT 18-SEP-2001 (first entry)  
XX DE Human complementary peptide, SEQ ID NO: 1808.  
XX KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX OS Homo sapiens.  
XX PN WO200142277-A2.  
XX PD 14-JUN-2001.  
XX PF 13-DEC-2000; 2000WO-GB04776.  
XX PR 13-DEC-1999; 99GB-0029464.  
XX PA (PROT-) PROTEOM LTD.  
XX PI Roberts GW, Heal JR;  
XX DR WPI; 2001-408419/43.  
XX  
PT A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -  
XX  
XX Example 4; Page 301; 646pp; English.  
XX CC The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 4 SVLS 7  
  
RESULT 56  
AAG95616  
ID AAG95616 standard; Peptide; 10 AA.  
XX AC AAG95616;  
XX DT 18-SEP-2001 (first entry)  
XX DE Human complementary peptide, SEQ ID NO: 1810.  
XX KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX OS Homo sapiens.  
XX PN WO200142277-A2.  
XX PD 14-JUN-2001.  
XX PF 13-DEC-2000; 2000WO-GB04776.  
XX PR 13-DEC-1999; 99GB-0029464.  
XX PA (PROT-) PROTEOM LTD.  
XX PI Roberts GW, Heal JR;  
XX DR WPI; 2001-408419/43.  
XX  
PT A set of peptide ligands consisting of specific complementary peptides  
PT to proteins encoded by genes of the human genome, useful in an assay  
PT for screening and identifying of one or more novel peptides which are  
PT drug candidates or pro-drugs -  
XX  
XX Example 4; Page 301; 646pp; English.  
XX CC The invention relates to a set of complementary peptide ligands  
CC generated from the human genome. The complementary peptides  
CC interact with their relevant target proteins encoded in the human  
CC genome. They can be used as reagents in drug discovery and as lead  
CC ligands to facilitate drug design and development. The present  
CC sequence is a complementary peptide provided in the specification.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 5 SVLS 8  
  
RESULT 57  
AAG85693  
ID AAG85693 standard; Peptide; 10 AA.  
XX AC AAG85693;  
XX DT 11-SEP-2001 (first entry)  
XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 642.  
XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX OS Saccharomyces cerevisiae.  
XX PN WO200142276-A1.  
XX PD 14-JUN-2001.  
XX PR 13-DEC-2000; 2000WO-GB04773.

XX The present invention describes a method of producing T cell epitopes,  
CC involving subjecting a precursor peptide to the action of a 20S  
CC proteasome, in order to locate the C-terminus of said epitope. This can  
CC be used in the production of vaccines, which can then be used to provoke  
CC a T cell response in the treatment of diseases such as cancer and  
CC infections. The present sequence is a peptide described in the  
CC exemplification of the invention.  
XX  
SQ Sequence 10 AA;  
  
Query Match 66.7%; Score 4; DB 22; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 SVLS 6  
Db 5 SVLS 8  
  
RESULT 57  
AAG85693  
ID AAG85693 standard; Peptide; 10 AA.  
XX AC AAG85693;  
XX DT 11-SEP-2001 (first entry)  
XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 642.  
XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;  
XX drug discovery; drug design.  
XX OS Saccharomyces cerevisiae.  
XX PN WO200142276-A1.  
XX PD 14-JUN-2001.  
XX PR 13-DEC-2000; 2000WO-GB04773.



XX PR 13-DEC-1999; 99GB-0029471.  
 XX PA (PROT-) PROTEOM LTD.  
 XX PI Roberts GW, Heal JR;  
 XX DR WPI; 2001-367863/38.  
 XX PT Identifying complementary peptides by analysis of protein and  
 PT nucleotide sequence databases, useful in drug design -  
 XX Example 3; Page 118; 488pp; English.  
 XX CC The invention relates to the identification of complementary peptides  
 CC by analysis of protein and nucleotide sequence databases from higher  
 CC eukaryotic genomes, excluding human and plants. The specific  
 CC complementary peptides interact with their relevant target proteins  
 CC encoded in the eukaryote genome. The peptides may be used as reagents  
 CC and drugs for drug discovery and as lead ligands for drug design and  
 CC development. The present sequence is a complementary peptide from  
 CC Saccharomyces cerevisiae.  
 XX SQ Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 DB 1 SVLS 4  
 RESULT 58  
 ABJ19987  
 ID ABJ19987 standard; Peptide; 10 AA.  
 AC ABJ19987;  
 XX DT 10-APR-2003 (first entry)  
 XX DE MHC binding peptide SEQ ID No 152.  
 XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;  
 KW antiinflammatory; major histocompatibility complex; MHC;  
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;  
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;  
 KW inflammation; gene therapy; MHC binding peptide.  
 XX OS Synthetic.  
 XX PN WO200294981-A2.  
 XX PD 28-NOV-2002.  
 XX PF 16-MAY-2002; 2002WO-IL00383.  
 XX PR 16-MAY-2001; 2001US-290958P.  
 XX PR 29-MAY-2001; 2001US-0865548.  
 XX PA (TECR ) TECHNTION RES & DEV FOUND LTD.  
 XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;  
 XX DR WPI; 2003-210043/20.  
 XX PT Identifying peptides that are capable of binding to major  
 PT histocompatibility complex (MHC) molecules of a particular haplotype by  
 PT analyzing peptides bound to the soluble and secreted form of the MHC  
 PT molecules of the particular haplotype -  
 XX Claim 37; Page 183; 238pp; English.

XX CC The invention relates to a novel method for identifying peptides  
 CC originating from a particular cell type, which are capable of binding to  
 CC major histocompatibility complex (MHC) molecules of a particular  
 CC haplotype. The method comprises analysing peptides bound to the soluble  
 CC and secreted form of the MHC molecules of the particular haplotype. The  
 CC method is useful for identifying peptides for treating an autoimmune  
 CC disease, such as T or B cell and/or allergic disease or condition,  
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,  
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The  
 CC sequences of the invention may be used in a gene therapy application.  
 CC This sequence represents a peptide relating to the method for identifying  
 CC MHC binding peptides of the invention.  
 XX SQ Sequence 10 AA;  
 SQ Query Match 66.7%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 DB 5 SVLS 8  
 RESULT 59  
 ABJ19627  
 ID ABJ19627 standard; Peptide; 10 AA.  
 XX AC ABJ19627;  
 XX DT 03-APR-2003 (first entry)  
 XX DE Neuronal nitric oxide synthase related peptide fragment SEQ ID No 85.  
 XX KW Antidiabetic; neuronal nitric oxide synthase; nNOS; enzyme; PIN;  
 KW inhibitor; insulin response; prediabetic; hyperinsulinic;  
 KW type 2 diabetes; rat.  
 XX OS Synthetic.  
 XX PN WO200283936-A2.  
 XX PD 24-OCT-2002.  
 XX PF 17-APR-2002; 2002WO-FR01327.  
 XX PR 18-APR-2001; 2001FR-0005248.  
 XX PA (INNO-) INNODIA.  
 XX PI Gross R, Lajoix A, Ribes G;  
 XX DR WPI; 2003-111816/10.  
 XX PT Identifying compounds that modulate interaction of neuronal nitric  
 PT oxide synthase and its inhibitor, useful e.g. for treating prediabetic  
 PT states -  
 XX PS Claim 10; Page 43; 89pp; French.  
 XX CC The invention relates to a novel method for detecting compounds that  
 CC modulate the complexation between neuronal nitric oxide synthase (nNOS)  
 CC and the inhibitor of nNOS (PIN). The nNOS protein comprises a 1429 amino  
 CC acid sequence, fully defined in the specification, or its variants. The  
 CC nNOS protein, its peptide fragments identified by the new method, and the  
 CC compound 1-(4-ethoxyphenyl)-5-(5-(benzimidazol-2-ylthio)-fur-2-  
 CC ylmethylidene)-hexahydropyrimidin-2,4,6-trione are used to treat altered  
 CC insulin responses in prediabetic and hyperinsulinic states, and in  
 CC subjects with type 2 diabetes. This sequence represents an nNOS peptide  
 CC fragment relating to the invention.  
 XX SQ Sequence 10 AA;

Query Match 66.7%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 4 SVLS 7

## RESULT 60

AAR67271  
 ID AAR67271 standard; peptide; 11 AA.

XX AC AAR67271;

XX 27-JUL-1995 (first entry)

XX Ubiquitin peptide extension, CRAS.

XX Ubiquitin; peptide extension; assay; protein kinase; C-terminal;  
 KW Ha-RAS protein; farnesyl-protein transferase;  
 KW carboxy methyl transferase.

XX OS Synthetic.

XX PN US5366871-A.

XX XX 22-NOV-1994.

XX PF 13-NOV-1991; 91US-0791935.

XX PR 13-NOV-1991; 91US-0791935.

XX PA (UTAH ) UNIV UTAH.

XX PI Rechsteiner MC, Yoo YJ;

XX DR WPI; 1995-005826/01.

XX DR N-PSDB; AAQ75292.

XX Assay for enzymes that modify peptide chains - using a substrate  
 PT comprising a ubiquitin-peptide extension contg. a sequence  
 PT modified by the enzyme

XX PS Example 1; Column 8; 14pp; English.

XX CC This sequence represents a ubiquitin-peptide extension which is used  
 CC in the method of the invention for assaying enzymes that modify peptide  
 CC chains. This peptide sequence represents an extension which is known  
 CC to be modified in the presence of an enzyme being assayed for, and the  
 CC reaction mixture formed is then analysed. This method may be used for  
 CC assaying protein kinases or enzymes which modify the C-terminal end of  
 CC Ha-RAS protein, such as farnesyl-protein transferase, or carboxy methyl  
 CC transferase. Peptides such as this are less expensive to synthesise  
 CC than standard peptides used in these methods and they may be purified  
 CC from bacterial extracts by simple acid extraction.

XX SQ Sequence 11 AA;

Query Match 66.7%; Score 4; DB 16; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 8 SVLS 11

## RESULT 61

AAR67272  
 ID AAR67272 standard; peptide; 11 AA.

XX

AC AAR67272;

XX 27-JUL-1995 (first entry)

XX Ubiquitin peptide extension, Ha-RAS.

XX Ubiquitin; peptide extension; assay; protein kinase; C-terminal;  
 KW Ha-RAS protein; farnesyl-protein transferase;  
 KW carboxy methyl transferase.

XX OS Synthetic.

XX PN US5366871-A.

XX PD 22-NOV-1994.

XX PF 13-NOV-1991; 91US-0791935.

XX PR 13-NOV-1991; 91US-0791935.

XX PA (UTAH ) UNIV UTAH.

XX PI Rechsteiner MC, Yoo YJ;

XX DR WPI; 1995-005826/01.

XX Assay for enzymes that modify peptide chains - using a substrate  
 PT comprising a ubiquitin-peptide extension contg. a sequence  
 PT modified by the enzyme

XX PS Example 1; Column 9; 14pp; English.

XX CC This sequence represents a ubiquitin-peptide extension which is used  
 CC in the method of the invention for assaying enzymes that modify peptide  
 CC chains. This peptide sequence represents an extension which is known  
 CC to be modified in the presence of an enzyme being assayed for, and the  
 CC reaction mixture formed is then analysed. This method may be used for  
 CC assaying protein kinases or enzymes which modify the C-terminal end of  
 CC Ha-RAS protein, such as farnesyl-protein transferase, or carboxy methyl  
 CC transferase. Peptides such as this are less expensive to synthesise  
 CC than standard peptides used in these methods and they may be purified  
 CC from bacterial extracts by simple acid extraction.

XX SQ Sequence 11 AA;

Query Match 66.7%; Score 4; DB 16; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
 Db 8 SVLS 11

## RESULT 62

AAB56247  
 ID AAB56247 standard; Protein; 11 AA.

XX AC AAB56247;

XX 13-MAR-2001 (first entry)

XX Human secreted protein sequence encoded by gene 17 SEQ ID NO.341.

XX Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;  
 KW antineumatic; antiproliferative; cytostatic; cardiant; vasotropic;  
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;  
 KW fungicide; ophthalmological; gene therapy; pathological condition;  
 KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
 KW neoplasm; cardiovascular disorder; cardiac arrest; cerebral ischaemia;  
 KW cerebrovascular disorder; angiogenesis; nervous system disorder;  
 KW Alzheimer's disease; infection; ocular disorder; corneal infection;  
 KW wound healing; skin aging; food additive; preservative.

XX OS	Human immunodeficiency virus type 1.	OS	Human immunodeficiency virus type 1.
XX FN	WO200124810-A1.	XX FN	WO200124810-A1.
XX PD	12-APR-2001.	XX PD	12-APR-2001.
XX PF	05-OCT-2000; 2000WO-US27766.	XX PF	05-OCT-2000; 2000WO-US27766.
XX PR	05-OCT-1999; 99US-0412863.	XX PR	05-OCT-1999; 99US-0412863.
XX PA	(EPIM-) EPIMMUNE INC.	XX PA	(EPIM-) EPIMMUNE INC.
XX PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;	XX PI	Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI	Baker DM, Celis E, Kubo RT, Grey HM;	XX PI	Baker DM, Celis E, Kubo RT, Grey HM;
XX DR	WPI; 2001-354887/37.	XX DR	WPI; 2001-354887/37.
XX PT	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)	XX PT	Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX PS	Claim 32; Page 166; 448pp; English.	XX PS	Claim 32; Page 166; 448pp; English.
XX CC	The present invention describes a composition (I) comprising a prepared	XX CC	The present invention describes a composition (I) comprising a prepared
XX CC	human immunodeficiency virus-1 (HIV-1) group comprising an amino acid	XX CC	human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX CC	sequence selected from 51 defined amino acid sequences (AB25347 to	XX CC	sequence selected from 51 defined amino acid sequences (AB25347 to
XX CC	AB25397). (I) has virucide activity and can be used in vaccines. (I)	XX CC	AB25397). (I) has virucide activity and can be used in vaccines. (I)
XX CC	may be used for immunising subjects against HIV-1 infections. The use of	XX CC	may be used for immunising subjects against HIV-1 infections. The use of
XX CC	group-based vaccines has several advantages over traditional vaccines,	XX CC	group-based vaccines has several advantages over traditional vaccines,
XX CC	particularly when compared to the use of whole antigens in vaccine	XX CC	particularly when compared to the use of whole antigens in vaccine
XX CC	compositions. There is evidence that the immune response to whole	XX CC	compositions. There is evidence that the immune response to whole
XX CC	antigens is directed largely toward variable regions of the antigen,	XX CC	antigens is directed largely toward variable regions of the antigen,
XX CC	allowing for immune escape due to mutations. The groups for inclusion in	XX CC	allowing for immune escape due to mutations. The groups for inclusion in
XX CC	an group-based vaccine may be selected from conserved regions of viral or	XX CC	an group-based vaccine may be selected from conserved regions of viral or
XX CC	tumour-associated antigens, which therefore reduces the likelihood of	XX CC	tumour-associated antigens, which therefore reduces the likelihood of
XX CC	escape mutants. Furthermore, immunosuppressive groups that may be present	XX CC	escape mutants. Furthermore, immunosuppressive groups that may be present
XX CC	in whole antigens can be avoided with the use of group-based vaccines.	XX CC	in whole antigens can be avoided with the use of group-based vaccines.
XX CC	An additional advantage of an group-based vaccine approach is the ability	XX CC	An additional advantage of an group-based vaccine approach is the ability
XX CC	to combine selected groups (CTL and HTL), and further, to modify the	XX CC	to combine selected groups (CTL and HTL), and further, to modify the
XX CC	composition of the groups, achieving, for example, enhanced	XX CC	composition of the groups, achieving, for example, enhanced
XX CC	immunogenicity. Accordingly, the immune response can be modulated, as	XX CC	immunogenicity. Accordingly, the immune response can be modulated, as
XX CC	appropriate, for the target disease. Similar engineering of the response	XX CC	appropriate, for the target disease. Similar engineering of the response
XX CC	is not possible with traditional approaches. ABP1501 to ABP25412	XX CC	is not possible with traditional approaches. ABP1501 to ABP25412
XX CC	represent peptide sequences used in the exemplification of the present	XX CC	represent peptide sequences used in the exemplification of the present
XX CC	invention.	XX CC	invention.
XX SQ	Sequence 11 AA;	XX SQ	Sequence 11 AA;
<hr/>			
XX	Query Match	66.7%; Score 4; DB 22; Length 11;	
XX	Best Local Similarity	100.0%; Pred. No. 2.9e+02;	
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3 SVLS 6		
DB	5 SVLS 8		
<hr/>			
XX	RESULT 64		
XX	ABP17201		
XX	ID	ABP17201 standard; Peptide; 11 AA.	
XX	AC	ABP17201;	
XX	DT	15-JUL-2002 (first entry)	
XX	DE	HIV B27 super motif gag peptide #77.	
XX	KW	HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;	
XX	KW	vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;	
XX	KW	antigen; vaccine; HIV infection; immunisation; virucide.	
XX	OS	Human immunodeficiency virus type 1.	
XX	FN	WO200124810-A1.	
<hr/>			
XX OS	Homo sapiens.	OS	Homo sapiens.
XX FN	WO200070042-A1.	XX FN	WO200070042-A1.
XX PD	23-NOV-2000.	XX PD	23-NOV-2000.
XX PF	11-MAY-2000; 2000WO-US12788.	XX PF	11-MAY-2000; 2000WO-US12788.
XX PR	13-MAY-1999; 99US-0134068.	XX PR	13-MAY-1999; 99US-0134068.
XX PA	(HUMA-) HUMAN GENOME SCI INC.	XX PA	(HUMA-) HUMAN GENOME SCI INC.
XX PI	Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;	XX PI	Rosen CA, Ruben SM, Moore PA, Young PE, Komatsoulis GA, Birse CE;
XX PI	Duan RD, Florence KA, Soppet DR;	XX PI	Duan RD, Florence KA, Soppet DR;
XX DR	WPI; 2000-679828/66.	XX DR	WPI; 2000-679828/66.
XX PT	Isolated nucleic acid molecule encoding a human secreted protein is	XX PT	Isolated nucleic acid molecule encoding a human secreted protein is
XX PS	used in preventing, treating or ameliorating a medical condition -	XX PS	used in preventing, treating or ameliorating a medical condition -
XX CC	Disclosure; Page 1012; 1065pp; English.	XX CC	Disclosure; Page 1012; 1065pp; English.
XX CC	The polynucleotide sequences given in AAC99818 to AAC99977 encode the	XX CC	The polynucleotide sequences given in AAC99818 to AAC99977 encode the
XX CC	human secreted proteins given in AAB56077 to AAB56362. Human secreted	XX CC	human secreted proteins given in AAB56077 to AAB56362. Human secreted
XX CC	proteins have activities based on the tissues and cells the genes are	XX CC	proteins have activities based on the tissues and cells the genes are
XX CC	expressed in. Examples of activities include: immunosuppressive;	XX CC	expressed in. Examples of activities include: immunosuppressive;
XX CC	antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;	XX CC	antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
XX CC	vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;	XX CC	vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
XX CC	virucide; fungicide; and ophthalmological. The human secreted	XX CC	virucide; fungicide; and ophthalmological. The human secreted
XX CC	polynucleotides and proteins can be used to prevent, treat or ameliorate	XX CC	polynucleotides and proteins can be used to prevent, treat or ameliorate
XX CC	a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,	XX CC	a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX CC	dogs, chickens or sheep. They are also used in diagnosing a pathological	XX CC	dogs, chickens or sheep. They are also used in diagnosing a pathological
XX CC	condition or susceptibility to a pathological condition. Disorders which	XX CC	condition or susceptibility to a pathological condition. Disorders which
XX CC	are diagnosed or treated include autoimmune diseases e.g. rheumatoid	XX CC	are diagnosed or treated include autoimmune diseases e.g. rheumatoid
XX CC	arthritis, hyperproliferative disorders e.g. neoplasms of the breast or	XX CC	arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
XX CC	liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular	XX CC	liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
XX CC	disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders	XX CC	disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders
XX CC	e.g. Alzheimer's disease, infections caused by bacteria, viruses and	XX CC	e.g. Alzheimer's disease, infections caused by bacteria, viruses and
XX CC	fungi and ocular disorders e.g. corneal infection. The proteins can also	XX CC	fungi and ocular disorders e.g. corneal infection. The proteins can also
XX CC	be used to aid wound healing and epithelial cell proliferation, to	XX CC	be used to aid wound healing and epithelial cell proliferation, to
XX CC	prevent skin aging due to sunburn, to maintain organs before	XX CC	prevent skin aging due to sunburn, to maintain organs before
XX CC	transplantation, for supporting cell culture of primary tissues, to	XX CC	transplantation, for supporting cell culture of primary tissues, to
XX CC	regenerate tissues and in chemotaxis. The proteins can also be used as a	XX CC	regenerate tissues and in chemotaxis. The proteins can also be used as a
XX CC	food additive or preservative to increase or decrease storage	XX CC	food additive or preservative to increase or decrease storage
XX CC	capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used	XX CC	capabilities. AAC99809 to AAC99817 and AAB56076 represent sequences used
XX CC	in the exemplification of the present invention.	XX CC	in the exemplification of the present invention.
XX SQ	Sequence 11 AA;	XX SQ	Sequence 11 AA;
<hr/>			
XX	Query Match	66.7%; Score 4; DB 21; Length 11;	
XX	Best Local Similarity	100.0%; Pred. No. 2.9e+02;	
XX	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	3 SVLS 6		
DB	8 SVLS 11		
<hr/>			
XX	RESULT 63		
XX	ABP14552		
XX	ID	ABP14552 standard; Peptide; 11 AA.	
XX	AC	ABP14552;	
XX	DT	15-JUL-2002 (first entry)	
XX	DE	HIV A03 super motif gag peptide #14.	
XX	KW	HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;	
XX	KW	vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;	
XX	KW	antigen; vaccine; HIV infection; immunisation; virucide.	



XX PA (EPIM-) EPIMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-354887/37.

XX PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

XX PT peptide groups, useful for vaccinating against HIV-1 -

XX PS Claim 32; Page 254; 448pp; English.

XX CC The present invention describes a composition (I) comprising a prepared

XX CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

XX CC sequence selected from 51 defined amino acid sequences (ABL25347 to

XX CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)

XX CC may be used for immunising subjects against HIV-1 infections. The use of

XX CC group-based vaccines has several advantages over traditional vaccines,

XX CC particularly when compared to the use of whole antigens in vaccine

XX CC compositions. There is evidence that the immune response to whole

XX CC antigens is directed largely toward variable regions of the antigen,

XX CC allowing for immune escape due to mutations. The groups for inclusion in

XX CC an group-based vaccine may be selected from conserved regions of viral or

XX CC tumour-associated antigens, which therefore reduces the likelihood of

XX CC escape mutants. Furthermore, immunosuppressive groups that may be present

XX CC in whole antigens can be avoided with the use of group-based vaccines.

XX CC An additional advantage of an group-based vaccine approach is the ability

XX CC to combine selected groups (CTL and HTL), and further, to modify the

XX CC composition of the groups, achieving, for example, enhanced

XX CC immunogenicity. Accordingly, the immune response can be modulated, as

XX CC appropriate, for the target disease. Similar engineering of the response

XX CC is not possible with traditional approaches. ABL1501 to ABP25412

XX CC represent peptide sequences used in the exemplification of the present

XX CC invention.

XX SQ Sequence 11 AA;

Query Match 66.7%; Score 4; DB 22; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 1 SVLS 4

RESULT 67

AAW80388

ID AAW80388 standard; Peptide; 12 AA.

XX AC AAW80388;

XX DT 14-JAN-1999 (first entry)

XX DE Peptide eluted after biopanning against maltose binding protein.

XX KW Intervening protein sequence; IVPS; protein splicing;

XX KW protein production; maltose binding protein.

XX OS Synthetic.

XX PN US5834247-A.

XX PD 10-NOV-1998.

XX PF 05-MAR-1997; 97US-0811492.

XX PR 05-MAR-1997; 97US-0811492.

XX PR 09-DEC-1992; 92US-0004139.

XX PR 03-NOV-1993; 93US-0146885.

XX PR 28-JUN-1995; 95US-0496247.

XX PR 29-DEC-1995; 95US-0580555.

XX PA (NEWE ) NEW ENGLAND BIOLABS INC.

XX PI Adam E, Chong SSC, Comb DG, Hodges RA, Jack WE;

XX PI Noren CJ, Perler FB, Southworth M, Xu M;

XX DR WPI; 1999-008713/01.

XX PT New modified target proteins - which have controllable intervening

XX PT protein sequence which can facilitate production, purification,

XX PT labelling or isolation of target proteins

XX PS Example 22; Fig 36; 123pp; English.

XX CC AAW80372-93 represent peptides eluted after biopanning against

XX CC maltose binding protein, in the course of the invention. The

XX CC specification describes IVPS (intervening protein sequence)

XX CC regions which encode peptides which are removed via protein

XX CC splicing to form the native protein. The specification describes

XX CC a modified protein comprising a target protein or portion, fused

XX CC either internally or terminally, to a IVPS, or to an amino- or

XX CC carboxyl-terminal element of a IVPS. The IVPS are capable of

XX CC excision from or cleavage of the modified protein upon predetermined

XX CC conditions, in cis or trans, e.g. temperature increase, deglycosylation,

XX CC unblocking of amino acid residues, treatment with chemical reagents.

XX CC The methods can be used for modifying, producing, purifying, labelling

XX CC or isolating target proteins such as enzymes, toxins, cytokines,

XX CC glycoproteins and growth factors.

XX SQ Sequence 12 AA;

Query Match 66.7%; Score 4; DB 20; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6

Db 7 SVLS 10

RESULT 68

AAW806328

ID AAW806328 standard; peptide; 12 AA.

XX AC AAW806328;

XX DT 03-OCT-2000 (first entry)

XX DE Sterol-regulatory element-binding protein 2 10mer.

XX KW Sterol-regulatory element-binding protein 2; SREBP-2;

XX KW subtilisin-kexin isoenzyme 1; SKI-1;

XX KW pro-brain-derived neurotrophic factor; proBDNF; antilipaeamic;

XX KW cytosstatic; vasotropic; SKI-1 inhibitor; hypercholesterolaemia;

XX KW liver steatosis; Ras-dependent cancer; restenosis;

XX KW amyloid protein formation.

XX OS Mammalia.

XX OS Synthetic.

XX PN WO2000026348-A2.

XX PD 11-MAY-2000.

XX PF 04-NOV-1999; 99WO-CA01058.

XX PR 04-NOV-1998; 98CA-2249648.

XX PR (RECL-) INST RECH CLINIQUES MONTREAL.

XX PA Seidah N, Chretien M, Marcinkiewicz M, Laaksonen R, Davignon J;

XX PI WPI; 2000-365601/31.

XX Novel soluble proteic fragment of subtilisin-kexin isoenzyme for  
 PT producing a polypeptide useful for treating hypercholesterolemia, liver  
 PT steatosis and amyloidosis, comprises a specific amino acid se  
 XX  
 PS Example 6; Page 53; 119pp; English.  
 XX  
 CC The present sequence is a 10mer of sterol-regulatory element-binding  
 CC protein 2 (SREBP-2), which is cleaved by subtilisin-kexin isoenzyme 1  
 CC (SKI-1), a type-1 membrane-bound proteinase. Fluorescence resonance  
 CC energy transfer (FRET)-based proteolysis assays were performed on a large  
 CC number of synthetic peptides based on potential cleavage sites in the  
 CC SKI-1 prodomain, proBNF and the loop region of SREBP-2. Like SREBP-2,  
 CC proBNF is processed by SKI-1. The present peptide was efficiently  
 CC cleaved by recombinant SKI-1. Peptides which bind to and are cleaved by  
 CC SKI-1 may be used for monitoring SKI-1 activity, for screening inhibitors  
 CC of SKI-1 activity, or for screening enhancers of SKI-1 activity. Proteic  
 CC fragments of SKI-1 which bind to the SKI-1 catalytic site may be used as  
 CC inhibitors of SKI-1 activity. They may be used to treat diseases  
 CC involving overexpression of SKI-1 or SKI-1 substrate. Such diseases  
 CC include hypercholesterolemia, high levels of fatty acids, lipids or  
 CC farnesyl pyrophosphate, liver steatosis, Ras-dependent cancer, restenosis  
 CC and amyloid protein formation.  
 XX  
 SQ Sequence 12 AA;

Query Match 66.7%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
 ||||  
 DB 6 SVLS 9

RESULT 69  
 ABG78536  
 ID ABG78536 standard; Peptide; 12 AA.  
 XX  
 AC ABG78536;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Multiple sclerosis associated feature (MSP) tryptic digest peptide #24.  
 XX  
 KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;  
 KW human; multiple sclerosis-associated protein isoform; MSPI;  
 KW antiinflammatory; neuroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200259604-A2.  
 XX  
 PD 01-AUG-2002.  
 XX  
 PF 25-JAN-2002; 2002WO-GB00330.  
 XX  
 PR 26-JAN-2001; 2001US-264404P.  
 PR 20-NOV-2001; 2001US-331647P.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMAC, Perekh RB, Rohlff C;  
 XX  
 DR WPI; 2002-599812/64.  
 XX  
 PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.  
 PT determining the stage or severity of MS, comprises detecting the  
 PT presence of MS-associated features or protein isoforms by 2-dimensional  
 PT electrophoresis -  
 XX  
 PS Disclosure; Page 20; 128pp; English.  
 XX

CC This invention relates to a novel method for screening or diagnosing  
 CC multiple sclerosis (MS) in a subject to determine the stage or severity  
 CC of MS, to identify a subject at risk of developing MS or to monitor the  
 CC effect of a therapy administered. The method comprises analysing a  
 CC sample body fluid from the subject by two-dimensional electrophoresis  
 CC and detecting the presence of multiple sclerosis-associated features  
 CC (MSFs), or multiple sclerosis-associated protein isoforms (MSPIs).  
 CC The MSFs of the invention correspond to spots identified on a 2D gel  
 CC these proteins may have antiinflammatory or neuroprotective activity.  
 CC The methods of the invention and the compositions are useful for  
 CC clinical screening, diagnosis and treatment of MS, for monitoring the  
 CC effectiveness of MS treatment, for selecting participants in clinical  
 CC trials, for identifying patients most likely to respond to a particular  
 CC therapeutic treatment and for screening and developing drugs for  
 CC treatment of MS. Agents that modulate the expression or activity of an  
 CC MSPI are useful for treating MS, for preventing or delaying the onset or  
 CC development of MS, to prevent or delay the progression of MS, or to  
 CC ameliorate the symptoms MS. Nucleic acids comprising a sequence encoding  
 CC an MSPI, MSPI-related polypeptide, or their fragments are useful for  
 CC promoting MSPI function by gene therapy. The present sequence represents  
 CC a human multiple sclerosis associated feature tryptic digest  
 XX  
 SQ Sequence 12 AA;

Query Match 66.7%; Score 4; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POSV 4  
 ||||  
 DB 5 POSV 8

RESULT 70  
 AAP50642  
 ID AAP50642 standard; Protein; 13 AA.  
 XX  
 AC AAP50642;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 09-JAN-2003 (updated)  
 DT 21-NOV-1991 (first entry)  
 XX  
 DE Sequence (b) of a synthetic polypeptide corresponding in amino acid  
 DE sequence to at least a portion of a naturally occurring proteinoid  
 DE translated from a messenger RNA present substantially only in brain  
 DE cells.  
 XX  
 KW Neurotransmitter; neuromodulator; neuroactive; brain cell proteinoid.  
 XX  
 OS Synthetic.  
 XX  
 PN AU8430813-A.  
 XX  
 PD 24-JAN-1985.  
 XX  
 PF 19-JUL-1984; 84AU-0030813.  
 XX  
 PR 21-JUL-1983; 83US-0516136.  
 PR 03-JUN-1987; 87US-0058620.  
 XX  
 PA (SCRI ) SCRIPPS CLINIC & RES FOUND.  
 XX  
 PI Sutcliffe JG;  
 XX  
 DR WPI; 1985-062448/11.  
 XX  
 PT New synthetic poly:peptide(s) - useful as neuro-active agents and  
 PT for diagnosis of brain cell proteinoid(s)  
 XX  
 PS Claim 4; Page 80; 97pp; English.  
 XX

CC The peptides of the invention (AAP50641-P50648) can pass from the  
CC blood stream through the blood-brain barrier and into brain cell  
CC tissues. They may be neuroactive, e.g. some cpds. have  
CC neurotransmitter-like and neuromodulating activity. The patent  
CC application outlines procedures that are useful in identifying  
CC proteinoids that are translated from brain-specific mRNA and for  
CC preparing synthetic polypeptides whose AA residue sequences  
CC correspond substantially to the AA residue sequences of at least a  
CC portion of those proteinoids. The adult male rat was chosen as a  
CC model. Four brain-specific clones of Class III were described as  
CC exemplary. These clones are designated p1A75, p1B236, p1B208 and  
CC p0-40 (see AAN50473-N50475, AAN50520).  
CC (Updated on 09-JAN-2003 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|||||

Db 8 SVLS 11  
|||||

RESULT 71  
AAW92320  
ID AAW92320 standard; peptide; 13 AA.  
XX AC AAW92320;  
XX  
DT 09-APR-1999 (first entry)  
DE E2A/pbx1 immunogenic fusion peptide #5.  
XX  
KW E2A; pbx1; fusion protein; antigen; monoclonal antibody; diagnosis;  
KW epitope; acute lymphoblastic leukemia.  
XX  
OS Synthetic.  
XX  
PN US5858682-A.  
XX  
PD 12-JAN-1999.  
XX  
PF 02-AUG-1996; 96US-0691997.  
XX  
PR 02-AUG-1996; 96US-0691997.  
XX  
PA (PHAR-) PHARMINGEN.  
XX  
PI Gruenwald S, Monell C, Sang B;  
XX  
DR WPI; 1999-119870/10.  
XX  
PT Monoclonal antibody specific for E2A/pbx1 fusion protein - useful  
PT for diagnosis of acute lymphoblastic leukemia  
XX  
PS Disclosure; Column 25-26; 21pp; English.  
XX  
CC This sequence represents a peptide used in a method for constructing  
CC antigenic E2A/pbx1 fusion proteins used for raising monoclonal  
CC antibodies which specifically bind with an E2A/pbx1 fusion epitope. This  
CC peptide can be used for the diagnosis of acute lymphoblastic leukemia.  
XX  
SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 20; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|||||

Db 5 SVLS 8

RESULT 72  
AAG68083  
ID AAG68083 standard; peptide; 13 AA.  
XX AC AAG68083;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Antitumour peptide hck 503-515.  
XX  
KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;  
KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;  
KW cyclophilin B gene; HLA-A2402.  
XX  
OS Homo sapiens.  
XX  
PN JP2001245675-A.  
XX  
PD 11-SEP-2001.  
XX  
PF 25-DEC-2000; 2000JP-0393047.  
XX  
PR 28-DEC-1999; 99JP-0374322.  
XX  
PA (ITOY/) ITO Y.  
XX  
DR WPI; 2001-610076/70.  
XX  
PT New peptides for recognizing cancer cells with tumor specific cytotoxic  
PT T lymphocytes and for treating cancer -  
XX  
PS Claim 8; Page 2; 14pp; Japanese.  
XX  
CC The present invention describes peptides recognising cancer cells with  
CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising  
CC cancer cells with tumour specific CTLs are selected from: (1) peptides  
CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above  
CC mentioned sequences; (3) peptides having 70 % or more of homogeneity  
CC with the above mentioned sequences; and (4) peptides with one or more  
CC deleted, substituted, added or inserted amino acid(s) of the above  
CC mentioned sequences, particularly those having recognising property due  
CC to HLA-A2402 binding CTL, especially having at least 5 amino acids,  
CC used for medicine, particularly anticancer agents, derived from  
CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or  
CC cyclophilin B genes. The antitumour peptides have cytostatic activities.  
CC The peptides are used for the treatment of cancer. The peptides cause  
CC activation of CTL in cancer patients. The present sequence represents  
CC a peptide from the present invention.  
XX  
SQ Sequence 13 AA;

Query Match 66.7%; Score 4; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5  
|||||

Db 6 QSVL 9  
|||||

RESULT 73  
AAG68084  
ID AAG68084 standard; peptide; 13 AA.  
XX AC AAG68084;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Antitumour peptide blk 482-494.  
XX

KW Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;  
 KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;  
 KW cyclophilin B gene; HLA-A2402.  
 XX  
 OS Homo sapiens.  
 XX JP2001245675-A.  
 XX  
 XX 11-SEP-2001.  
 XX  
 XX 25-DEC-2000; 2000JP-0393047.  
 XX  
 XX 28-DEC-1999; 99JP-0374322.  
 XX  
 XX (ITOY/) ITO Y.  
 XX  
 XX WPI; 2001-610076/70.  
 XX  
 XX  
 XX PT New peptides for recognizing cancer cells with tumor specific cytotoxic  
 PT T lymphocytes and for treating cancer -  
 XX  
 XX Claim 8; Page 2; 14pp; Japanese.  
 XX  
 XX The present invention describes peptides recognising cancer cells with  
 CC tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising  
 CC cancer cells with tumour specific CTLs are selected from: (1) peptides  
 CC of sequences (AAG68066 to AAG68069); (2) peptides containing the above  
 CC mentioned sequences; (3) peptides having 70 % or more of homogeneity  
 CC with the above mentioned sequences; and (4) peptides with one or more  
 CC deleted, substituted, added or inserted amino acid(s) of the above  
 CC mentioned sequences, particularly those having recognising property due  
 CC to HLA-A2402 binding CTL, especially having at least 5 amino acids,  
 CC used for medicine, particularly anticancer agents, derived from  
 CC antitumour antigenic peptides of lck, src family, SART-1, SART-3 or  
 CC cyclophilin B genes. The antitumour peptides have cytostatic activities.  
 CC The peptides are used for the treatment of cancer. The peptides cause  
 CC activation of CTL in cancer patients. The present sequence represents  
 CC a peptide from the present invention.  
 XX  
 XX SQ Sequence 13 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 QSVL 5  
 Db 6 QSVL 9  
 XX  
 XX  
 XX RESULT 74  
 XX AAB31919  
 XX ID AAB31919 standard; peptide; 13 AA.  
 XX AC  
 XX AAB31919;  
 XX  
 XX 15-MAY-2001 (first entry)  
 XX  
 XX Amino acid sequence of a peptide fragment of a human protein.  
 DE  
 XX  
 XX Human; perlecan; retinol-binding plasma protein; calgranulin B; vaccine;  
 KW ganglioside GM2 activator; saposin B; degenerative disease; glial cell;  
 KW neurological disease; auto-immune disease; multiple sclerosis; toxicity;  
 KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;  
 KW rheumatoid polyarthritis; lupus erythematosus; gene therapy.  
 XX  
 XX Homo sapiens.  
 XX  
 XX WO200105422-A2.  
 XX  
 XX 25-JAN-2001.  
 XX  
 XX 17-JUL-2000; 2000WO-FR02057.

XX 15-JUL-1999; 99FR-0009372.  
 XX (INMR ) BIOMERIEUX STELHYS.  
 XX  
 XX Roecklin D, Kolbe H, Charles M, Malcus C, Santoro L, Perron H;  
 XX WPI; 2001-159475/16.  
 XX  
 XX Detecting, preventing and treating degenerative, neurological and  
 PT autoimmune diseases, particularly multiple sclerosis, using specified  
 PT polypeptides or related nucleic acid or ligand -  
 XX  
 XX Claim 7; Page 205; 209pp; French.  
 XX  
 XX The present sequence represents a peptide fragment of a human protein,  
 CC which is used in the method of the invention. The specification describes  
 CC a method which uses at least one polypeptide or polynucleotide sequence  
 CC belonging to the perlecan, precursor of the retinol-binding plasma  
 CC protein, precursor of the ganglioside GM2 activator, calgranulin B or  
 CC saposin B protein families. The method is used for detecting,  
 CC preventing or treating a degenerative, neurological and/or auto-immune  
 CC disease. The polynucleotides and polypeptides are used for diagnosis,  
 CC prognosis, prevention and treatment of multiple sclerosis (in its  
 CC various forms and phases). They may also be useful in cases of  
 CC e.g. Alzheimer's and Parkinson's diseases, amyotrophic lateral sclerosis,  
 CC rheumatoid polyarthritis and lupus erythematosus, including use as  
 CC vaccines and in gene therapy (expression of sense or antisense  
 CC sequences). They can also be used to assess efficacy of potential  
 CC therapeutic agents, particularly compounds that reduce or inhibit  
 CC toxicity towards glial cells.  
 XX  
 XX SQ Sequence 13 AA;  
 Query Match 66.7%; Score 4; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 SVLS 6  
 Db 3 SVLS 6  
 XX  
 XX  
 XX RESULT 75  
 XX AAB73149  
 XX ID AAB73149 standard; Peptide; 13 AA.  
 XX AC  
 XX AAB73149;  
 XX  
 XX 09-MAY-2001 (first entry)  
 XX  
 XX Tumour antigen peptide #33.  
 DE  
 XX  
 XX Src protein; lck protein; vaccine; colon cancer; small-cell lung cancer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200111044-A1.  
 XX  
 XX 15-FEB-2001.  
 XX  
 XX 03-AUG-2000; 2000WO-JP05220.  
 XX  
 XX 05-AUG-1999; 99JP-0222101.  
 XX  
 XX (ITOY/) ITOH K.  
 XX  
 XX Itoh K;  
 PI  
 XX WPI; 2001-191541/19.  
 XX  
 XX Tumor antigen peptides which induce tumor-specific cytotoxic T-cells  
 PT and polynucleotides encoding them for treatment of cancer -



XX  
PS Example 6; Page 36; 75pp; Japanese.  
XX  
CC The present invention relates to peptides which are partial sequences of  
CC src/lck family proteins. The present sequence is one such peptide. The  
CC peptides are useful for producing vaccines for the treatment of cancer,  
CC including colon cancer and small-cell lung cancer.  
XX  
SQ Sequence 13 AA;  
Query Match 66.7%; Score 4; DB 22; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 QSVL 5  
Db ||||  
6 QSVL 9

Search completed: November 25, 2003, 19:27:14  
Job time : 16.314 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 9.62791 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 POSVLS 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications\_AA:  
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10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	6	100.0	6	15	US-10-281-652-26
2	4	66.7	7	12	Sequence 26, Appl
3	4	66.7	8	12	Sequence 22, Appl
4	4	66.7	8	12	Sequence 5, Appl
5	4	66.7	8	15	Sequence 58, Appl
6	4	66.7	9	14	Sequence 64, Appl
7	4	66.7	9	14	Sequence 7, Appl
8	4	66.7	9	14	Sequence 8, Appl
9	4	66.7	10	11	Sequence 1808, Ap
10	4	66.7	10	11	Sequence 1810, Ap
11	4	66.7	10	11	Sequence 152, App
12	4	66.7	11	11	Sequence 341, App
13	4	66.7	12	10	Sequence 9, Appl
14	4	66.7	12	15	Sequence 214, App
15	4	66.7	14	10	Sequence 8, Appl

4	66.7	14	15	US-10-097-065-571	Sequence 571, App
4	66.7	15	10	US-09-791-378-194	Sequence 194, App
4	66.7	15	12	US-09-933-767-582	Sequence 582, App
4	66.7	15	13	US-10-023-282-582	Sequence 582, Appl
4	66.7	17	11	US-09-563-222-14	Sequence 23, Appl
4	66.7	17	12	US-10-272-248-21	Sequence 34123, A
4	66.7	17	12	US-10-029-386-34123	Sequence 142, App
4	66.7	19	11	US-09-876-904A-142	Sequence 128, App
4	66.7	19	15	US-10-219-834-128	Sequence 48427, A
4	66.7	20	9	US-09-864-761-48427	Sequence 116, App
4	66.7	20	12	US-10-195-730-116	Sequence 24, Appl
4	66.7	20	12	US-10-272-248-24	Sequence 1150, Ap
4	66.7	20	12	US-09-962-756-1150	Sequence 1, Appl
4	66.7	4	8	US-08-839-248-1	Sequence 538, App
4	66.7	4	8	US-08-424-550B-538	Sequence 1, Appl
4	66.7	4	9	US-09-770-367-1	Sequence 1, Appl
4	66.7	4	9	US-09-858-369-1	Sequence 2, Appl
4	66.7	4	9	US-09-757-251-2	Sequence 1, Appl
4	66.7	4	9	US-09-784-897A-1	Sequence 1, Appl
4	66.7	4	9	US-09-770-983-1	Sequence 1, Appl
4	66.7	4	9	US-09-834-765-742	Sequence 742, App
4	66.7	4	9	US-09-853-918-12	Sequence 12, Appl
4	66.7	4	9	US-09-828-325A-2	Sequence 2, Appl
4	66.7	4	9	US-09-757-217A-2	Sequence 2, Appl
4	66.7	4	10	US-09-828-259A-2	Sequence 2, Appl
4	66.7	4	10	US-09-751-100B-20	Sequence 20, Appl
4	66.7	4	10	US-09-784-818-1	Sequence 1, Appl
4	66.7	4	12	US-09-756-248-1	Sequence 1, Appl
4	66.7	4	12	US-09-932-165-1436	Sequence 1436, Ap
4	66.7	4	12	US-10-087-942-6	Sequence 6, Appl
4	66.7	4	12	US-10-083-894-17	Sequence 17, Appl
4	66.7	4	12	US-10-352-704-27	Sequence 27, Appl
4	66.7	4	12	US-10-317-644-6	Sequence 6, Appl
4	66.7	4	15	US-10-087-905-6	Sequence 6, Appl
4	66.7	4	15	US-10-211-088-360	Sequence 360, App
4	66.7	5	9	US-09-803-854-4	Sequence 4, Appl
4	66.7	5	10	US-09-924-824-16	Sequence 16, Appl
4	66.7	5	10	US-09-924-824-17	Sequence 17, Appl
4	66.7	5	10	US-09-751-100B-43	Sequence 43, Appl
4	66.7	5	12	US-10-268-552-16	Sequence 16, Appl
4	66.7	5	12	US-10-268-552-17	Sequence 17, Appl
4	66.7	5	12	US-10-076-047A-197	Sequence 197, App
4	66.7	5	12	US-10-076-047A-251	Sequence 251, App
4	66.7	5	12	US-10-076-047A-296	Sequence 296, App
4	66.7	5	12	US-10-319-402-25	Sequence 25, Appl
4	66.7	5	12	US-10-352-704-29	Sequence 29, Appl
4	66.7	5	15	US-10-206-699-55	Sequence 55, Appl
4	66.7	6	8	US-08-681-219-11	Sequence 11, Appl
4	66.7	6	9	US-09-742-582-22	Sequence 22, Appl
4	66.7	6	10	US-09-924-824-27	Sequence 27, Appl
4	66.7	6	10	US-09-924-824-28	Sequence 28, Appl
4	66.7	6	10	US-09-924-824-37	Sequence 37, Appl
4	66.7	6	10	US-09-924-824-38	Sequence 38, Appl
4	66.7	6	10	US-09-924-824-44	Sequence 44, Appl
4	66.7	6	10	US-09-873-233A-15	Sequence 15, Appl
4	66.7	6	11	US-09-742-580-22	Sequence 22, Appl
4	66.7	6	11	US-09-742-581-22	Sequence 22, Appl
4	66.7	6	12	US-10-268-552-30	Sequence 30, Appl
4	66.7	6	12	US-10-268-552-31	Sequence 31, Appl
4	66.7	6	12	US-10-268-552-40	Sequence 40, Appl
4	66.7	6	12	US-10-268-552-41	Sequence 41, Appl
4	66.7	6	12	US-10-268-552-47	Sequence 47, Appl
4	66.7	6	12	US-09-935-384-746	Sequence 746, App
4	66.7	6	12	US-10-092-138-9	Sequence 9, Appl
4	66.7	6	12	US-10-319-402-27	Sequence 27, Appl
4	66.7	6	12	US-10-352-704-31	Sequence 31, Appl
4	66.7	6	12	US-09-230-111C-9	Sequence 9, Appl
4	66.7	6	14	US-10-156-820-54	Sequence 54, Appl
4	66.7	7	9	US-09-799-576A-9	Sequence 9, Appl
4	66.7	7	9	US-09-896-251-30	Sequence 30, Appl
4	66.7	7	9	US-09-896-251-32	Sequence 32, Appl
4	66.7	7	9	US-09-896-251-33	Sequence 33, Appl
4	66.7	7	9	US-09-896-251-40	Sequence 40, Appl

89 3 50.0 7 9 US-09-896-251-45 Sequence 45, Appl  
90 3 50.0 7 9 US-09-896-245-30 Sequence 30, Appl  
91 3 50.0 7 9 US-09-896-245-32 Sequence 32, Appl  
92 3 50.0 7 9 US-09-896-245-33 Sequence 33, Appl  
93 3 50.0 7 9 US-09-896-245-40 Sequence 40, Appl  
94 3 50.0 7 9 US-09-896-245-45 Sequence 45, Appl  
95 3 50.0 7 9 US-09-799-540-9 Sequence 9, Appl  
96 3 50.0 7 9 US-09-989-789-751 Sequence 751, App  
97 3 50.0 7 9 US-09-989-789-953 Sequence 953, App  
98 3 50.0 7 9 US-09-989-789-955 Sequence 955, App  
99 3 50.0 7 9 US-09-989-789-3232 Sequence 3232, Ap  
100 3 50.0 7 9 US-09-989-789-3955 Sequence 3955, Ap

## ALIGNMENTS

RESULT 1  
US-10-281-652-26  
; Sequence 26, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-10-281-652-26

Query Match 100.0%; Score 6; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PQSVLS 6  
Db 1 PQSVLS 6  
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RESULT 2  
US-10-271-708-22  
; Sequence 22, Application US/10271708  
; Publication No. US20030162200A1  
; GENERAL INFORMATION:  
; APPLICANT: CHOO, Yen  
; APPLICANT: LIU, Xiaohai  
; APPLICANT: BALASUBRAMANIAN, Shankar  
; APPLICANT: PATEL, Sachin D.  
; APPLICANT: ISALAN, Mark  
; TITLE OF INVENTION: METHODS FOR MODULATING TELOMERASE ACTIVITY  
; FILE REFERENCE: SABI-036/01US (8325-2014.01)  
; CURRENT APPLICATION NUMBER: US/10/271,708  
; CURRENT FILING DATE: 2002-10-15  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 22  
; LENGTH: 7  
; TYPE: PRT

; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: F2 residue  
US-10-271-708-22

Query Match 66.7%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 3 SVLS 6  
|||||

RESULT 3  
US-10-209-187A-5  
; Sequence 5, Application US/10209187A  
; Publication No. US20030148383A1  
; GENERAL INFORMATION:  
; APPLICANT: Maurer-Stroh, Sebastian  
; APPLICANT: Eisenhaber, Birgit  
; APPLICANT: Eisenhaber, Frank  
; TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoylat  
; FILE REFERENCE: 0652.2560000  
; CURRENT APPLICATION NUMBER: US/10/209,187A  
; CURRENT FILING DATE: 2002-08-01  
; PRIOR APPLICATION NUMBER: EP 01 118 627.7  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Synthetic octapeptide  
US-10-209-187A-5

Query Match 66.7%; Score 4; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 5 SVLS 8  
|||||

RESULT 4  
US-10-061-395-58  
; Sequence 58, Application US/10061395  
; Publication No. US20020192675A1  
; GENERAL INFORMATION:  
; APPLICANT: Zauderer, Maurice  
; APPLICANT: Smith, Ernest S.  
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules  
; FILE REFERENCE: 1821.0080003  
; CURRENT APPLICATION NUMBER: US/10/061,395  
; CURRENT FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/271,423  
; PRIOR FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: 60/265,880  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/265,589  
; PRIOR FILING DATE: 2001-02-02  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 58  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Myristoylation signal sequence from HIV (HTLV-III) gag  
US-10-061-395-58



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;
; FEATURE:
; OTHER INFORMATION: sequence located in EVX1 at 384-393 and may interact with Sequenc
; OTHER INFORMATION: in this patent.
US-09-572-404B-1808

Query Match          66.7%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 SVLS 6
   ||||
Db  4 SVLS 7

RESULT 10
US-09-572-404B-1810
; Sequence 1810, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1810
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in EVX1 at 383-392 and may interact with Sequenc
; OTHER INFORMATION: in this patent.
US-09-572-404B-1810

Query Match          66.7%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 SVLS 6
   ||||
Db  5 SVLS 8

RESULT 11
US-09-865-548A-152
; Sequence 152, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 152
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-152

Query Match          66.7%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 SVLS 6
   ||||
Db  5 SVLS 8

RESULT 12
US-09-986-480-341
; Sequence 341, Application US/09986480
; Publication No. US20030027999A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 143 Human Secreted Proteins
; FILE REFERENCE: PSS00P1
; CURRENT APPLICATION NUMBER: US/09/986,480
; CURRENT FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: PCT/US00/12788
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/134,068
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 456
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 341
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-986-480-341

Query Match          66.7%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 3 SVLS 6
   ||||
Db  8 SVLS 11

RESULT 13
US-09-242-450A-9
; Sequence 9, Application US/09242450A
; Patent No. US2002015552A1
; GENERAL INFORMATION:
; APPLICANT: Bergmann, Johanna
; TITLE OF INVENTION: "PRIONINS", HIGHLY SPECIFIC MARKERS FOR NONINVASIVE PRE-SYMP
; TITLE OF INVENTION: DETECTION OF TSE DISEASES AND TARGETS FOR THERAPEUTIC REAGEN
; TITLE OF INVENTION: CONTROL TSE DISEASES IN ANIMALS AND HUMANS
; FILE REFERENCE: 830006-2001
; CURRENT APPLICATION NUMBER: US/09/242,450A
; CURRENT FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; US-09-242-450A-9

Query Match          66.7%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 1 PQSV 4
   ||||
Db  5 PQSV 8

RESULT 14
US-10-254-446A-214
; Sequence 214, Application US/10254446A
; Publication No. US20030113714A1
; GENERAL INFORMATION:
; APPLICANT: Belcher, Angela M
; APPLICANT: Smalley, Richard E.
```

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; APPLICANT: Ryan, Esther
; APPLICANT: Lee, Seung-Wuk
; TITLE OF INVENTION: BIOLOGICAL CONTROL OF NANOPARTICLES
; FILE REFERENCE: 119927-1066
; CURRENT APPLICATION NUMBER: US/10/254,446A
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/325,664
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 245
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 214
; LENGTH: 12
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide with peptide binding sequence retrieved from phage biopar
US-10-254-446A-214

Query Match      66.7%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 POSV 4
      |||||
Db      8 POSV 11

RESULT 15
US-09-242-450A-8
; Sequence 8, Application US/09242450A
; Patent No. US2002015552A1
; GENERAL INFORMATION:
; APPLICANT: Bergmann, Johanna
; TITLE OF INVENTION: "PRIONINS", HIGHLY SPECIFIC MARKERS FOR NONINVASIVE PRE-SYMPTOM
; TITLE OF INVENTION: DETECTION OF TSE DISEASES AND TARGETS FOR THERAPEUTIC REAGENTS
; TITLE OF INVENTION: CONTROL TSE DISEASES IN ANIMALS AND HUMANS
; FILE REFERENCE: 830006-2001
; CURRENT APPLICATION NUMBER: US/09/242,450A
; CURRENT FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-242-450A-8

Query Match      66.7%; Score 4; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 POSV 4
      |||||
Db      7 POSV 10

RESULT 16
US-10-097-065-571
; Sequence 571, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057

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; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 571
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-065-571

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Query Match      66.7%; Score 4; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 SVLS 6
      |||||
Db      5 SVLS 8

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```

RESULT 17
US-09-791-378-194
; Sequence 194, Application US/09791378
; Patent No. US20020142303A1
; GENERAL INFORMATION:
; APPLICANT: Parekh, Rajesh
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: SCHIZOPHRENIA
; FILE REFERENCE: 9195-061-999
; CURRENT APPLICATION NUMBER: US/09/791,378
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/750,395
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 677
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 194
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-378-194

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Query Match      66.7%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 SVLS 6
      |||||
Db      7 SVLS 10

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RESULT 18
US-09-933-767-582
; Sequence 582, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:

```

; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P2  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: PCT/US01/05614  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/184,836  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/193,170  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/205,258  
; PRIOR FILING DATE: 1998-12-04  
; PRIOR APPLICATION NUMBER: PCT/US98/11422  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: 60/048,885  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,375  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,881  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,917  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/048,883  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,897  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,898  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,962  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,963  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 582  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-582

Query Match 66.7%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 11 SVLS 14

RESULT 19  
US-10-023-282-582  
; Sequence 582, Application US/10023282  
; Publication No. US20030092893A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/10/023,282  
; CURRENT FILING DATE: 2001-12-20  
; EARLIER APPLICATION NUMBER: 09/205,258  
; EARLIER FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04

EARLIER APPLICATION NUMBER: 60/048,885  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,375  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,881  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,880  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,896  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,020  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,876  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,895  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,884  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,894  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,971  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923

EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 582  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-282-582

Query Match 66.7%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 11 SVLS 14  
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RESULT 20  
US-09-563-222-14  
Sequence 14, Application US/09563222  
Publication No. US20030079253A1  
GENERAL INFORMATION:  
APPLICANT: Hiatt, Andrew  
APPLICANT: Hein, Mich B.  
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
FILE REFERENCE: 310098.406  
CURRENT APPLICATION NUMBER: US/09/563,222  
CURRENT FILING DATE: 2000-05-02  
NUMBER OF SEQ ID NOS: 197  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapien  
US-09-563-222-14

Query Match 66.7%; Score 4; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5  
Db 4 QSVL 7  
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RESULT 21  
US-10-272-248-23  
Sequence 23, Application US/10272248  
Publication No. US20030176337A1  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
Karunaratne, Nedra  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:



APPLICATION NUMBER: US/10/272,248  
FILING DATE: 15-Oct-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/593,321  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 09/307,200  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-10-272-248-23

Query Match 66.7%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 14 SVLS 17

RESULT 22  
US-10-029-386-34123  
Sequence 34123, Application US/10029386  
Publication No. US20030194704A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Hanzel, David R.  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G  
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
FILE REFERENCE: AEMICA-X-2  
CURRENT APPLICATION NUMBER: US/10/029,386  
CURRENT FILING DATE: 2001-12-20  
NUMBER OF SEQ ID NOS: 34288  
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
SEQ ID NO 34123  
LENGTH: 17  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC007281.3  
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1  
US-10-029-386-34123

Query Match 66.7%; Score 4; DB 12; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 10 SVLS 13

RESULT 23  
US-09-876-904A-142  
Sequence 142, Application US/09876904A  
Publication No. US20030072794A1  
GENERAL INFORMATION:  
APPLICANT: BOULIKAS, TENI  
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC  
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES  
FILE REFERENCE: TB-2002.00  
CURRENT APPLICATION NUMBER: US/09/876,904A  
CURRENT FILING DATE: 2001-06-08  
PRIOR APPLICATION NUMBER: US 60/210,925  
PRIOR FILING DATE: 2000-06-09  
NUMBER OF SEQ ID NOS: 629  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 142  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Bos sp.  
FEATURE:  
OTHER INFORMATION: Karyophilic peptide  
US-09-876-904A-142

Query Match 66.7%; Score 4; DB 11; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5  
|||  
Db 15 QSVL 18

RESULT 24  
US-10-219-834-128  
Sequence 128, Application US/10219834  
Publication No. US20030096751A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE  
FILE REFERENCE: D0191 NP  
CURRENT APPLICATION NUMBER: US/10/219,834  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: US 60/313,658  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: US 60/340,703  
PRIOR FILING DATE: 2001-10-30  
PRIOR APPLICATION NUMBER: US 60/318,675  
PRIOR FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: US 60/355,596  
PRIOR FILING DATE: 2002-02-06  
PRIOR APPLICATION NUMBER: US 60/333,417  
PRIOR FILING DATE: 2001-11-26  
PRIOR APPLICATION NUMBER: US 60/338,367  
PRIOR FILING DATE: 2001-12-06  
NUMBER OF SEQ ID NOS: 192  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 128  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-219-834-128

Query Match 66.7%; Score 4; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 5 SVLS 8

RESULT 25  
US-09-864-761-48427  
Sequence 48427, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng

```
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48427
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78810.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: EST_HUMAN HIT: B5621144.1, EVALUATE 2.00e-03
US-09-864-761-48427

Query Match 66.7%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 12 SVLS 15

RESULT 26
US-10-195-730-116
; Sequence 116, Application US/10195730
; Publication No. US2003014492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: PZ017P1
; CURRENT APPLICATION NUMBER: US/10/195,730

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48427
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78810.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.96
; OTHER INFORMATION: EST_HUMAN HIT: B5621144.1, EVALUATE 2.00e-03
US-09-864-761-48427

Query Match 66.7%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 12 SVLS 15

RESULT 26
US-10-195-730-116
; Sequence 116, Application US/10195730
; Publication No. US2003014492A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et. al
; TITLE OF INVENTION: 101 Human Secreted Proteins
; FILE REFERENCE: PZ017P1
; CURRENT APPLICATION NUMBER: US/10/195,730
```

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; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US/09/281,976
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/060,837
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: 60/060,862
; PRIOR FILING DATE: 1997-10-02
; NUMBER OF SEQ ID NOS: 390
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 116
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (20)
; OTHER INFORMATION: Xaa equals stop translation
US-10-195-730-116

Query Match 66.7%; Score 4; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 5 SVLS 8

RESULT 27
US-10-272-248-24
; Sequence 24, Application US/10272248
; Publication No. US20030176337A1
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/10/272,248
; APPLICATION NUMBER: US/10/272,248
; FILING DATE: 15-Oct-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/593,321
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 09/307,200
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-272-248-24
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Query Match 66.7%; Score 4; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5  
Db 16 QSVL 19  
|||

## RESULT 28

US-09-962-756-1150  
; Sequence 1150, Application US/09962756  
; Publication No. US20030195147A1  
; GENERAL INFORMATION:  
; APPLICANT: PILLUTLA, RENUKA  
; APPLICANT: BRISSETTE, RENEE  
; APPLICANT: BLUME, ARTHUR J.  
; APPLICANT: SCHAEFER, LAUGE  
; APPLICANT: BRANDT, JAKOB  
; APPLICANT: GOLDSTEIN, NEIL I.  
; APPLICANT: SPETZLER, JANE  
; APPLICANT: OSTERGAARD, SOREN  
; APPLICANT: HANSEN, PER HERTZ  
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS  
; FILE REFERENCE: 1878-4051US1  
; CURRENT APPLICATION NUMBER: US/09/962,756  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 09/538,038  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: 09/146,127  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1150  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (11)  
; OTHER INFORMATION: Unknown amino acid; translation read-through at  
; OTHER INFORMATION: TGA stop codon

US-09-962-756-1150  
Query Match 66.7%; Score 4; DB 12; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5  
Db 2 QSVL 5  
|||

## RESULT 29

US-08-839-248-1  
; Sequence 1, Application US/08839248A  
; Publication No. US20020034725A1  
; GENERAL INFORMATION:  
; APPLICANT: McKenna, Gillies  
; APPLICANT: Muschel, Ruth J  
; APPLICANT: Bernhard, Eric J  
; APPLICANT: Sebti, Said M  
; APPLICANT: Hamilton, Andrew D  
; TITLE OF INVENTION: Sensitization of Cells to Radiation Therapy  
; FILE REFERENCE: 09596-2U1  
; CURRENT APPLICATION NUMBER: US/08/839,248A  
; CURRENT FILING DATE: 1997-04-15  
; EARLIER APPLICATION NUMBER: 60/015,477  
; EARLIER FILING DATE: 1996-04-15  
; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: H-ras farnesyltransferase recognition motif  
US-08-839-248-1

Query Match 50.0%; Score 3; DB 8; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
Db 2 VLS 4  
|||

## RESULT 30

US-08-424-550B-538  
; Sequence 538, Application US/08424550B  
; Publication No. US20020119447A1  
; GENERAL INFORMATION:  
; APPLICANT: JOHN N. SIMONS  
; APPLICANT: TAMI J. PILOT-MATIAS  
; APPLICANT: GEORGE J. DAWSON  
; APPLICANT: GEORGE G. SCHLAUDER  
; APPLICANT: SURESH M. DESAI  
; APPLICANT: THOMAS P. LEARY  
; APPLICANT: ANTHONY SCOTT MUEHROFF  
; APPLICANT: JAMES C. ERKER  
; APPLICANT: SHERI L. BUIOK  
; APPLICANT: ISA K. MUSHAWAR  
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 716  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D  
; STREET: 100 ABBOTT PARK ROAD  
; CITY: ABBOTT PARK  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/424,550B  
; FILING DATE:  
; CLASSIFICATION: 435435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: POREMSKI, PRISCILLA E.  
; REGISTRATION NUMBER: 33,207  
; REFERENCE/DOCKET NUMBER: 5527.PC.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 708-937-6365  
; TELEFAX: 708-938-2623  
; INFORMATION FOR SEQ ID NO: 538:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-424-550B-538

Query Match 50.0%; Score 3; DB 8; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POS 3  
|||

Db 2 PQS 4

RESULT 31

US-09-770-967-1

; Sequence 1, Application US/09770967

; Patent No. US20020010184A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Dinsmore, Christopher J.

; APPLICANT: Bergman, Jeffrey M.

; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase

; FILE REFERENCE: 20495

; CURRENT APPLICATION NUMBER: US/09/770,967

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/183,651

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homosapien

US-09-770-967-1

Query Match 50.0%; Score 3; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

RESULT 32

US-09-858-369-1

; Sequence 1, Application US/09858369

; Patent No. US20020022633A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Williams, Theresa M.

; APPLICANT: Stump, Craig A.

; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase

; FILE REFERENCE: 20673

; CURRENT APPLICATION NUMBER: US/09/858,369

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: 60/215,655

; PRIOR FILING DATE: 2000/06/30

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homosapien

US-09-858-369-1

Query Match 50.0%; Score 3; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

RESULT 33

US-09-757-251-2

; Sequence 2, Application US/09757251

; Patent No. US20020049217A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: S. Jane deSolms

; APPLICANT: Suzanne C. MacTough

; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase

; FILE REFERENCE: 20309

; CURRENT APPLICATION NUMBER: US/09/770,983

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/183,650

; PRIOR FILING DATE: 2000-02-18

US-09-770-967-1

Query Match 50.0%; Score 3; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

RESULT 34

US-09-784-897A-1

; Sequence 1, Application US/09784897A

; Patent No. US20020052363A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Dinsmore, Christopher J.

; APPLICANT: Bergman, Jeffrey M.

; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS

; FILE REFERENCE: 20497

; CURRENT APPLICATION NUMBER: US/09/784,897A

; CURRENT FILING DATE: 2001-06-20

; PRIOR APPLICATION NUMBER: 60/183,449

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: completely synthetic sequence

US-09-784-897A-1

Query Match 50.0%; Score 3; DB 9; Length 4;

Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

RESULT 35

US-09-770-983-1

; Sequence 1, Application US/09770983

; Patent No. US20020052380A1

; GENERAL INFORMATION:

; APPLICANT: Merck & Co., Inc.

; APPLICANT: Dinsmore, Christopher J.

; APPLICANT: Bergman, Jeffrey M.

; TITLE OF INVENTION: Inhibitors of Prenyl-Protein Transferase

; FILE REFERENCE: 20309

; CURRENT APPLICATION NUMBER: US/09/770,983

; CURRENT FILING DATE: 2001-01-26

; PRIOR APPLICATION NUMBER: 60/183,650

; PRIOR FILING DATE: 2000-02-18

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; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-770-983-1

Query Match
Best Local Similarity 50.0%; Score 3; DB 9; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 2 VLS 4

RESULT 36
US-09-834-765-742
; Sequence 742, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USUI
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 742
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-742

Query Match
Best Local Similarity 50.0%; Score 3; DB 9; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
Db 1 SVL 3

RESULT 37
US-09-853-918-12
; Sequence 12, Application US/09853918
; Patent No. US20020068346A1
; GENERAL INFORMATION:
; APPLICANT: Krystek, Stanley R.
; APPLICANT: Sheriff, Steven
; APPLICANT: Witmer, Mark R.
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Van, Ning
; APPLICANT: Mouravieff, Julie E.
; APPLICANT: Einspahr, Howard M.
; APPLICANT: Kish, Kevin
; TITLE OF INVENTION: MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
; FILE REFERENCE: DR24NP
; CURRENT APPLICATION NUMBER: US/09/853,918
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 60/203,448
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 65

; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-918-12

Query Match
Best Local Similarity 50.0%; Score 3; DB 9; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POS 3
Db 2 POS 4

RESULT 38
US-09-828-325A-2
; Sequence 2, Application US/09828325A
; Patent No. US20020068747A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Craig A. Stump
; APPLICANT: Theresa M. Williams
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20636Y
; CURRENT APPLICATION NUMBER: US/09/828,325A
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/196,244
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-828-325A-2

Query Match
Best Local Similarity 50.0%; Score 3; DB 9; Length 4;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 2 VLS 4

RESULT 39
US-09-757-217A-2
; Sequence 2, Application US/09757217A
; Patent No. US20020099007A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: S. Jane desolms
; APPLICANT: Gerald E. Stokker
; APPLICANT: Anthony W. Shaw
; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE
; FILE REFERENCE: 20603Y
; CURRENT APPLICATION NUMBER: US/09/757,217A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/175,801
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: N-terminus of Ras protein
US-09-757-217A-2
```

Query Match 50.0%; Score 3; DB 9; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

RESULT 40  
 US-09-828-259A-2  
 ; Sequence 2, Application US/09828259A  
 ; Patent No. US20020123497A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Diem N. Nguyen  
 ; APPLICANT: Craig A. Stump  
 ; APPLICANT: Theresa M. Williams  
 ; TITLE OF INVENTION: INHIBITORS OF PRENYL-PROTEIN TRANSFERASE  
 ; FILE REFERENCE: 20637Y  
 ; CURRENT APPLICATION NUMBER: US/09/828,259A  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: 60/195,951  
 ; PRIOR FILING DATE: 2000-04-10  
 ; NUMBER OF SEQ ID NOS: 25  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: N-terminus of Ras protein  
 US-09-828-259A-2

Query Match 50.0%; Score 3; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

RESULT 41  
 US-09-751-100B-20  
 ; Sequence 20, Application US/09751100B  
 ; Patent No. US20020142436A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Medical Research Council  
 ; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor  
 ; FILE REFERENCE: P27948A  
 ; CURRENT APPLICATION NUMBER: US/09/751,100B  
 ; CURRENT FILING DATE: 2000-12-28  
 ; NUMBER OF SEQ ID NOS: 104  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Mouse  
 US-09-751-100B-20

Query Match 50.0%; Score 3; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

RESULT 42  
 US-09-784-818-1

; Sequence 1, Application US/09784818  
 ; Publication No. US20020193283A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; APPLICANT: Bergman, Jeffrey M.  
 ; TITLE OF INVENTION: PRENYL-PROTEIN TRANSFERASE INHIBITORS  
 ; FILE REFERENCE: 20496  
 ; CURRENT APPLICATION NUMBER: US/09/784,818  
 ; CURRENT FILING DATE: 2001-02-16  
 ; PRIOR APPLICATION NUMBER: 60/183,451  
 ; PRIOR FILING DATE: 2000-02-18  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: completely synthetic sequence  
 US-09-784-818-1

Query Match 50.0%; Score 3; DB 10; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

RESULT 43  
 US-09-756-248-1  
 ; Sequence 1, Application US/09756248  
 ; Publication No. US20030134860A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Dinsmore, Christopher J.  
 ; TITLE OF INVENTION: Inhibitors Of Prenyl-Protein Transferase  
 ; FILE REFERENCE: 20341  
 ; CURRENT APPLICATION NUMBER: US/09/756,248  
 ; CURRENT FILING DATE: 2001-01-08  
 ; PRIOR APPLICATION NUMBER: 60/175,706  
 ; PRIOR FILING DATE: 2000-01-12  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 4  
 ; TYPE: PRT  
 ; ORGANISM: Homosapien  
 US-09-756-248-1

Query Match 50.0%; Score 3; DB 12; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

RESULT 44  
 US-09-932-165-1436  
 ; Sequence 1436, Application US/09932165  
 ; Publication No. US20030134784A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: CHALLITA-EID, PIA M.  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: SAFFRAN, DOUGLAS  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: HUBERT, RENE

```
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITS, AYA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
; TITLE OF INVENTION: 83P2H3 AND CatIF2E11 USEFUL IN TREATMENT AND
; TITLE OF INVENTION: DETECTION OF CANCER
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1436
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-932-165-1436
Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 SVL 5
Db      1 SVL 3

RESULT 45
US-10-087-942-6
; Sequence 6, Application US/10087942
; Publication No. US20030165808A1
; GENERAL INFORMATION:
; APPLICANT: Haaland, Perry D.
; APPLICANT: Sherman, Douglas B.
; APPLICANT: Stewart II, Walter W.
; APPLICANT: Lloyd, Sheila A.
; APPLICANT: Campbell, Robert L.
; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR
; TITLE OF INVENTION: FORMULATING CULTURE MEDIA
; FILE REFERENCE: P3250
; CURRENT APPLICATION NUMBER: US/10/087,942
; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US/09/359,260
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
US-10-087-942-6
Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VLS 6
Db      1 VLS 3

RESULT 46
US-10-083-894-17
; Sequence 17, Application US/10083894
; Publication No. US20030170766A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Goldstein, Joseph L.
```

```
; Reiss, Yuval
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; IDENTIFICATION, CHARACTERIZATION, AND INHIBITION OF
; FARNESYL PROTEIN TRANSFERASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,894
; FILING DATE: 27-Feb-2002
; CLASSIFICATION: UNKNOWN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/937,893
; FILING DATE: 18-APR-1991
; APPLICATION NUMBER: US 07/615,713
; FILING DATE: 20-NOV-1990
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990
; APPLICATION NUMBER: NOT APPLICABLE
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:249/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512-320-7200
; TELEFAX: 512-474-7577
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-083-894-17
Query Match          50.0%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VLS 6
Db      2 VLS 4

RESULT 47
US-10-352-704-27
; Sequence 27, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C
; STATE: D.C
; COUNTRY: U.S.A.
```

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/352,704  
FILING DATE: 28-Jan-2003  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/358,556A  
FILING DATE: 14-DEC-1994  
APPLICATION NUMBER: FR 9315164  
FILING DATE: 16-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Player, William B.  
REGISTRATION NUMBER: 31,409  
REFERENCE/DOCKET NUMBER: 10577/P58418  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-10-352-704-27

Query Match 50.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
Db 2 QSV 4

RESULT 48  
US-10-317-644-6  
Sequence 6, Application US/10317644  
Publication No. US20030181355A1  
GENERAL INFORMATION:  
APPLICANT: Glenn, Jeffrey S.  
FILE OF INVENTION: METHOD FOR INHIBITION OF VIRAL INFECTION  
FILE REFERENCE: 24004-20524.21  
CURRENT APPLICATION NUMBER: US/10/317,644  
CURRENT FILING DATE: 2002-12-11  
PRIOR APPLICATION NUMBER: US 09/687,267  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 09/028,655  
PRIOR FILING DATE: 1998-02-24  
PRIOR APPLICATION NUMBER: US 08/347,448  
PRIOR FILING DATE: 1995-06-23  
PRIOR APPLICATION NUMBER: US 07/890,754  
PRIOR FILING DATE: 1992-05-29  
PRIOR APPLICATION NUMBER: PCT/US98/05247  
PRIOR FILING DATE: 1993-06-01  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Mimic of a prenyl group  
US-10-317-644-6

Query Match 50.0%; Score 3; DB 12; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VLS 6  
Db 2 VLS 4

RESULT 49  
US-10-087-905-6  
Sequence 6, Application US/10087905  
Publication No. US20030022152A1  
GENERAL INFORMATION:  
APPLICANT: Haaland, Perry D.  
APPLICANT: Sherman, Douglas B.  
APPLICANT: Stewart II, Walter W.  
APPLICANT: Lloyd, Sheila A.  
APPLICANT: Campbell, Robert L.  
TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAM PRODUCTS FOR  
FILE REFERENCE: P3250  
CURRENT APPLICATION NUMBER: US/10/087,905  
CURRENT FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US/09/359,260  
PRIOR FILING DATE: 1999-07-22  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 6  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: hypothetical  
US-10-087-905-6

Query Match 50.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
Db 1 VLS 3

RESULT 50  
US-10-211-088-360  
Sequence 360, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai  
TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/309,395  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/341,589  
PRIOR FILING DATE: 2001-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 360  
LENGTH: 4  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Post-translational modification site  
US-10-211-088-360

Query Match 50.0%; Score 3; DB 15; Length 4;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 4 VLS 6  
|||  
Db 2 VLS 4

## RESULT 51

US-09-803-854-4  
; Sequence 4, Application US/09803854  
; Patent No. US20010046686A1  
; GENERAL INFORMATION:  
; APPLICANT: Albert J. Wong  
; APPLICANT: David K. Moscatello  
; APPLICANT: Allan Lipson  
; APPLICANT: Kim E. Leitzel  
; TITLE OF INVENTION: Sensitive Detection of Wild-Type and  
; TITLE OF INVENTION: Mutant EGFR by Specific ELISA Assays in Any Biological  
; TITLE OF INVENTION: Sample  
; FILE REFERENCE: W001-NP003  
; CURRENT APPLICATION NUMBER: US/09/803,854  
; CURRENT FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: 60/188,424  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-803-854-4

Query Match 50.0%; Score 3; DB 9; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6  
|||  
Db 1 VLS 3

## RESULT 52

US-09-924-824-16  
; Sequence 16, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Feng, Dong-Mei  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183V  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
US-09-924-824-16

Query Match 50.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4  
|||  
Db 3 QSV 5

## RESULT 53

US-09-924-824-17  
; Sequence 17, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Feng, Dong-Mei  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183V  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: clcIhexylglycine  
US-09-924-824-17

Query Match 50.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4  
|||  
Db 3 QSV 5

## RESULT 54

US-09-751-100B-43  
; Sequence 43, Application US/09751100B  
; Patent No. US20020142436A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical Research Council  
; TITLE OF INVENTION: Human Adenylate Cyclase and Use Therefor  
; FILE REFERENCE: P27948A  
; CURRENT APPLICATION NUMBER: US/09/751,100B  
; CURRENT FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 43  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-751-100B-43

Query Match 50.0%; Score 3; DB 10; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6  
|||  
Db 3 VLS 5

## RESULT 55

US-10-268-552-16  
; Sequence 16, Application US/10268552  
; Publication No. US20030133927A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: DeFeo-Jones, Deborah  
; APPLICANT: Jones, Raymond E.  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
US-10-268-552-16

; FILE REFERENCE: 20771  
; CURRENT APPLICATION NUMBER: US/10/268,552  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: 60/328,351  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
US-10-268-552-16

Query Match 50.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 3 QSV 5

RESULT 56  
US-10-268-552-17  
; Sequence 17, Application US/10268552  
; Publication No. US20030133927A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: DeFeo-Jones, Deborah  
; APPLICANT: Jones, Raymond E.  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20771  
; CURRENT APPLICATION NUMBER: US/10/268,552  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: 60/328,351  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa = cyclohexylglycine  
US-10-268-552-17

Query Match 50.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 3 QSV 5

RESULT 57  
US-10-076-047A-197  
; Sequence 197, Application US/10076047A  
; Publication No. US20030152935A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-026  
; CURRENT APPLICATION NUMBER: US/10/076,047A  
; CURRENT FILING DATE: 2002-02-13

; PRIOR APPLICATION NUMBER: GB 9919258.5  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: GB 0007754.5  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/03143  
; PRIOR FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 351  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 197  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-047A-197

Query Match 50.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 1 SVL 3

RESULT 58  
US-10-076-047A-251  
; Sequence 251, Application US/10076047A  
; Publication No. US20030152935A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-026  
; CURRENT APPLICATION NUMBER: US/10/076,047A  
; CURRENT FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: GB 9919258.5  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: GB 0007754.5  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/03143  
; PRIOR FILING DATE: 2000-08-14  
; NUMBER OF SEQ ID NOS: 351  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 251  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-047A-251

Query Match 50.0%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 1 SVL 3

RESULT 59  
US-10-076-047A-296  
; Sequence 296, Application US/10076047A  
; Publication No. US20030152935A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-026  
; CURRENT APPLICATION NUMBER: US/10/076,047A  
; CURRENT FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: GB 9919258.5  
; PRIOR FILING DATE: 1999-08-13  
; PRIOR APPLICATION NUMBER: GB 0007754.5  
; PRIOR FILING DATE: 2000-03-30  
; PRIOR APPLICATION NUMBER: PCT/GB00/03143

```
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-047A-296

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
Db 1 SVL 3

RESULT 60
US-10-319-402-25
; Sequence 25, Application US/10319402
; Publication No. US20030176689A1
; GENERAL INFORMATION:
; APPLICANT: Joyce, Michael
; APPLICANT: Williams, Mark
; APPLICANT: Hindsgaul, Ole
; APPLICANT: Tyrrell, D. Lorne
; TITLE OF INVENTION: Inhibitors of Hepatitis C Virus Protease
; FILE REFERENCE: UALB-002
; CURRENT APPLICATION NUMBER: US/10/319,402
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/340,574
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain in NS4A that binds to NS3 as discussed in the specification
; OTHER INFORMATION: (e.g. page 37)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: This sequence is shown in the specification using one-letter code
US-10-319-402-25

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 1 VLS 3

RESULT 61
US-10-352-704-29
; Sequence 29, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; STATE: D.C.

; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 351
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-047A-296

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5
Db 1 SVL 3

RESULT 60
US-10-319-402-25
; Sequence 25, Application US/10319402
; Publication No. US20030176689A1
; GENERAL INFORMATION:
; APPLICANT: Joyce, Michael
; APPLICANT: Williams, Mark
; APPLICANT: Hindsgaul, Ole
; APPLICANT: Tyrrell, D. Lorne
; TITLE OF INVENTION: Inhibitors of Hepatitis C Virus Protease
; FILE REFERENCE: UALB-002
; CURRENT APPLICATION NUMBER: US/10/319,402
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/340,574
; PRIOR FILING DATE: 2001-12-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain in NS4A that binds to NS3 as discussed in the specification
; OTHER INFORMATION: (e.g. page 37)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(5)
; OTHER INFORMATION: This sequence is shown in the specification using one-letter code
US-10-319-402-25

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VLS 6
Db 1 VLS 3

RESULT 61
US-10-352-704-29
; Sequence 29, Application US/10352704
; Publication No. US20030176690A1
; GENERAL INFORMATION:
; APPLICANT: Chatelain, Francois
; APPLICANT: Kumarev, Viktor
; TITLE OF INVENTION: Process for Preparing Polynucleotides on
; a Solid Support and Apparatus Permitting its
; Implementation
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; STATE: D.C.

; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,704
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,556A
; FILING DATE: 14-DEC-1994
; APPLICATION NUMBER: FR 9315164
; FILING DATE: 16-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William B.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: 10577/P58418
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-352-704-29

Query Match          50.0%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4
Db 2 QSV 4

RESULT 62
US-10-206-699-55
; Sequence 55, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundaramoorthy, M.
; APPLICANT: Hudson, B.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NC1 Domain Hexamer
; FILE REFERENCE: MHB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/308,523
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US 60/385,362
; PRIOR FILING DATE: 2002-06-03
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-206-699-55

Query Match          50.0%; Score 3; DB 15; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 POS 3  
|||  
Db 1 POS 3

## RESULT 63

US-08-681-219-11  
; Sequence 11, Application US/08681219  
; Publication No. US20020058607A1  
; GENERAL INFORMATION:  
; APPLICANT: Takaaki Sato and Junn Yanagisawa  
; TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN  
; SIGNAL-TRANSDUCING PROTEINS AND THE GLGF  
; TITLE OF INVENTION: (PDZ/DHR) DOMAIN AND USES THEREOF  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/681,219  
; FILING DATE: 22-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/48962/JPW/JKM  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-681-219-11

Query Match 50.0%; Score 3; DB 8; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 3 QSV 5

## RESULT 64

US-09-742-582-22  
; Sequence 22, Application US/09742582  
; Patent No. US20010012615A1  
; GENERAL INFORMATION:  
; APPLICANT: Heidler, Steven A  
; APPLICANT: Radding, Jeffrey A  
; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI  
; FILE REFERENCE: X-11242 Sequence 1st  
; Patent No. US20010012615A1  
; CURRENT APPLICATION NUMBER: US/09/742,582  
; CURRENT FILING DATE: 2000-12-20  
; PRIOR APPLICATION NUMBER: 09/041,075  
; PRIOR FILING DATE: 1998-03-10  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22

; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Cryptococcus neoformans  
US-09-742-582-22

Query Match 50.0%; Score 3; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVL 5  
|||  
Db 2 SVL 4

## RESULT 65

US-09-924-824-27  
; Sequence 27, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Feng, Dong-Mei  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183Y  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
US-09-924-824-27

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 4 QSV 6

## RESULT 66

US-09-924-824-28  
; Sequence 28, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; APPLICANT: Feng, Dong-Mei  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183Y  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: cyclohexylglycine  
US-09-924-824-28

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 4 QSV 6

RESULT 67  
US-09-924-824-37  
; Sequence 37, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183Y  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 37  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
US-09-924-824-37

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 4 QSV 6

RESULT 68  
US-09-924-824-38  
; Sequence 38, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183Y  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 38  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: cyclohexylglycine  
US-09-924-824-38

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 4 QSV 6

RESULT 69  
US-09-924-824-44  
; Sequence 44, Application US/09924824  
; Patent No. US20020103136A1  
; GENERAL INFORMATION:  
; APPLICANT: Merck & Co., Inc.  
; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
; TITLE OF INVENTION: PROSTATE CANCER  
; FILE REFERENCE: 20183Y  
; CURRENT APPLICATION NUMBER: US/09/924,824  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/076,860  
; PRIOR FILING DATE: 1998-03-05  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: completely synthetic amino acid sequence  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: cyclohexylglycine  
US-09-924-824-44

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 4 QSV 6

RESULT 70  
US-09-973-233A-15  
; Sequence 15, Application US/09873233A  
; Patent No. US20020146434A1  
; GENERAL INFORMATION:  
; APPLICANT: UEDA, Shigeharu  
; APPLICANT: WATANABE, Michiko  
; APPLICANT: KAWANISHI, Hitomi  
; TITLE OF INVENTION: GENE CODING FOR THE MEASLES VIRUS MUTANT ANTIGEN  
; FILE REFERENCE: 0216-0451P  
; CURRENT APPLICATION NUMBER: US/09/873,233A  
; CURRENT FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Measles virus  
; FEATURE:  
; OTHER INFORMATION: Attenuated measles virus NA strain  
US-09-973-233A-15

Query Match 50.0%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
|||  
Db 2 QSV 4

RESULT 71  
 US-09-742-580-22  
 ; Sequence 22, Application US/09742580  
 ; Publication No. US20030022342A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heidler, Steven A  
 ; APPLICANT: Radding, Jeffrey A  
 ; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI  
 ; FILE REFERENCE: X-11242 Sequence Let  
 ; CURRENT APPLICATION NUMBER: US/09/742,580  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: 09/041,075  
 ; PRIOR FILING DATE: 1998-03-10  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Cryptococcus neoformans  
 US-09-742-580-22

Query Match 50.0%; Score 3; DB 11; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 2 SVL 4

RESULT 72  
 US-09-742-581-22  
 ; Sequence 22, Application US/09742581  
 ; Publication No. US20030022343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heidler, Steven A  
 ; APPLICANT: Radding, Jeffrey A  
 ; TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI  
 ; FILE REFERENCE: X-11242 Sequence Let  
 ; CURRENT APPLICATION NUMBER: US/09/742,581  
 ; CURRENT FILING DATE: 2000-12-20  
 ; PRIOR APPLICATION NUMBER: 09/041,075  
 ; PRIOR FILING DATE: 1998-03-10  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 22  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Cryptococcus neoformans  
 US-09-742-581-22

Query Match 50.0%; Score 3; DB 11; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVL 5  
 |||  
 Db 2 SVL 4

RESULT 73  
 US-10-268-552-30  
 ; Sequence 30, Application US/10268552  
 ; Publication No. US20030133927A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Defeo-Jones, Deborah  
 ; APPLICANT: Jones, Raymond E.  
 ; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
 ; TITLE OF INVENTION: PROSTATE CANCER  
 ; FILE REFERENCE: 20771  
 ; CURRENT APPLICATION NUMBER: US/10/268,552  
 ; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: 60/328,351  
 ; PRIOR FILING DATE: 2001-10-10  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 30  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
 US-10-268-552-30

Query Match 50.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4  
 |||  
 Db 4 QSV 6

RESULT 74  
 US-10-268-552-31  
 ; Sequence 31, Application US/10268552  
 ; Publication No. US20030133927A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Defeo-Jones, Deborah  
 ; APPLICANT: Jones, Raymond E.  
 ; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
 ; TITLE OF INVENTION: PROSTATE CANCER  
 ; FILE REFERENCE: 20771  
 ; CURRENT APPLICATION NUMBER: US/10/268,552  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: 60/328,351  
 ; PRIOR FILING DATE: 2001-10-10  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO 31  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence  
 ; NAME/KEY: VARIANT  
 ; LOCATION: (3)...(3)  
 ; OTHER INFORMATION: Xaa = cyclohexylglycine  
 US-10-268-552-31

Query Match 50.0%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSV 4  
 |||  
 Db 4 QSV 6

RESULT 75  
 US-10-268-552-40  
 ; Sequence 40, Application US/10268552  
 ; Publication No. US20030133927A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Merck & Co., Inc.  
 ; APPLICANT: Defeo-Jones, Deborah  
 ; APPLICANT: Jones, Raymond E.  
 ; TITLE OF INVENTION: CONJUGATES USEFUL IN THE TREATMENT OF  
 ; TITLE OF INVENTION: PROSTATE CANCER  
 ; FILE REFERENCE: 20771  
 ; CURRENT APPLICATION NUMBER: US/10/268,552  
 ; CURRENT FILING DATE: 2002-10-10  
 ; PRIOR APPLICATION NUMBER: 60/328,351

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; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Completely Synthetic Amino Acid Sequence
US-10-268-552-40
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Query Match      50.0%; Score 3; DB 12; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2 QSV 4
         |||
Db      4 QSV 6
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Search completed: November 25, 2003, 20:37:03
Job time : 10.6279 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 4.84884 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-26

Perfect score: 6

Sequence: 1 PQSVLS 6

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/aaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/aaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/aaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/aaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/aaa/PTCUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/aaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6	100.0	20	3	US-08-505-250-12
3	6	100.0	20	4	US-08-505-250-12
4	6	100.0	20	4	US-08-505-250-12
5	4	66.7	5	2	US-08-691-997-12
6	4	66.7	5	2	US-08-691-997-11
7	4	66.7	5	4	US-09-360-237-10
8	4	66.7	5	4	US-09-522-666-31
9	4	66.7	7	4	US-08-691-997-3
10	4	66.7	7	4	US-09-537-817B-7
11	4	66.7	8	2	US-08-373-190-39
12	4	66.7	8	2	US-08-350-260A-382
13	4	66.7	8	2	US-08-438-190A-39
14	4	66.7	8	3	US-08-350-215-39
15	4	66.7	8	3	US-09-287-145A-39
16	4	66.7	8	4	US-09-556-111-39
17	4	66.7	8	4	US-09-104-337A-382
18	4	66.7	9	2	US-08-691-997-9
19	4	66.7	10	4	US-09-298-924-39
20	4	66.7	11	1	US-07-791-935B-13
21	4	66.7	12	2	US-08-811-492-150
22	4	66.7	13	2	US-08-691-997-8
23	4	66.7	13	4	US-09-522-666-30
24	4	66.7	13	6	US-09-257-825B-22
25	4	66.7	14	1	US-07-791-935B-9
26	4	66.7	14	2	US-08-691-997-4
27	4	66.7	15	1	US-08-268-251-5

28	4	66.7	15	1	US-08-342-411A-21	Sequence 21, Appl
29	4	66.7	15	1	US-08-397-633A-80	Sequence 80, Appl
30	4	66.7	15	1	US-08-397-633A-81	Sequence 81, Appl
31	4	66.7	15	1	US-08-397-633A-83	Sequence 83, Appl
32	4	66.7	15	3	US-08-684-187-4	Sequence 4, Appl
33	4	66.7	15	4	US-09-537-817B-2	Sequence 2, Appl
34	4	66.7	15	4	US-09-205-258-582	Sequence 582, App
35	4	66.7	15	5	PCT-US93-01112-5	Sequence 5, Appl
36	4	66.7	16	2	US-08-480-190-37	Sequence 37, Appl
37	4	66.7	16	2	US-08-488-379-37	Sequence 37, Appl
38	4	66.7	16	4	US-09-360-237-55	Sequence 55, Appl
39	4	66.7	16	4	US-08-475-399A-37	Sequence 37, Appl
40	4	66.7	16	5	PCT-US93-07545-37	Sequence 37, Appl
41	4	66.7	17	1	US-08-360-125-19	Sequence 19, Appl
42	4	66.7	17	2	US-08-450-578-19	Sequence 19, Appl
43	4	66.7	17	2	US-09-017-628-19	Sequence 19, Appl
44	4	66.7	17	2	US-09-014-880-19	Sequence 19, Appl
45	4	66.7	17	3	US-08-658-857B-23	Sequence 23, Appl
46	4	66.7	17	3	US-08-763-226C-23	Sequence 23, Appl
47	4	66.7	17	3	US-09-307-200-23	Sequence 23, Appl
48	4	66.7	17	4	US-08-450-363-19	Sequence 19, Appl
49	4	66.7	17	4	US-09-593-321-23	Sequence 23, Appl
50	4	66.7	19	1	US-08-519-777-15	Sequence 15, Appl
51	4	66.7	19	1	US-08-742-035-15	Sequence 15, Appl
52	4	66.7	19	2	US-08-777-019-15	Sequence 15, Appl
53	4	66.7	19	2	US-08-777-143-15	Sequence 15, Appl
54	4	66.7	19	3	US-08-775-414-15	Sequence 15, Appl
55	4	66.7	19	3	US-08-931-858E-15	Sequence 15, Appl
56	4	66.7	19	3	US-08-981-739-15	Sequence 15, Appl
57	4	66.7	19	4	US-09-128-026-15	Sequence 15, Appl
58	4	66.7	19	4	US-09-257-825B-23	Sequence 23, Appl
59	4	66.7	20	3	US-08-658-857B-24	Sequence 24, Appl
60	4	66.7	20	3	US-08-763-226C-24	Sequence 24, Appl
61	4	66.7	20	3	US-09-307-200-24	Sequence 24, Appl
62	4	66.7	20	4	US-09-593-321-24	Sequence 24, Appl
63	3	50.0	4	1	US-07-772-087-8	Sequence 8, Appl
64	3	50.0	4	1	US-08-199-778-4	Sequence 4, Appl
65	3	50.0	4	1	US-08-240-712-5	Sequence 5, Appl
66	3	50.0	4	1	US-08-387-156-22	Sequence 22, Appl
67	3	50.0	4	1	US-08-443-890-5	Sequence 5, Appl
68	3	50.0	4	2	US-08-667-001-13	Sequence 13, Appl
69	3	50.0	4	2	US-08-694-865-28	Sequence 28, Appl
70	3	50.0	4	2	US-08-358-556A-27	Sequence 27, Appl
71	3	50.0	4	2	US-08-637-759B-200	Sequence 200, App
72	3	50.0	4	2	US-08-429-964-19	Sequence 19, Appl
73	3	50.0	4	2	US-08-878-748-22	Sequence 22, Appl
74	3	50.0	4	2	US-08-707-082A-18	Sequence 18, Appl
75	3	50.0	4	2	US-08-582-076-2	Sequence 2, Appl
76	3	50.0	4	3	US-08-871-355A-200	Sequence 200, App
77	3	50.0	4	3	US-09-124-431-28	Sequence 28, Appl
78	3	50.0	4	3	US-09-195-578-11	Sequence 11, Appl
79	3	50.0	4	3	US-08-894-173-20	Sequence 20, Appl
80	3	50.0	4	3	US-09-140-557-11	Sequence 11, Appl
81	3	50.0	4	3	US-09-170-951-11	Sequence 11, Appl
82	3	50.0	4	3	US-09-164-482-11	Sequence 11, Appl
83	3	50.0	4	3	US-09-330-970-16	Sequence 16, Appl
84	3	50.0	4	3	US-09-330-970-34	Sequence 34, Appl
85	3	50.0	4	3	US-09-058-562-5	Sequence 5, Appl
86	3	50.0	4	3	US-09-398-193-20	Sequence 20, Appl
87	3	50.0	4	3	US-09-167-180-11	Sequence 11, Appl
88	3	50.0	4	4	US-09-360-237-11	Sequence 11, Appl
89	3	50.0	4	4	US-09-360-237-38	Sequence 38, Appl
90	3	50.0	4	4	US-09-426-533-1	Sequence 1, Appl
91	3	50.0	4	4	US-09-516-945-1	Sequence 1, Appl
92	3	50.0	4	4	US-09-201-945-200	Sequence 200, App
93	3	50.0	4	4	US-09-757-218-2	Sequence 2, Appl
94	3	50.0	4	4	US-09-516-757-1	Sequence 1, Appl
95	3	50.0	4	4	US-09-516-750-1	Sequence 1, Appl
96	3	50.0	4	4	US-09-342-577-2	Sequence 2, Appl
97	3	50.0	4	4	US-09-516-756-1	Sequence 1, Appl
98	3	50.0	4	4	US-09-828-061A-2	Sequence 2, Appl
99	3	50.0	4	4	US-09-463-917-2	Sequence 2, Appl
100	3	50.0	4	4	US-09-347-673-2	Sequence 2, Appl



## ALIGNMENTS

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RESULT 1
US-09-641-803-26
; Sequence 26, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/09/641.803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-26

Query Match      100.0%; Score 6; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6
Db 1 PQSVLS 6

RESULT 2
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6183983
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Sakagami, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: PCT/JP95/00298
; EARLIER FILING DATE: 1995-02-27
; EARLIER APPLICATION NUMBER: JP 198187/94
; EARLIER FILING DATE: 1994-08-23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12

Query Match      100.0%; Score 6; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6
Db 1 PQSVLS 6

RESULT 3
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: PCT/JP95/00298
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: JP 198187/94
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12

Query Match      100.0%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6
Db 2 PQSVLS 7

RESULT 4
US-08-691-997-12
; Sequence 12, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
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Qy 1 PQSVLS 6
Db 2 PQSVLS 7

RESULT 3
US-08-505-250-12
; Sequence 12, Application US/08505250
; Patent No. 6322996
; GENERAL INFORMATION:
; APPLICANT: Sato, Haruya
; APPLICANT: Yamamoto, Keiji
; APPLICANT: Suzuki, Kokichi
; APPLICANT: Ikeda, Masahiro
; APPLICANT: Taniguchi, Makoto
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
; FILE REFERENCE: 110-511
; CURRENT APPLICATION NUMBER: US/08/505,250
; CURRENT FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: PCT/JP95/00298
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: JP 198187/94
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-08-505-250-12

Query Match      100.0%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PQSVLS 6
Db 2 PQSVLS 7

RESULT 4
US-08-691-997-12
; Sequence 12, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
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;/ FILING DATE:  
;/ CLASSIFICATION: 424  
;/ PRIOR APPLICATION DATA:  
;/ APPLICATION NUMBER:  
;/ FILING DATE:  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Guise, Jeffrey W.  
;/ REGISTRATION NUMBER: 34,613  
;/ REFERENCE/DOCKET NUMBER: 219/251  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (213) 489-1600  
;/ TELEFAX: (213) 955-0440  
;/ TELEX: 67-3510  
;/ INFORMATION FOR SEQ ID NO: 12:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 4 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-691-997-12

Query Match 66.7%; Score 4; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 1 SVLS 4

RESULT 5  
US-08-691-997-11  
; Sequence 11, Application US/08691997  
; Patent No. 585682  
; GENERAL INFORMATION:  
; APPLICANT: Gruenwald, Stefan  
; APPLICANT: Sang, Bi-Ching  
; APPLICANT: Monell, Craig  
; TITLE OF INVENTION: E2A/px1 FUSION PROTEIN  
; TITLE OF INVENTION: SPECIFIC MONOCLONAL  
; TITLE OF INVENTION: ANTIBODIES  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/691,997  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Guise, Jeffrey W.  
; REGISTRATION NUMBER: 34,613  
; REFERENCE/DOCKET NUMBER: 219/251  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 11:

;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 5 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: peptide  
;/ US-08-691-997-11

Query Match 66.7%; Score 4; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 2 SVLS 5

RESULT 6  
US-09-360-237-10  
; Sequence 10, Application US/09360237  
; Patent No. 6322962  
; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: CHENG, DONG  
; APPLICANT: ESPENSHADE, PETER J.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: RAWSON, ROBERT B.  
; APPLICANT: SAKAI, JURO  
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF  
; TITLE OF INVENTION: MODULATORS THEREOF  
; FILE REFERENCE: UTXD:567  
; CURRENT APPLICATION NUMBER: US/09/360,237  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/096,571  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE  
; US-09-360-237-10

Query Match 66.7%; Score 4; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 2 SVLS 5

RESULT 7  
US-09-522-666-31  
; Sequence 31, Application US/09522666  
; Patent No. 6333167  
; GENERAL INFORMATION:  
; APPLICANT: Shuey, David  
; APPLICANT: Quinet, Elaine  
; TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of  
; TITLE OF INVENTION: Proteolysis of Membrane-Associated Proteins  
; FILE REFERENCE: 6-00  
; CURRENT APPLICATION NUMBER: US/09/522,666  
; CURRENT FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 31  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence within human, hamster SREBP-2 recognized
; OTHER INFORMATION: by Site-1 protease
US-09-522-666-31

Query Match          66.7%; Score 4; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 2 SVLS 5

RESULT 8
US-08-691-997-3
; Sequence 3, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-997-3

Query Match          66.7%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 3 SVLS 6
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```
RESULT 9
US-09-537-817B-7
; Sequence 7, Application US/09537817B
; Patent No. 6417327
; GENERAL INFORMATION:
; APPLICANT: Shuichi Oka
; APPLICANT: Yoshimitsu Yamazaki
; APPLICANT: Toru Imamura
; APPLICANT: Yasuko Fujita
; APPLICANT: Saori Yamamoto
; APPLICANT: Yukiko Okita
; APPLICANT: Kazuo Ozawa
; APPLICANT: Reiko Akakura
; APPLICANT: Chikako Ito
; TITLE OF INVENTION: PEPTIDE CAPABLE OF REGULATING
; TITLE OF INVENTION: PHYSIOLOGICAL FUNCTION OF FGF-5 AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITION CONTAINING THE PEPTIDE
; FILE REFERENCE: 08206-012001
; CURRENT APPLICATION NUMBER: US/09/537,817B
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: JP 88364/1999
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: JP 6643/2000
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:7 represents a partial sequence
; OTHER INFORMATION: (corresponding to amino acids 111-117) of the
; OTHER INFORMATION: amino acid sequence of mouse FGF-5.
US-09-537-817B-7

Query Match          66.7%; Score 4; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 4 SVLS 7

RESULT 10
US-08-373-190-39
; Sequence 39, Application US/08373190
; Patent No. 5851829
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; APPLICANT: HASELTINE, WILLIAM
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
; NUMBER OF SEQUENCES: 79
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/373,190
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06735
```

; FILING DATE: 16-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: RESNICK, DAVID S  
; REGISTRATION NUMBER: 34,235  
; REFERENCE/DOCKET NUMBER: 41956-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-523-3400  
; TELEFAX: 617-523-6440  
; TELEX: STRE UR 2002  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; US-08-373-190-39

Query Match 66.7%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 5 SVLS 8

RESULT 11  
US-08-350-260A-382  
; Sequence 382, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/350,260A  
; FILING DATE: 05-DEC-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9110549.4  
; FILING DATE: 15-MAY-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01134  
; FILING DATE: 10-JUL-1991  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/00883  
; FILING DATE: 15-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/00605  
; FILING DATE: 24-MAR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/150,002  
; FILING DATE: 31-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/307,619  
; FILING DATE: 16-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clough, David W  
; REGISTRATION NUMBER: 36,107  
; REFERENCE/DOCKET NUMBER: 28111/32372  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; INFORMATION FOR SEQ ID NO: 382:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-350-260A-382

Query Match 66.7%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 1 SVLS 4

RESULT 12  
US-08-438-190A-39  
; Sequence 39, Application US/08438190A  
; Patent No. 5965371  
; GENERAL INFORMATION:  
; APPLICANT: MARASCO, WAYNE  
; APPLICANT: HASELTINE, WILLIAM  
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF  
; NUMBER OF SEQUENCES: 78  
; TITLE OF INVENTION: PROTEINS  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &  
; ADDRESS: CUSHMAN  
; STREET: 130 WATER STREET  
; CITY: BOSTON  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/438,190A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: EISENSTEIN, RONALD I.  
; REGISTRATION NUMBER: 30628  
; REFERENCE/DOCKET NUMBER: 41956  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 523-3400  
; TELEX: 200291 STRE UR  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid

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; TOPOLOGY: linear
US-08-438-190A-39
Query Match      66.7%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 13
US-08-350-215-39
; Sequence 39, Application US/08350215
; Patent No. 6004940
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE A.
; TITLE OF INVENTION: INTRACELLULAR TARGETING OF ENDOGENOUS
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/287,145A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,190
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-287-145A-39
Query Match      66.7%; Score 4; DB 3; Length 8;
Best Local Similarity 100.0%; Pred.No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 5 SVLS 8

RESULT 15
US-09-556-111-39
; Sequence 39, Application US/09556111
; Patent No. 6329173
; GENERAL INFORMATION:
; APPLICANT: MARASCO, WAYNE
; TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
; PROTEINS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/556,111
; FILING DATE: 21-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,190

```

```
;
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: EISENSTEIN, RONALD I.
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41956
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-556-111-39

Query Match          66.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
Db      5 SVLS 8

RESULT 16
US-09-104-337A-382
; Sequence 382, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Abuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
```

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;
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 382:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 382:
US-09-104-337A-382

Query Match          66.7%; Score 4; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
Db      1 SVLS 4

RESULT 17
US-08-691-997-9
; Sequence 9, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/691,997
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Guise, Jeffrey W.
; REGISTRATION NUMBER: 34,613
; REFERENCE/DOCKET NUMBER: 219/251
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-691-997-9
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Query Match 66.7%; Score 4; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|  
|  
|  
|  
Db 4 SVLS 7

RESULT 18  
US-09-298-924-39  
; Sequence 39, Application US/09298924  
; Patent No. 6391595  
; GENERAL INFORMATION:  
; APPLICANT: KATO, Masaru  
; MIURA, Yutaka  
; KETTOKU, Masako  
; IWAMATSU, Akihiro  
; KOBAYASHI, Kazuo  
; KOMEDA, Toshihiro  
; TITLE OF INVENTION: NOVEL TRANSFERASE AND AMYLASE, PROCESS  
; FOR PRODUCING THE ENZYMES, USE THEREOF, AND GENE CODING  
; FOR THE SAME  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/298,924  
; FILING DATE: 26-Apr-1999  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/750,569  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 7-120673  
; FILING DATE: 21-APR-1995  
; APPLICATION NUMBER: JP 6-311185  
; FILING DATE: 21-NOV-1994  
; APPLICATION NUMBER: JP 6-286917  
; FILING DATE: 21-NOV-1994  
; APPLICATION NUMBER: JP 6-290394  
; FILING DATE: 31-OCT-1994  
; APPLICATION NUMBER: JP 6-194223  
; FILING DATE: 18-AUG-1994  
; APPLICATION NUMBER: JP 6-133354  
; FILING DATE: 16-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 49441/110  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-298-924-39

Query Match 66.7%; Score 4; DB 4; Length 10;

Best Local Similarity 100.0%; Pred.No. 64;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|  
|  
|  
|  
Db 2 SVLS 5

RESULT 19  
US-07-791-935B-13  
; Sequence 13, Application US/07791935B  
; Patent No. 5366871  
; GENERAL INFORMATION:  
; APPLICANT: RECHSTEINER, MARTIN C.  
; APPLICANT: YOO, YUNG JOON  
; TITLE OF INVENTION: UBIQUITIN-PEPTIDE EXTENSIONS AS  
; ENZYME SUBSTRATES  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Thorpe, No. 5366871th & Western  
; STREET: 9035 South 700 East, Suite 200  
; CITY: Sandy  
; STATE: Utah  
; COUNTRY: USA  
; ZIP: 84070  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage  
; COMPUTER: compaq LTE/286  
; OPERATING SYSTEM: DOS 4.01  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,935B  
; FILING DATE: 19911113  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: none  
; FILING DATE: na  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Western, M. Wayne  
; REGISTRATION NUMBER: 22,788  
; REFERENCE/DOCKET NUMBER: T310  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (801) 566-6633  
; TELEFAX: (801) 566-0750  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acid residues  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
US-07-791-935B-13

Query Match 66.7%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred.No. 70;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|  
|  
|  
|  
Db 8 SVLS 11

RESULT 20  
US-08-811-492-150  
; Sequence 150, Application US/08811492  
; Patent No. 5834247  
; GENERAL INFORMATION:  
; APPLICANT: COMB, DONALD G.  
; APPLICANT: PERLER, FRANCINE B.  
; APPLICANT: JACK, WILLIAM E.  
; APPLICANT: XU, MING-QUN  
; APPLICANT: HODGES, ROBERT A.  
; APPLICANT: NOREN, CHRISTOPHER J.  
; APPLICANT: CHONG, SHAO-RONG S.C.  
; APPLICANT: ADAM, ERIC

APPLICANT: SOUTHWORTH, MAURICE  
TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR  
PRODUCTION AND METHODS FOR PURIFICATION OF TARGET  
PROTEINS  
NUMBER OF SEQUENCES: 155  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.  
STREET: 32 TOZER ROAD  
CITY: BEVERLY  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 01915  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC\DOS\MS\DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/811,492  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/580,555  
FILING DATE: 29-DEC-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/496,247  
FILING DATE: 28-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/146,885  
FILING DATE: 03-NOV-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/004,139  
FILING DATE: 09-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Gregory D  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-036C4  
TELEPHONE: 508-927-5054  
TELEFAX: 509-927-1705  
TELEX:  
INFORMATION FOR SEQ ID NO: 150:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-811-492-150  
Query Match 66.7%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVLS 6  
DB 7 SVLS 10  
RESULT 21  
US-08-691-997-8  
Sequence 8, Application US/08691997  
Patent No. 5858682  
GENERAL INFORMATION:  
APPLICANT: Gruenwald, Stefan  
APPLICANT: Sang, Bi-Chang  
APPLICANT: Monell, Craig  
TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN  
TITLE OF INVENTION: SPECIFIC MONOCLONAL

TITLE OF INVENTION: ANTIBODIES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/691,997  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 219/251  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-691-997-8  
Query Match 66.7%; Score 4; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 SVLS 6  
DB 5 SVLS 8  
RESULT 22  
US-09-522-666-30  
Sequence 30, Application US/09522666  
Patent No. 6333167  
GENERAL INFORMATION:  
APPLICANT: Shuey, David  
APPLICANT: Quinet, Elaine  
TITLE OF INVENTION: Methods and Reagents for Identifying Inhibitors of  
Proteolysis of Membrane-Associated Proteins  
FILE REFERENCE: 6-00  
CURRENT APPLICATION NUMBER: US/09/522,666  
CURRENT FILING DATE: 2000-03-10  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 30  
LENGTH: 13  
TYPE: PPT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: amino acid  
OTHER INFORMATION: sequence encompassing Site-1 protease cleavage  
OTHER INFORMATION: site within SREPB-2  
US-09-522-666-30



```
Query Match          66.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      8 SVLS 11

RESULT 23
US-09-257-825B-22
; Sequence 22, Application US/09257825B
; Patent No. 6403352
; GENERAL INFORMATION:
; APPLICANT: Poovaiyah, Bachettira W.
; APPLICANT: Patil, Shameekumar
; APPLICANT: Takezawa, Daisuke
; TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants
; FILE REFERENCE: 4630-51993
; CURRENT APPLICATION NUMBER: US/09/257,825B
; CURRENT FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: US 08/655,352
; PRIOR FILING DATE: 1996-05-23
; PRIOR APPLICATION NUMBER: US 60/014,743
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Lilium longiflorum
US-09-257-825B-22

Query Match          66.7%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      9 SVLS 12

RESULT 24
5242798-11
; Patent No. 5242798
; APPLICANT: SUTCLIFFE, J. GEROR
; TITLE OF INVENTION: SYNTHETIC POLYPEPTIDES CORRESPONDING
; TO PORTIONS OF PROTEINIDS TRANSLATED FROM BRAIN-SPECIFIC MENAS,
; RECEPTORS, METHODS AND DIAGNOSTICS USING THE SAME
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/476,961
; FILING DATE: 07-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 58 620
; FILING DATE: 03-JUN-1987
; APPLICATION NUMBER: 516,136
; FILING DATE: 21-JUL-1983
; SEQ ID NO:11
; LENGTH: 13
5242798-11

Query Match          66.7%; Score 4; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      8 SVLS 11

RESULT 25
US-07-791-935B-9
```

```
; Sequence 9, Application US/07791935B
; Patent No. 5366871
; GENERAL INFORMATION:
; APPLICANT: RECHSTEINER, MARTIN C.
; APPLICANT: YOO, YUNG JOON
; TITLE OF INVENTION: UBIQUITIN-PEPTIDE EXTENSIONS AS
; TITLE OF INVENTION: ENZYME SUBSTRATES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thorpe, No. 5366871th & Western
; STREET: 9035 South 700 East, Suite 200
; CITY: Sandy
; STATE: Utah
; COUNTRY: USA
; ZIP: 84070
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 720 Kb storage
; COMPUTER: Compaq LTE/286
; OPERATING SYSTEM: DOS 4.01
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,935B
; FILING DATE: 19911113
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: none
; FILING DATE: na
; ATTORNEY/AGENT INFORMATION:
; NAME: Western, M. Wayne
; REGISTRATION NUMBER: 22,788
; REFERENCE/DOCKET NUMBER: T310
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (801) 566-6633
; TELEFAX: (801) 566-0750
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
US-07-791-935B-9

Query Match          66.7%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 SVLS 6
      |||||
Db      11 SVLS 14

RESULT 26
US-08-691-997-4
; Sequence 4, Application US/08691997
; Patent No. 5858682
; GENERAL INFORMATION:
; APPLICANT: Gruenwald, Stefan
; APPLICANT: Sang, Bi-Ching
; APPLICANT: Monell, Craig
; TITLE OF INVENTION: E2A/pbx1 FUSION PROTEIN
; TITLE OF INVENTION: SPECIFIC MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
```

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/691.997  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Guise, Jeffrey W.  
REGISTRATION NUMBER: 34,613  
REFERENCE/DOCKET NUMBER: 219/251  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-691-997-4

Query Match 66.7%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 3 SVLS 6

RESULT 27  
US-08-268-251-5  
Sequence 5, Application US/08268251  
Patent No. 5585475  
GENERAL INFORMATION:  
APPLICANT: Jamieson, Gordon A  
APPLICANT: Dedman, John R  
APPLICANT: Kaetzel, Marcia A  
TITLE OF INVENTION: Calmodulin-Binding Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,251  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/831,219  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Grant D  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 272.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-268-251-5  
Query Match 66.7%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 10 SVLS 13

RESULT 28  
US-08-342-411A-21  
Sequence 21, Application US/08342411A  
Patent No. 5639616  
GENERAL INFORMATION:  
APPLICANT: LIAO, Shutsung  
APPLICANT: SONG, Ching  
TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR:  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: TX  
COUNTRY: USA  
ZIP: 77210-4433  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/342,411A  
FILING DATE: 18-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KITCHELL, BARBARA S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: ARCD154  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-342-411A-21

Query Match 66.7%; Score 4; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 8 SVLS 11

RESULT 29  
US-08-397-633A-80  
Sequence 80, Application US/08397633A  
Patent No. 5773577

```

; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMTIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-80

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

RESULT 30
US-08-397-633A-81
; Sequence 81, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMTIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

RESULT 31
US-08-397-633A-83
; Sequence 83, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMTIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-81

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

```

```

; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-81

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

RESULT 31
US-08-397-633A-83
; Sequence 83, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMTIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83

Query Match 66.7%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6
Db 1 SVLS 4

```

Db 1 SVLS 4

RESULT 32

US-08-684-187-4

Sequence 4, Application US/08684187A

Patent No. 6020171

GENERAL INFORMATION:

APPLICANT: SAITO, ATSUSHI

APPLICANT: SHINAGAWA, HIDEO

APPLICANT: NAKATA, ATSUO

TITLE OF INVENTION: METHOD OF PREPARING PLASMID HAVING BOTH EXPRESSING

TITLE OF INVENTION: ABILITY OF RETROVIRAL GENE AND PROCESSING ABILITY AFTER

TITLE OF INVENTION: TRANSLATION, AND RESULTANT PLASMID AND EXPRESSION

TITLE OF INVENTION: PRODUCTS THEROF

FILE REFERENCE: 96-0747/lc(wmc)/653

CURRENT APPLICATION NUMBER: US/08/684,187A

CURRENT FILING DATE: 1996-07-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: N-TERMINAL

OTHER INFORMATION: AMINO ACID SEQUENCE

US-08-684-187-4

Query Match 66.7%; Score 4; DB 3; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6

Db 5 SVLS 8

RESULT 33

US-09-537-817B-2

Sequence 2, Application US/09537817B

Patent No. 6417327

GENERAL INFORMATION:

APPLICANT: Shuichi Oka

APPLICANT: Yoshimitsu Yamazaki

APPLICANT: Toru Imamura

APPLICANT: Yasuko Fujita

APPLICANT: Saori Yamamoto

APPLICANT: Yukiko Okita

APPLICANT: Kazuo Ozawa

APPLICANT: Reiko Akakura

APPLICANT: Chikako Ito

TITLE OF INVENTION: PEPTIDE CAPABLE OF REGULATING

TITLE OF INVENTION: PHYSIOLOGICAL FUNCTION OF FGF-5 AND PHARMACEUTICAL

TITLE OF INVENTION: COMPOSITION CONTAINING THE PEPTIDE

FILE REFERENCE: 08206-012001

CURRENT APPLICATION NUMBER: US/09/537,817B

CURRENT FILING DATE: 2001-08-23

PRIOR APPLICATION NUMBER: JP 88364/1999

PRIOR FILING DATE: 1999-03-30

PRIOR APPLICATION NUMBER: JP 6643/2000

PRIOR FILING DATE: 2000-01-14

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: SEQ ID NO:2 represents a partial sequence

OTHER INFORMATION: (corresponding to amino acids 103-117) of the

OTHER INFORMATION: amino acid sequence of mouse FGF-5.

US-09-537-817B-2

Query Match 66.7%; Score 4; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6

Db 12 SVLS 15

RESULT 34

US-09-205-258-582

Sequence 582, Application US/09205258

Patent No. 6525174

GENERAL INFORMATION:

APPLICANT: Young et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

FILE REFERENCE: P2007P1

CURRENT APPLICATION NUMBER: US/09/205,258

CURRENT FILING DATE: 1998-12-04

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER FILING DATE: 1998-06-04

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,880

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,020

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,876

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,895

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,884

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,894

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,971

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,964

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,882

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,899

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,893

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,900

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,892

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,915

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,019

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,970

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,972

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,916

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,373

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,875

EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/049,374

EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,897  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,898  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
EARLIER FILING DATE: 1998-07-30  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 582  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-205-258-582

Query Match 66.7% Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 11 SVLS 14

RESULT 35  
PCT-US93-01112-5  
Sequence 5, Application PC/TUS9301112  
GENERAL INFORMATION:  
APPLICANT: Jamieson, Gordon A  
APPLICANT: Dedman, John R  
APPLICANT: Kaetzel, Marcia A  
TITLE OF INVENTION: Calmodulin-Binding Peptides  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Chiron Corporation  
STREET: 4560 Horton Street  
CITY: Emeryville  
STATE: CA  
COUNTRY: USA  
ZIP: 94608  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/01112  
FILING DATE: 19930208  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/831,219  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:

NAME: Green, Grant D  
REGISTRATION NUMBER: 31,259  
REFERENCE/DOCKET NUMBER: 272.001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (510) 601-2706  
TELEFAX: (510) 655-3542  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: AMINO ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US93-01112-5

Query Match 66.7% Score 4; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 10 SVLS 13

RESULT 36  
US-08-480-190-37  
Sequence 37, Application US/08480190  
Patent No. 5827516  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 274  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 50Z or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,190  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/077,255  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-480-190-37

Query Match 66.7%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 5 SVLS 8

RESULT 37  
US-08-488-379-37  
; Sequence 37, Application US/08488379  
; Patent No. 5880103  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Urban  
; APPLICANT: Roman M. Chicz  
; APPLICANT: Dario A. A. Vignali  
; APPLICANT: Mary L. Hedley  
; APPLICANT: Lawrence J. Stern  
; APPLICANT: Jack L. Strominger  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; COMPUTER: IBM PS/2 Model 502 or 55SX  
; OPERATING SYSTEM: MS-DOS (Version 5.0)  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/488,379  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: June 15, 1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: August 11, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Clark, Paul T.  
; REGISTRATION NUMBER: 30,162  
; REFERENCE/DOCKET NUMBER: 00246/168001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 200154  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear

Query Match 66.7%; Score 4; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 5 SVLS 8

RESULT 38  
US-09-360-237-55  
; Sequence 55, Application US/09360237  
; Patent No. 6322962

; GENERAL INFORMATION:  
; APPLICANT: BROWN, MICHAEL S.  
; APPLICANT: CHENG, DONG  
; APPLICANT: ESPENSHADE, PETER J.  
; APPLICANT: GOLDSTEIN, JOSEPH L.  
; APPLICANT: RAWSON, ROBERT B.  
; APPLICANT: SAKAI, JURO  
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF  
; FILE REFERENCE: UTXD:567  
; CURRENT APPLICATION NUMBER: US/09/360,237  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: 60/096,571  
; EARLIER FILING DATE: 1998-08-14  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 55  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC  
; OTHER INFORMATION: PEPTIDE

US-09-360-237-55  
Query Match 66.7%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|||  
Db 7 SVLS 10

RESULT 39  
US-08-475-399A-37  
; Sequence 37, Application US/08475399A  
; Patent No. 6509033  
; GENERAL INFORMATION:  
; APPLICANT: Urban, Robert G.  
; APPLICANT: Chicz, Roman M.  
; APPLICANT: Vignali, Dario A.A.  
; APPLICANT: Hedley, Mary L.  
; APPLICANT: Stern, Lawrence J.  
; APPLICANT: Strominger, Jack L.  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
; NUMBER OF SEQUENCES: 276  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: US  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,399A  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/077,255  
; FILING DATE: 15-JUN-1993  
; APPLICATION NUMBER: 07/925,460  
; FILING DATE: 11-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fraser, Janis K.  
; REGISTRATION NUMBER: 34,819  
; REFERENCE/DOCKET NUMBER: 00246/168003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617/542-507

TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-475-399A-37

Query Match 66.7%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|  
|  
|  
|  
DB 5 SVLS 8

RESULT 40  
PCT-US93-07545-37  
Sequence 37, Application PC/TUS9307545  
GENERAL INFORMATION:  
APPLICANT: Robert G. Urban  
APPLICANT: Roman M. Chicz  
APPLICANT: Dario A. A. Vignali  
APPLICANT: Mary L. Hedley  
APPLICANT: Lawrence J. Stern  
APPLICANT: Jack L. Strominger  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/07545  
FILING DATE: 19930811  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/925,460  
FILING DATE: August 11, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Clark, Paul T.  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 00246/168001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154

INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
PCT-US93-07545-37

Query Match 66.7%; Score 4; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
|  
|  
|  
|  
DB 5 SVLS 8

RESULT 41  
US-08-360-125-19  
Sequence 19, Application US/08360125  
Patent No. 5767246  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 5767246ihiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/360,125  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-8850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody GAH  
CELL LINE:  
ORGANELLE:  
IMMEDIATE SOURCE:  
LIBRARY:  
CLONE:  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT:  
MAP POSITION:  
UNITS:  
FEATURE:  
NAME/KEY:

```

; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-360-125-19
    Query Match 66.7%; Score 4; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 42
US-08-450-578-19
; Sequence 19, Application US/08450578
; Patent No. 5837845
; GENERAL INFORMATION:
; APPLICANT: Saiko HOSOKAWA
; APPLICANT: Toshiaki TAGAWA
; APPLICANT: Yoko HIRAKAWA
; APPLICANT: NO. 5837845hiko ITO
; APPLICANT: Kazuhiro NAGAIKE
; TITLE OF INVENTION: Human Monoclonal Antibody
; TITLE OF INVENTION: Specifically Binding to Surface Antigen of Cancer
; TITLE OF INVENTION: Cell Membrane
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,578
; FILING DATE: May 25, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/360,125
; FILING DATE: December 20, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/905,534
; FILING DATE: June 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE: Hybridoma producing human antibody GAH
; CELL LINE:
; ORGANELLER:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-450-578-19
    Query Match 66.7%; Score 4; DB 2; Length 17;
    Best Local Similarity 100.0%; Pred. No. 1.1e+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5
Db 4 QSVL 7

RESULT 43
US-09-017-628-19
; Sequence 19, Application US/09017628
; Patent No. 5990287
; GENERAL INFORMATION:
; APPLICANT: HOSOKAWA, Saiko
; APPLICANT: TAGAWA, Toshiaki
; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITO, No. 5990287hiko
; APPLICANT: NAGAIKE, Kazuhiro
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY BINDING TO
; FILE REFERENCE: 177/527361KH
; CURRENT APPLICATION NUMBER: US/09/017,628
; CURRENT FILING DATE: 1998-02-02
; EARLIER APPLICATION NUMBER: 08/360,125
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 17
```



TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Hybridoma producing human antibody GAH  
US-09-017-628-19

Query Match 66.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5  
Db 4 QSVL 7

RESULT 44  
US-09-014-880-19  
Sequence 19, Application US/09014880  
Patent No. 5990297  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA et al.  
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY SPECIFICALLY  
BINDING TO SURFACE ANTIGEN OF CANCER CELL MEMBRANE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., #800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/014,880  
FILING DATE: January 28, 1998  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/450,578  
FILING DATE: May 25, 1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
CELL TYPE: Hybridoma producing human antibody GAH  
US-09-014-880-19

Query Match 66.7%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5

Db 4 QSVL 7

RESULT 45  
US-08-658-857B-23  
Sequence 23, Application US/08658857B  
Patent No. 6040435  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
APPLICANT: Karunaratne, Nedra  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,857B  
FILING DATE: May 31, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/460,464  
FILING DATE: June 2, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-658-857B-23

Query Match 66.7%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 14 SVLS 17

RESULT 46  
US-08-763-226C-23  
Sequence 23, Application US/08763226C  
Patent No. 6057291  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
APPLICANT: Karunaratne, Nedra  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/763,226C  
FILING DATE: 10-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/658,857  
FILING DATE: 31-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-763-226C-23

Query Match 66.7%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e-02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 14 SVLS 17

RESULT 47  
US-09-307-200-23  
Sequence 23, Application US/09307200  
Patent No. 6297215  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
APPLICANT: Karunaratne, Nedra  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/307,200  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/763,226  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-09-307-200-23

Query Match 66.7%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6  
Db 14 SVLS 17

RESULT 48  
US-08-450-363-19  
Sequence 19, Application US/08450363  
Patent No. 6436434  
GENERAL INFORMATION:  
APPLICANT: Saiko HOSOKAWA  
APPLICANT: Toshiaki TAGAWA  
APPLICANT: Yoko HIRAKAWA  
APPLICANT: No. 6436434hiko ITO  
APPLICANT: Kazuhiro NAGAIKE  
TITLE OF INVENTION: Human Monoclonal Antibody  
SPECIFICALLY BINDING TO SURFACE ANTIGEN OF CANCER  
TITLE OF INVENTION: Cell Membrane  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,363  
FILING DATE: May 25, 1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/360,125  
FILING DATE: December 20, 1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/905,534  
FILING DATE: June 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Warren M. Cheek, Jr.  
REGISTRATION NUMBER: 33,367  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-9850  
TELEFAX:  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL:  
ANTI-SENSE:  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
ORGANISM:  
STRAIN:  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE: Hybridoma producing human antibody GAH

; CELL LINE:  
; ORGANELLE:  
; IMMEDIATE SOURCE:  
; LIBRARY:  
; CLONE:  
; POSITION IN GENOME:  
; CHROMOSOME/SEGMENT:  
; MAP POSITION:  
; UNITS:  
; FEATURE:  
; NAME/KEY:  
; LOCATION:  
; IDENTIFICATION METHOD:  
; OTHER INFORMATION:  
; PUBLICATION INFORMATION:  
; AUTHORS:  
; TITLE:  
; JOURNAL:  
; VOLUME:  
; ISSUE:  
; PAGES:  
; DATE:  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO:  
; US-08-450-363-19

Query Match 66.7%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5  
Db 4 QSVL 7

RESULT 49  
US-09-593-321-23  
; Sequence 23, Application US/09593321  
; Patent No. 6465429  
; GENERAL INFORMATION:  
; APPLICANT: Hancock, Robert E. W.  
; APPLICANT: Karunarathne, Nedra  
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/593,321  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/307,200  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Haile, Lisa A.  
; REGISTRATION NUMBER: 38,347  
; REFERENCE/DOCKET NUMBER: 07420/014001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619/678-5070  
; TELEFAX: 619/678-5099  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-593-321-23

Query Match 66.7%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 14 SVLS 17

RESULT 50  
US-08-519-777-15  
; Sequence 15, Application US/08519777  
; Patent No. 5739307  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 78  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROGERS, HOWELL & HAFFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/519,777  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 953095  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-519-777-15

Query Match 66.7%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 16 SVLS 19

RESULT 51  
US-08-742-035-15  
; Sequence 15, Application US/08742035  
; Patent No. 5747655  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.

```
/ APPLICANT: KOTZBAUER, PAUL T.
/ APPLICANT: LAMPE, PATRICIA A.
/ TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
/ NUMBER OF SEQUENCES: 78
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
/ STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
/ CITY: ST. LOUIS
/ STATE: MISSOURI
/ COUNTRY: US
/ ZIP: 63105-1817
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/742,035
/ FILING DATE: 01-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/519,777
/ FILING DATE: 28-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HOLLAND, DONALD R.
/ REGISTRATION NUMBER: 35,197
/ REFERENCE/DOCKET NUMBER: 953095
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 727-5188
/ TELEFAX: (314) 727-6092
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-742-035-15

Query Match 66.7%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 16 SVLS 19

RESULT 52
US-08-777-019-15
/ Sequence 15, Application US/08777019
/ Patent No. 5817622
/ GENERAL INFORMATION:
/ APPLICANT: JOHNSON JR., EUGENE M.
/ APPLICANT: MILBRANDT, JEFFREY D.
/ APPLICANT: KOTZBAUER, PAUL T.
/ APPLICANT: LAMPE, PATRICIA A.
/ TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
/ NUMBER OF SEQUENCES: 78
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
/ STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
/ CITY: ST. LOUIS
/ STATE: MISSOURI
/ COUNTRY: US
/ ZIP: 63105-1817
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/777,019
/ FILING DATE: 30-DEC-1996
```

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/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/519,777
/ FILING DATE: 28-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HOLLAND, DONALD R.
/ REGISTRATION NUMBER: 35,197
/ REFERENCE/DOCKET NUMBER: 953095
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 727-5188
/ TELEFAX: (314) 727-6092
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-777-019-15

Query Match 66.7%; Score 4; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVLS 6
Db 16 SVLS 19

RESULT 53
US-08-777-143-15
/ Sequence 15, Application US/08777143
/ Patent No. 5843914
/ GENERAL INFORMATION:
/ APPLICANT: JOHNSON JR., EUGENE M.
/ APPLICANT: MILBRANDT, JEFFREY D.
/ APPLICANT: KOTZBAUER, PAUL T.
/ APPLICANT: LAMPE, PATRICIA A.
/ TITLE OF INVENTION: NEURTURIN AND RELATED GROWTH FACTORS
/ NUMBER OF SEQUENCES: 78
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: ROGERS, HOWELL & HAFERKAMP, L.C.
/ STREET: 7733 FORSYTH BOULEVARD, SUITE 1400
/ CITY: ST. LOUIS
/ STATE: MISSOURI
/ COUNTRY: US
/ ZIP: 63105-1817
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION NUMBER: US/08/777,143
/ FILING DATE: 30-DEC-1996
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/519,777
/ FILING DATE: 28-AUG-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: HOLLAND, DONALD R.
/ REGISTRATION NUMBER: 35,197
/ REFERENCE/DOCKET NUMBER: 953095
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 727-5188
/ TELEFAX: (314) 727-6092
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-777-143-15
```

Query Match 66.7%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 16 SVLS 19

RESULT 54  
US-08-775-414-15  
; Sequence 15, Application US/08775414  
; Patent No. 6090778  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: NEUTURIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/775,414  
; FILING DATE: 31-DEC-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 965805  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314) 727-5188  
; TELEFAX: (314) 727-6092  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-775-414-15

Query Match 66.7%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 16 SVLS 19

RESULT 55  
US-08-931-858E-15  
; Sequence 15, Application US/08931858E  
; Patent No. 6222022  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON, EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; APPLICANT: KLEIN, ROBERT  
; APPLICANT: DESAUVAGE, FRED  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTOR  
; NUMBER OF SEQUENCES: 239

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MO  
; COUNTRY: USA  
; ZIP: 63105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/931,858E  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.  
; REGISTRATION NUMBER: 35,197  
; REFERENCE/DOCKET NUMBER: 971486  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 314-727-5188  
; TELEFAX: 314-727-6092  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-931-858E-15

Query Match 66.7%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
Db 16 SVLS 19

RESULT 56  
US-08-981-739-15  
; Sequence 15, Application US/08981739  
; Patent No. 6232449  
; GENERAL INFORMATION:  
; APPLICANT: JOHNSON JR., EUGENE M.  
; APPLICANT: MILBRANDT, JEFFREY D.  
; APPLICANT: KOTZBAUER, PAUL T.  
; APPLICANT: LAMPE, PATRICIA A.  
; TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
; NUMBER OF SEQUENCES: 176  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
; STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
; CITY: ST. LOUIS  
; STATE: MISSOURI  
; COUNTRY: US  
; ZIP: 63105-1817  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/981,739  
; FILING DATE: 31-Aug-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US97/03461  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HOLLAND, DONALD R.

REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-08-981-739-15

Query Match 66.7%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|||  
Db 16 SVLS 19

RESULT 57  
US-09-128-026-15  
Sequence 15, Application US/09128026  
Patent No. 6403335  
GENERAL INFORMATION:  
APPLICANT: JOHNSON JR., EUGENE M.  
APPLICANT: MILBRANDT, JEFFREY D.  
APPLICANT: KOTZBAUER, PAUL T.  
APPLICANT: LAMPE, PATRICIA A.  
TITLE OF INVENTION: PERSEPHIN AND RELATED GROWTH FACTORS  
NUMBER OF SEQUENCES: 176  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: HOWELL & HAFERKAMP, L.C.  
STREET: 7733 FORSYTH BOULEVARD, SUITE 1400  
CITY: ST. LOUIS  
STATE: MISSOURI  
COUNTRY: US  
ZIP: 63105-1817  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOLLAND, DONALD R.  
REGISTRATION NUMBER: 35,197  
REFERENCE/DOCKET NUMBER: 976163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 727-5188  
TELEFAX: (314) 727-6092  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-128-026-15

Query Match 66.7%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|||

Db 16 SVLS 19

RESULT 58  
US-09-257-825B-23  
Sequence 23, Application US/09257825B  
Patent No. 6403352  
GENERAL INFORMATION:  
APPLICANT: Pooviah, Bachettira W.  
APPLICANT: Patil, Shameekumar  
APPLICANT: Takezawa, Daisuke  
TITLE OF INVENTION: Compositions and Methods for Production of Male-Sterile Plants  
FILE REFERENCE: 4630-51993  
CURRENT APPLICATION NUMBER: US/09/257,825B  
CURRENT FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: US 08/655,352  
PRIOR FILING DATE: 1996-05-23  
PRIOR APPLICATION NUMBER: US 60/014,743  
PRIOR FILING DATE: 1996-03-28  
NUMBER OF SEQ ID NOS: 28  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 23  
LENGTH: 19  
TYPE: PRT  
ORGANISM: Lilium longiflorum  
US-09-257-825B-23

Query Match 66.7%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SVLS 6  
|||  
Db 15 SVLS 18

RESULT 59  
US-08-658-857B-24  
Sequence 24, Application US/08658857B  
Patent No. 6040435  
GENERAL INFORMATION:  
APPLICANT: Hancock, Robert E. W.  
APPLICANT: Karunaratne, Nedra  
TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,857B  
FILING DATE: May 31, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/460,464  
FILING DATE: June 2, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haile, Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-857B-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19

RESULT 60
US-08-763-226C-24
; Sequence 24, Application US/08763226C
; Patent No. 6057291
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,200
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/763,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-307-200-24

Query Match 66.7%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSVL 5
Db 16 QSVL 19

RESULT 62
US-09-593-321-24
; Sequence 24, Application US/09593321
; Patent No. 6465429
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; APPLICANT: Karunaratne, Nedra
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/593,321
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,200
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/593,321
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/307,200
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347

```

REFERENCE/DOCKET NUMBER: 07420/014001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-593-321-24

Query Match 66.7%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSVL 5  
DB 16 QSVL 19

RESULT 63  
US-07-772-087-8  
Sequence 8, Application US/07772087  
Patent No. 5275945  
GENERAL INFORMATION:  
APPLICANT: HSIAO, Hung-Yu  
APPLICANT: FODGE, Douglas W.  
APPLICANT: LALONDE, James J.  
TITLE OF INVENTION: ALKALINE PROTEASES STABLE IN HEAVY-DUTY  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313-0299

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/772,087  
FILING DATE: 19911008  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 16754/115 CHCO  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149

INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Bacillus  
STRAIN: KP1239 from B. alcalophilis  
US-07-772-087-8

Query Match 50.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
DB 16 QSVL 19

Db 2 QSV 4

RESULT 64  
US-08-199-778-4  
Sequence 4, Application US/08199778  
Patent No. 5525479  
GENERAL INFORMATION:  
APPLICANT: Anthony, Neville J.  
APPLICANT: Pompliano, David L.  
TITLE OF INVENTION: A FLUORESCENCE ASSAY OF RAS FARNESYL  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Merck & Co., Inc.  
STREET: P.O. Box 2000  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: U.S.A.  
ZIP: 07065-0900

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/199,778  
FILING DATE: 17-FEB-1994  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Muthard, David A.  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 187781A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3903  
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-199-778-4

Query Match 50.0%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
DB 2 VLS 4

RESULT 65  
US-08-240-712-5  
Sequence 5, Application US/08240712  
Patent No. 5599907  
GENERAL INFORMATION:  
APPLICANT: ANDERSON, DAVID C.  
APPLICANT: MATHEWS, ANTONY JAMES  
APPLICANT: STETLER, GARY L.  
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:



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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,712
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-240-712-5

Query Match      50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VLS 6
Db      1 VLS 3

RESULT 66
US-08-387-156-22
; Sequence 22, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUN P.A.
; TITLE OF INVENTION: GRH-LEUKOTOKIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,156
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.21

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8959
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-387-156-22

Query Match      50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VLS 6
Db      2 VLS 4

RESULT 67
US-08-443-890-5
; Sequence 5, Application US/08443890
; Patent No. 5739011
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,890
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/240,712
; FILING DATE: 09-MAY-1994
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON=6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-443-890-5

Query Match      50.0%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 VLS 6  
Db 1 VLS 3

RESULT 68  
US-08-667-001-13  
; Sequence 13, Application US/08667001  
; Patent No. 5827827  
; GENERAL INFORMATION:  
; APPLICANT: Janda, Kim D.  
; APPLICANT: Wirsching, Peter  
; TITLE OF INVENTION: HIV-1 PROTEASE INHIBITOR  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE  
; STREET: 10666 No. 5827827th Torrey Pines Road, TPC-8  
; CITY: La Jolla  
; STATE: California  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/667,001  
; FILING DATE: 20-JUN-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/335,039  
; FILING DATE: 16-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lewis, Donald G.  
; REGISTRATION NUMBER: 28,636  
; REFERENCE/DOCKET NUMBER: TSI 282.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 554-2937  
; TELEFAX: (619) 554-6312  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 1  
; OTHER INFORMATION: /note= "sequence = R" in formula  
US-08-667-001-13

Query Match 50.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4  
Db 2 QSV 4

RESULT 69  
US-08-694-865-28  
; Sequence 28, Application US/08694865  
; Patent No. 5837268  
; GENERAL INFORMATION:  
; APPLICANT: POTTER, ANDREW A.  
; APPLICANT: MANNS, JOHN G.  
; TITLE OF INVENTION: GNBH-LEUKOTOXIN CHIMERAS  
; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: REED & ROBINS LLP  
; STREET: 285 HAMILTON AVENUE, SUITE 200  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/694,865  
; FILING DATE: 09-AUG-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MCCracken, THOMAS P.  
; REGISTRATION NUMBER: 38,548  
; REFERENCE/DOCKET NUMBER: 9001-0016.22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 327-3400  
; TELEFAX: (415) 327-3231  
; INFORMATION FOR SEQ ID NO: 28:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-694-865-28

Query Match 50.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
Db 2 VLS 4

RESULT 70  
US-08-358-556A-27  
; Sequence 27, Application US/08358556A  
; Patent No. 5869643  
; GENERAL INFORMATION:  
; APPLICANT: Chatelain, Francois  
; APPLICANT: Kumarev, Viktor  
; TITLE OF INVENTION: Process for Preparing Polynucleotides on  
; TITLE OF INVENTION: a Solid Support and Apparatus Permitting its  
; TITLE OF INVENTION: Implementation  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Jacobson, Price, Holman & Stern  
; STREET: 400 Seventh St. N.W.  
; CITY: Washington D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/358,556A  
; FILING DATE: 14-DEC-1994  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9315164  
; FILING DATE: 16-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E.  
; REGISTRATION NUMBER: 31,409

REFERENCE/DOCKET NUMBER: 10577/P58418  
TELEPHONE: (202) 638-6666  
TELEFAX: (202) 393-5350  
TELEX: RCA 248593 IDEA UR  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-358-556A-27

Query Match 50.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4

Db 2 QSV 4

RESULT 71  
US-08-637-759B-200  
Sequence 200, Application US/08637759B  
Patent No. 5876931  
GENERAL INFORMATION:  
APPLICANT: David William Holden  
TITLE OF INVENTION: Identification of Genes  
NUMBER OF SEQUENCES: 501  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 03-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER:  
APPLICATION NUMBER: PCT/GB95/02875  
FILING DATE: 11-DEC-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: RPMS 101  
TELEPHONE: (404) 873-8794  
TELEFAX: (404) 873-8795  
INFORMATION FOR SEQ ID NO: 200:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-637-759B-200

Query Match 50.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QSV 4

Db 1 QSV 3

RESULT 72  
US-08-429-964-19  
Sequence 19, Application US/08429964  
Patent No. 5962243  
GENERAL INFORMATION:  
APPLICANT: BROWN, MICHAEL S.  
APPLICANT: GOLDSTEIN, JOSEPH L.  
APPLICANT: REISS, YUVAL  
APPLICANT: JAMES, GUY L.  
TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL  
TRANSFERASE INHIBITORS  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARNOLD, WHITE & DURKEE  
STREET: P.O. BOX 4433  
CITY: HOUSTON  
STATE: TEXAS  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/429,964  
FILING DATE: 27-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,625  
FILING DATE: 16-FEB-1993  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/822,011  
FILING DATE: ABANDONED  
CLASSIFICATION: 435  
APPLICATION NUMBER: PCT/US/91/02650  
FILING DATE: 18-APR-1991  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/615,715  
FILING DATE: 20-NOV-1990  
CLASSIFICATION: 435  
APPLICATION NUMBER: US 07/510,706  
FILING DATE: 18-APR-1990 (ABANDONED)  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: PARKER, DAVID L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:432/PAR  
TELEPHONE: (512) 418-3000  
TELEFAX: (713) 789-2679  
TELEX: 79-0924  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-429-964-19

Query Match 50.0%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6

Db 2 VLS 4

## RESULT 73

US-08-878-748-22  
 ; Sequence 22, Application US/08878748  
 ; Patent No. 5969126  
 ; GENERAL INFORMATION:  
 ; APPLICANT: POTTER, ANDREW A.  
 ; APPLICANT: REDMOND, MARK J.  
 ; APPLICANT: HUGHES, HUM P.A.  
 ; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS  
 ; NUMBER OF SEQUENCES: 28  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: REED & ROBINS  
 ; STREET: 635 BRYANT STREET  
 ; CITY: PALO ALTO  
 ; STATE: CALIFORNIA  
 ; COUNTRY: UNITED STATES OF AMERICA  
 ; ZIP: 94301  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/878,748  
 ; FILING DATE: 19-JUN-1997  
 ; CLASSIFICATION: 536  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/387,156  
 ; FILING DATE: 10-FEB-1995  
 ; APPLICATION NUMBER: US 07/960,932  
 ; FILING DATE: 14-OCT-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/779,171  
 ; FILING DATE: 16-OCT-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ROBINS, ROBERTA L.  
 ; REGISTRATION NUMBER: 33,208  
 ; REFERENCE/DOCKET NUMBER: 9001-0016.21  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (415) 617-8999  
 ; TELEFAX: (415) 327-3231  
 ; INFORMATION FOR SEQ ID NO: 22:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-878-748-22

Query Match 50.0%; Score 3; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

## RESULT 74

US-08-707-082A-18  
 ; Sequence 18, Application US/08707082A  
 ; Patent No. 5930277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexander Levitzki, Chaim Gilon and Hadas Reuveni  
 ; TITLE OF INVENTION: SEMIPEPTOID FARNESYL PROTEIN TRANSFERASE  
 ; TITLE OF INVENTION: INHIBITORS AND ANALOGS THEREOF  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein  
 ; STREET: 2940 Birchtree lane  
 ; CITY: Silver Spring  
 ; STATE: Maryland

; COUNTRY: United States of America  
 ; ZIP: 20906  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk  
 ; COMPUTER: Twinhead\* Slimnote-890TX  
 ; OPERATING SYSTEM: MS DOS version 6.2,  
 ; OPERATING SYSTEM: Windows version 3.11  
 ; SOFTWARE: Word for Windows version 2.0 converted to  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/707,082A  
 ; FILING DATE: 3 SEP 1996  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Friedman, Mark M.  
 ; REGISTRATION NUMBER: 33,883  
 ; REFERENCE/DOCKET NUMBER: 325/7  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 972-3-5625553  
 ; TELEFAX: 972-3-5625554  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 4  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-707-082A-18

Query Match 50.0%; Score 3; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLS 6  
 |||  
 Db 2 VLS 4

## RESULT 75

US-08-582-076-2  
 ; Sequence 2, Application US/08582076  
 ; Patent No. 6011175  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SEBTI, SAID  
 ; APPLICANT: HAMILTON, ANDREW  
 ; TITLE OF INVENTION: INHIBITION OF FARNESYLTRANSFERASE  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
 ; STREET: 1100 NEW YORK AVENUE, N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/582,076  
 ; FILING DATE: 02-JAN-1996  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KOKULIS, PAUL N.  
 ; REGISTRATION NUMBER: 16,773  
 ; REFERENCE/DOCKET NUMBER: 220007/6137  
 ; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-582-076-2

Query Match      50.0%; Score 3; DB 3; Length 4;
Best local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VLS 6
      |||
Db      2 VLS 4

Search completed: November 25, 2003, 20:30:02
Job time : 5.84884 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 15.093 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-27  
Perfect score: 22  
Sequence: 1 LSQPKVLVPQKAVPQDMPQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR 76:\*

1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	4	18.2	10	2 A61218	alpha-gliadin 4Ha
2	4	18.2	10	2 B61218	alpha-gliadin 6Ha
3	4	18.2	11	2 PC4267	ribosomal protein
4	4	18.2	13	2 S09395	hypothetical prote
5	4	18.2	15	2 A49155	vasotocin-associat
6	4	18.2	17	2 UQ2030	hypothetical 1.9K
7	4	18.2	18	2 P00149	beta-Gliadin 13 -
8	4	18.2	19	2 S69153	Neb-colloostatin -
9	4	18.2	19	2 A37968	neural surface pro
10	4	18.2	20	2 S63602	glutathione S-tran
11	4	13.6	6	2 A35890	RNA-directed DNA p
12	3	13.6	7	2 P00663	membrane protein -
13	3	13.6	7	2 PC1316	large granule L3 c
14	3	13.6	8	2 B24749	neuropeptide B - b
15	3	13.6	8	2 A14683	aspartate transami
16	3	13.6	9	2 S78426	52.5K protein - sp
17	3	13.6	9	2 PC7073	ubiquinol-cytochro
18	3	13.6	10	1 XASNPC	angiotensin-conver
19	3	13.6	10	2 A46491	C3 homolog HX - in
20	3	13.6	10	2 A44646	neurotoxin-associ
21	3	13.6	10	2 I44644	neurotoxin-associ
22	3	13.6	10	2 JP0072	ribosomal protein
23	3	13.6	10	2 PC4374	telomeric and tetr
24	3	13.6	11	2 D06091	phycobilisome 9K 1
25	3	13.6	11	2 S68637	acetylcholinester
26	3	13.6	12	1 A43975	locustamytropin -
27	3	13.6	12	2 S25485	transcription fact
28	3	13.6	12	2 S43013	hypothetical prote
29	3	13.6	12	2 PA0037	plastocyanin 2 - A

30	13.6	12	2	PA0030	protein QA300025 -
31	13.6	12	2	PA0098	ribosomal protein
32	13.6	12	2	A61503	sterol carrier pro
33	13.6	12	2	S74196	3-hydroxy-3-methyl
34	13.6	13	2	S12388	argA protein - Sal
35	13.6	13	2	G22565	R-phycocerythrin ga
36	13.6	13	2	S09018	hemolytic protein
37	13.6	13	2	PL0157	Ig kappa chain V-I
38	13.6	13	2	B56864	dipeptidyl-peptida
39	13.6	13	2	C61576	ribosomal protein
40	13.6	14	2	JN0389	histamine-releasin
41	13.6	14	2	C33098	223K exoantigen -
42	13.6	14	2	S45655	cathepsin L (EC 3.
43	13.6	14	2	S38307	DBB-A protein - fr
44	13.6	14	2	S14336	mastoparan B - hor
45	13.6	14	2	A23996	Beta-granin - rat
46	13.6	15	2	I49420	placental lactogen
47	13.6	15	2	PN0117	hemoglobin alpha c
48	13.6	15	2	PH0216	agarase (EC 3.2.1.
49	13.6	15	2	T09463	ribosomal protein
50	13.6	15	2	PA0056	protein QF200002 -
51	13.6	15	2	B61457	alpha-glucosidase
52	13.6	15	2	FR0090	alpha-glucosidase
53	13.6	15	2	D46743	corneal keratan su
54	13.6	15	2	G24417	interphotoreceptor
55	13.6	15	2	S62675	collagen type I -
56	13.6	15	2	PH1590	Ig H chain V-D-J r
57	13.6	15	2	A31902	bone acidic glycop
58	13.6	16	2	A27803	myosin light chain
59	13.6	16	2	PA0048	protein QA100047 -
60	13.6	16	2	PS0256	22K protein 4208 -
61	13.6	16	2	S38292	30K allergen - rye
62	13.6	16	2	A23992	melanin-mochochrome
63	13.6	16	2	S65709	major allergen Myr
64	13.6	16	2	S68730	bleomycin-binding
65	13.6	17	2	S165274	glutathione S-tran
66	13.6	17	2	A29834	trp leader peptide
67	13.6	17	2	A36727	cytochrome c551 -
68	13.6	17	2	A49237	45/47K antigen - M
69	13.6	17	2	S59481	hydroxyproline-ric
70	13.6	17	2	S28839	RNA-binding protei
71	13.6	17	2	A22595	bombolitin I - Ame
72	13.6	17	2	B22595	bombolitin II - Am
73	13.6	17	2	C22595	bombolitin III - A
74	13.6	17	2	D22595	bombolitin IV - Am
75	13.6	17	2	FR0234	Ig heavy chain CRD
76	13.6	18	1	DRUFDP	pigment-dispersing
77	13.6	18	2	A24749	neuropeptide A - b
78	13.6	18	2	I40062	shikimate 5-dehydr
79	13.6	18	2	S13974	chlorophyll a/b-bi
80	13.6	18	2	A45590	beta-pigment-dispe
81	13.6	18	2	B48408	21K high mobility
82	13.6	18	2	A56798	dermatan sulfate p
83	13.6	18	2	S09026	carboxylesterase (
84	13.6	18	2	S19914	choline O-acetyltr
85	13.6	18	2	S39009	oviductin - golden
86	13.6	19	2	C56049	superoxide dismuta
87	13.6	19	2	A41299	T-cell receptor al
88	13.6	19	2	D24417	interphotoreceptor
89	13.6	19	2	I40063	shikimate 5-dehydr
90	13.6	19	2	C61079	24K protein - list
91	13.6	19	2	PQ0678	photosystem I 8.0K
92	13.6	19	2	A48408	21K high mobility
93	13.6	19	2	A49192	transferrin - bu
94	13.6	19	2	A60326	cholecystokinin-58
95	13.6	19	2	S02808	nucléolin - bovine
96	13.6	19	2	S78411	ribosomal protein
97	13.6	19	2	S68394	H+-transporting tw
98	13.6	20	2	A39328	notechis II-5b non
99	13.6	20	2	S09022	carboxylesterase (
100	13.6	20	2	S09025	carboxylesterase (

## ALIGNMENTS

## RESULT 1

B61218  
 alpha-gliadin 4Ha - grass (Haynaldia villosa) (fragment)  
 C:Species: Haynaldia villosa, Dasyphyrum villosum  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
 C:Accession: A61218  
 R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
 Biochem. Genet. 29, 207-211, 1991  
 A>Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
 A:Reference number: A61218; MUID:91315394; PMID:1859356  
 A:Accession: A61218  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <SHE>  
 C:Keywords: seed; storage protein

Query Match 18.2%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQ 11

|||||  
 5 PVPQ 8

## RESULT 2

B61218  
 alpha-gliadin 6Ha - grass (Haynaldia villosa) (fragment)  
 C:Species: Haynaldia villosa, Dasyphyrum villosum  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-1999  
 C:Accession: B61218  
 R:Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafandra, D.  
 Biochem. Genet. 29, 207-211, 1991  
 A>Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa  
 A:Reference number: A61218; MUID:91315394; PMID:1859356  
 A:Accession: B61218  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <SHE>  
 C:Keywords: seed; storage protein

Query Match 18.2%; Score 4; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQ 11

|||||  
 4 PVPQ 7

## RESULT 3

PC4267  
 ribosomal protein L12.1 - rice (fragment)  
 C:Species: Oryza sativa (rice)  
 C>Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
 C:Accession: PC4267  
 R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.  
 submitted to JIPID, April 1997  
 A:Reference number: PC4267  
 A:Accession: PC4267  
 A:Molecule type: protein  
 A:Residues: 1-11 <KAW>  
 A:Experimental source: strain Japonica Nihonbare

Query Match 18.2%; Score 4; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7

.|||||

Db 7 PKVL 10

## RESULT 4

S09395  
 hypothetical protein - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C>Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 24-Jul-1997  
 C:Accession: S09395  
 R:Gisselmann, G.; Sewing, S.; Madsen, B.W.; Mallart, A.; Angaut-Petit, D.; Mueller-Hoerster, J.  
 EMBO J. 8, 2359-2364, 1989  
 A>Title: The interference of truncated with normal potassium channel subunits leads to a reduction in current  
 A:Reference number: S09395; MUID:90005442; PMID:2551680  
 A:Accession: S09395  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-13 <GIS>

Query Match 18.2%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10

|||||  
 5 LPVP 8

## RESULT 5

A49155  
 vasotocin-associated neurophysin - African toad (fragment)  
 N:Alternate names: MSEL-neurophysin  
 C:Species: Bufo regularis (African toad)  
 C>Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Apr-2001  
 C:Accession: A49155  
 R:Chauvet, J.; Ouedraogo, Y.; Michel, G.; Acher, R.  
 Comp. Biochem. Physiol. Comp. Physiol. 104, 497-502, 1993  
 A>Title: Vasotocin and hyalrin 2 (vasotocinyl-Gly) in the African toad Bufo regularis:  
 A:Reference number: A49155; MUID:93230882; PMID:8097151  
 A:Accession: A49155  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <CHA>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:129814)  
 C:Superfamily: oxytocin-neurophysin  
 C:Keywords: neuropeptide

Query Match 18.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQ 16

|||||  
 6 AVPQ 9

## RESULT 6

JQ2030  
 hypothetical 1.9K protein - Orgyia pseudotaugata multicapsid nuclear polyhedrosis virus  
 N:Alternate names: ORF2 mini gene protein  
 C:Species: Orgyia pseudotaugata multicapsid nuclear polyhedrosis virus, OpMNVPV  
 C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 08-Oct-1999  
 C:Accession: JQ2030  
 R:Russell, R.L.O.; Rohrmann, G.F.  
 J. Gen. Virol. 74, 1191-1195, 1993  
 A>Title: Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia pseudotaugata multicapsid nuclear polyhedrosis virus

A:Reference number: JQ2030; MUID:93286576; PMID:8389803  
 A:Accession: JQ2030  
 A:Molecule type: DNA  
 A:Residues: 1-17 <RUS>  
 A:Cross-references: DDBJ:DL3375; NID:g222217; PIDN:BAA02640.1; PID:d1003144; PID:g222217

Query Match 18.2%; Score 4; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
|  
|  
|  
|  
Db 2 VLPV 5

RESULT 7  
PN0149  
beta-Gliadine 13 - Aegilops longissima (fragment)  
C:Species: Aegilops longissima  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PN0149  
R:Odintsova, T.I.; Egorov, T.A.  
Biochimia 55, 509-516, 1990  
A:Title: N-Terminal sequences of omega-gliadins of Aegilops longissima: On the origin of  
A:Reference number: PN0146; MUID:90283493; PMID:2354218  
A:Accession: PN0149  
A:Molecule type: protein  
A:Residues: 1-18 <ODI>  
A:Experimental source: strain K-202  
C:Superfamily: gliadin

Query Match 18.2%; Score 4; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQ 11  
|  
|  
|  
|  
Db 4 PVPQ 7

RESULT 8  
S69153  
Neb-colloostatin - flesh fly (Sarcophaga bullata)  
C:Species: Sarcophaga bullata  
C:Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 19-May-2000  
C:Accession: S69153  
R:Bylemans, D.; Proost, P.; Samijn, B.; Borovsky, D.; Grauwels, L.; Huybrechts, R.; van  
Eur. J. Biochem. 228, 45-49, 1995  
A:Title: Neb-colloostatin, a second folliculastatin of the grey fleshfly, Neobellieria  
A:Reference number: S69153; MUID:95188911; PMID:7883009  
A:Accession: S69153  
A:Molecule type: protein  
A:Residues: 1-19 <BYL>

Query Match 18.2%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|  
|  
|  
|  
Db 7 LPVP 10

RESULT 9  
A37968  
neural surface protein Bravo - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 24-Jan-1992 #sequence\_revision 24-Jan-1992 #text\_change 15-Aug-1997  
C:Accession: A37968; A36345  
R:de la Rosa, E.J.; Kayyem, J.P.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 112, 1049, 1991  
A:Reference number: A37968; MUID:91154309; PMID:1999455  
A:Contents: erratum  
A:Accession: A37968  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-19 <DEL>  
R:de la Rosa, E.J.; Kayyem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.  
J. Cell Biol. 111, 3087-3096, 1990  
A:Title: Topologically restricted appearance in the developing chick retinotectal system  
A:Reference number: A36345; MUID:91100421; PMID:2269667

A:Accession: A36345  
A:Molecule type: protein  
A:Residues: 1-7,9-19 <DE2>

Query Match 18.2%; Score 4; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
|  
|  
|  
|  
Db 13 LSQP 16

RESULT 10  
S63602  
glutathione S-transferase chain T2-2 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S63602  
R:Mainwaring, G.W.; Nash, J.; Davidson, M.; Green, T.  
Biochem. J. 314, 445-448, 1996  
A:Title: Isolation of a mouse Theta glutathione S-transferase active with methylene ch  
A:Reference number: S63601; MUID:96239100; PMID:8670055  
A:Accession: S63602  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <MAI>  
C:Superfamily: glutathione transferase

Query Match 18.2%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
|  
|  
|  
|  
Db 9 LSQP 12

RESULT 11  
A35890  
RNA-directed DNA polymerase (EC 2.7.7.49) 66K chain - human immunodeficiency virus typ  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 09-Nov-1990 #sequence\_revision 09-Nov-1990 #text\_change 31-Dec-1993  
C:Accession: A35890  
R:Bathurst, I.C.; Moen, L.K.; Lujan, M.A.; Gibson, H.L.; Feucht, P.H.; Pichuanes, S.;  
Biochem. Biophys. Res. Commun. 171, 589-595, 1990  
A:Title: Characterization of the human immunodeficiency virus type-1 reverse transcript  
A:Reference number: A35890; MUID:90386627; PMID:1698361  
A:Accession: A35890  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <BAT>  
C:Keywords: nucleotidyltransferase

Query Match 13.6%; Score 3; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
|  
|  
|  
|  
Db 4 KVL 6

RESULT 12  
PQ0663  
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)  
C:Species: porcine epidemic diarrhea virus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 08-Oct-1999  
C:Accession: PQ0663  
R:Brigden, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.  
J. Gen. Virol. 74, 1795-1804, 1993  
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epidem  
issile gastroenteritis virus.



A:Reference number: JQ2191; MUID:93389433; PMID:8397280

A:Accession: PQ0663

A:Molecule type: mRNA

A:Residues: 1-7 <BRI>

A:Cross-references: GB:Z14976; NID:g311650; PIDN:CAA78699.1; PID:g584083

C:Comment: This virus is coronavirus related to human coronavirus 229E.

C:Keywords: membrane protein

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

Db 2 KVL 4

#### RESULT 13

PC1316

large granule L3 chain - horseshoe crab (Tachypleus tridentatus) (fragment)

C:Species: Tachypleus tridentatus

C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C:Accession: PC1316

R:Shigenaga, T.; Takavenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa

J.; Biochem. 114, 307-316, 1993

A:Title: Separation of large and small granules from horseshoe crab (Tachypleus tridentatus)

A:Reference number: PC1309; MUID:94110249; PMID:8282718

A:Accession: PC1316

A:Molecule type: protein

A:Residues: 1-7 <SHI>

C:Comment: This protein participates in immobilization of invading microbes.

Query Match 13.6%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4

Db 2 SQP 4

#### RESULT 14

B24749

neuropeptide B - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000

C:Accession: B24749

R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two b

A:Reference number: A94074; MUID:86067995; PMID:3865193

A:Accession: B24749

A:Molecule type: protein

A:Residues: 1-8 <YAN>

A:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17

Db 5 PQR 7

#### RESULT 15

A14683

aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (fragm

N:Alternate names: aspartate aminotransferase, mitochondrial

C:Species: Gallus gallus (chicken)

C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 31-Mar-2000

C:Accession: A14683

C:Keywords: membrane protein

R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.

FEBS Lett. 108, 98-102, 1979

A:Title: Microsequence analysis: IV. Automatic liquid-phase sequencing using DABITC.

A:Reference number: A14683; MUID:80092116; PMID:520566

A:Accession: A14683

A:Molecule type: protein

A:Residues: 1-8 <WIL>

C:Keywords: aminotransferase; mitochondrion

Query Match 13.6%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPK 5

Db 6 QPK 8

#### RESULT 16

S78426

52.5K protein - spiny lobster (fragment)

C:Species: Panulirus argus (spiny lobster)

C:Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 19-May-2000

C:Accession: S78426

R:James, M.O.; Boyle, S.M.; Trapido-Rosenthal, H.G.; Smith, W.C.; Greenberg, R.M.; Shi

Arch. Biochem. Biophys. 329, 31-38, 1996

A:Title: cDNA and protein sequence of a major form of P450, CYP2L, in the hepatopancre

A:Reference number: S68856; MUID:96201120; PMID:8619632

A:Accession: S78426

A:Molecule type: protein

A:Residues: 1-9 <JAM>

A:Experimental source: hepatopancreas microsomes

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7

Db 5 KVL 7

#### RESULT 17

PC7073

ubiquinol-cytochrome-c reductase (EC 1.10.2.2) core protein II - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 03-Jun-2002

C:Accession: PC7073

R:Teugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.

Electrophoresis 21, 1853-1871, 2000

A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles o

A:Reference number: PC7072

A:Accession: PC7073

A:Molecule type: protein

A:Residues: 1-9 <TSU>

C:Keywords: brain; core protein; oxidoreductase

Query Match 13.6%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6

Db 6 PKV 8

#### RESULT 18

XASNPC

angiotensin-converting enzyme inhibitor - aspici viper

C:Species: Vipera aspis (aspici viper)

C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 08-Dec-1995

C:Accession: A60377

R:Komori, Y.; Sugihara, H.

```

Int. J. Biochem. 22, 767-771, 1990
A:Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
A:Reference number: A60377; MUID:90382616; PMID:2169439
A:Accession: A60377
A:Molecule type: protein
A:Residues: 1-10 <KOM>
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
P1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match      13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
   |||
Db 6 PKV 8

RESULT 19
A46491
C3 homolog HX - inshore hagfish (fragment)
C:Species: Eptatretus burgeri (inshore hagfish)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C:Accession: A46491
R:Fujii, T.; Nakamura, T.; Sekizawa, A.; Tomonaga, S.
J. Immunol. 148, 117-123, 1992
A:Title: Isolation and characterization of a protein from hagfish serum that is homologous
A:Reference number: A46491; MUID:92091759; PMID:1727859
A:Accession: A46491
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <FUJ>
A:Experimental source: serum
A:Note: sequence extracted from NCBI backbone (NCBIP:71420)
C:Superfamily: alpha-2-macroglobulin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
   |||
Db 2 KVL 4

RESULT 20
A44646
neurotoxin-associated protein type A Hn+ 57K chain - Clostridium botulinum (fragment)
C:Species: Clostridium botulinum
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: A44646
R:Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A:Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without he
A:Reference number: A44644; MUID:92143938; PMID:1781887
A:Contents: type A
A:Accession: A44646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:83774)
A:Note: 6-Trp was also found
C:Keywords: hemagglutinin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
   |||
Db 7 VLP 9

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
   |||

```

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RESULT 21
I44644
neurotoxin-associated protein type B Hn+ 57K chain - Clostridium botulinum (fragment)
C:Species: Clostridium botulinum
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
C:Accession: I44644
R:Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A:Title: Clostridium botulinum types A, B, Cl, and E produce proteins with or without
A:Reference number: A44644; MUID:92143938; PMID:1781887
A:Contents: type B
A:Accession: I44644
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:83783)
C:Keywords: hemagglutinin

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
   |||
Db 7 VLP 9

RESULT 22
JP0072
ribosomal protein L32 - Lactobacillus plantarum (fragment)
C:Species: Lactobacillus plantarum
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: JP0072
R:Ochi, K.
submitted to JIPID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0042
A:Accession: JP0072
A:Molecule type: protein
A:Residues: 1-10 <OCH>
C:Keywords: protein biosynthesis; ribosome

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
   |||
Db 1 AVP 3

RESULT 23
PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4374
R:Sarig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the
A:Reference number: PC4371; MUID:97445086; PMID:9299414
A:Accession: PC4374
A:Molecule type: protein
A:Residues: 1-10 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecu

Query Match      13.6%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
   |||

```

Db 1 KVL 3

RESULT 24

D60691

Phycobilisome 9K linker protein - *Synechococcus* sp. (PCC 7002) (fragment)

C;Species: *Synechococcus* sp.

C;Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 07-May-1999

C;Accession: D60691

R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.

Arch. Microbiol. 153: 550-560, 1990

A;Title: Structural and compositional analyses of the phycobilisomes of *Synechococcus* sp.

S.

A;Reference number: A60691; MUID:90314662; PMID:2164365

A;Accession: D60691

A;Molecule type: protein

A;Residues: 1-11 <BR>

C;Comment: This protein, one of the eleven components detected in this species of the phycobilisome

C;Keywords: photosystem II

Query Match 13.6%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQ 3

Db 2 LSQ 4

RESULT 25

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)

C;Species: *Bos primigenius* taurus (cattle)

C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 30-Jan-1998

C;Accession: S68637

R;Boschetti, N.; Brodbeck, U.

FEBS Lett. 380, 133-136, 1996

A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a single transmembrane domain

A;Reference number: S68637; MUID:96181683; PMID:8603722

A;Accession: S68637

A;Molecule type: protein

A;Residues: 1-11 <BOS>

A;Experimental source: brain

C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 13.6%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 POK 12

Db 2 POK 4

RESULT 26

A43975

locustamyotropin - migratory locust

N;Alternate names: Lom-MT

C;Species: *Locusta migratoria* (migratory locust)

C;Date: 11-Feb-1993 #sequence\_revision 02-Jun-1994 #text\_change 08-Dec-1995

C;Accession: A43975

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Tips, A.; Nachman, R.J.; Vandesande, F.; De Loof, L.

Peptides 11, 427-433, 1990

A;Title: Isolation, identification and synthesis of locustamyotropin (Lom-MT), a novel bioactive peptide

A;Reference number: A43975; MUID:90341077; PMID:1974346

A;Accession: A43975

A;Molecule type: protein

A;Residues: 1-12 <SCH>

A;Note: the amino end of this peptide is not blocked

A;Note: synthetic locustamyotropin mimics natural locustamyotropin only in the amidated form

C;Comment: This peptide was shown to stimulate visceral muscle contractions in locust ovary

C;Superfamily: pyrokinin

C;Keywords: amidated carboxyl end; neuropeptide

F;12/Modified site: amidated carboxyl end (leu) #status experimental

Query Match 13.6%; Score 3; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15

Db 2 AVP 4

RESULT 27

S25485

transcription factor NF1 - rat

N;Alternate names: HNF1 protein; LFBI protein

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 15-Oct-1999

C;Accession: S25485; S50121

R;Tomei, L.; Piaggio, G.; Toniatti, C.; Lazzaro, D.; de Francesco, R.; Pozzi, L.; Gerardi, L.

submitted to the EMBL Data Library, August 1992

A;Description: LFBI/HNF1 acts as a repressor of its own transcription.

A;Reference number: S25485

A;Accession: S25485

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <TOM>

A;Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576

R;Piaggio, G.; Tomei, L.; Toniatti, C.; de Francesco, R.; Gerstner, J.; Cortese, R.

Nucleic Acids Res. 22, 4284-4290, 1994

A;Title: LFBI/HNF1 acts as a repressor of its own transcription.

A;Reference number: S50121; MUID:95023202; PMID:7937157

A;Accession: S50121

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <PIA>

A;Cross-references: EMBL:X67649; NID:G56575; PIDN:CAA47891.1; PID:G56576

C;Superfamily: transcription factor HNF-1; homeobox homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 13.6%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQ 3

Db 5 LSQ 7

RESULT 28

S43013

hypothetical protein URF-2X - *Yersinia enterocolitica* transposon TN3926

C;Species: *Yersinia enterocolitica*

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999

C;Accession: S43013

R;Osbourne, S.E.V.; Turner, A.K.; Grinstead, J.

submitted to the EMBL Data Library, March 1994

A;Description: The structure of the bacterial transposable element, TN3926.

A;Reference number: S43013

A;Accession: S43013

A;Molecule type: DNA

A;Residues: 1-12 <OSB>

A;Cross-references: EMBL:X78059; NID:G460067; PIDN:CAA54979.1; PID:G460070

C;Genetics: transposon TN3926

A;Mobile element: transposon TN3926

Query Match 13.6%; Score 3; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4

Db 4 SQP 6

## RESULT 29

PA0037  
 plastocyanin 2 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 23-Mar-1995  
 C:Accession: PA0037  
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0037  
 A:Molecule type: protein  
 A:Residues: 1-12 <KAW>  
 A:Experimental source: stem

Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 5 VLP 7

## RESULT 30

PA0030  
 protein QA300025 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C>Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C:Accession: PA0030  
 R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0030  
 A:Molecule type: protein  
 A:Residues: 1-12 <KAW>  
 A:Experimental source: seed  
 C:Keywords: seed

Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 PIQ 22  
 |||  
 Db 4 PIQ 6

## RESULT 31

PA0098  
 ribosomal protein S3 - fungus (Fusarium sporotrichioides) (fragment)  
 C:Species: Fusarium sporotrichioides  
 C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C:Accession: PA0098  
 R;Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A:Reference number: PA0051  
 A:Accession: PA0098  
 A:Molecule type: protein  
 A:Residues: 1-12 <CHO>

Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10  
 |||  
 Db 5 PVP 7

## RESULT 32

A61503  
 sterol carrier protein-2-like protein - chicken (fragment)  
 C:Species: Gallus gallus (chicken)  
 C>Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 11-May-2000  
 C:Accession: A61503  
 R;Reinhart, M.P.; Avart, S.J.; Foglia, T.  
 Comp. Biochem. Physiol. B 100, 243-248, 1991  
 A:Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken sterol carrier protein-2-like protein  
 A:Reference number: A61503; MUID:92191564; PMID:1799965  
 A:Accession: A61503  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <REI>

Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6  
 |||  
 Db 6 PKV 8

## RESULT 33

S74196  
 3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 01-May-1998  
 C:Accession: S74196  
 R;Taketani, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.;  
 Eur. J. Biochem. 230, 760-765, 1995  
 A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of bovine erythroid cells  
 A:Reference number: S65629; MUID:95331315; PMID:7607249  
 A:Accession: S74196  
 A:Molecule type: protein  
 A:Residues: 1-12 <TAK>  
 A:Experimental source: liver

Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15  
 |||  
 Db 5 AVP 7

## RESULT 34

S12388  
 argA protein - Salmonella typhimurium (fragment)  
 C:Species: Salmonella typhimurium  
 C>Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
 C:Accession: S12388  
 R;Shyamala, V.; Schneider, E.; Ames, G.F.L.  
 EMBO J. 9, 939-946, 1990  
 A:Title: Tandem chromosomal duplications: role of REP sequences in the recombination of the argA gene  
 A:Reference number: S12388; MUID:90183995; PMID:2178927  
 A:Accession: S12388  
 A:Molecule type: DNA  
 A:Residues: 1-13 <SHY>  
 C:Genetics:  
 A:Gene: argA

Query Match 13.6%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
 |||  
 Db 6 KVL 8

## RESULT 35

G22565  
R-phycoerythrin gamma-B chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: G22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: G22565  
A;Molecule type: protein  
A;Residues: 1-13 <KLO>

Query Match 13.6%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VPQ 11  
|||  
Db 6 VPQ 8

## RESULT 36

S09018  
hemolytic protein A1 - edible frog (fragment)  
C;Species: Rana esculenta (edible frog)  
C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 18-Jun-1993  
C;Accession: S09018  
R;Simmaco, M.; De Biase, D.; Severini, C.; Alta, M.; Erspamer, G.F.; Barra, D.; Borea, F.  
Biochim. Biophys. Acta 1033, 318-323, 1990  
A;Title: Purification and characterization of bioactive peptides from skin extracts of R.  
A;Reference number: S09018; MUID:90198965; PMID:2317508  
A;Accession: S09018  
A;Molecule type: protein  
A;Residues: 1-13 <SIM>

Query Match 13.6%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQ 3  
|||  
Db 9 LSQ 11

## RESULT 37

PL0157  
Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PEC) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-Feb-1997  
C;Accession: PL0157; C61458  
R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1989  
A;Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associated glycoprotein.  
A;Reference number: A61458; MUID:90039128; PMID:2478651  
A;Accession: PL0157  
A;Molecule type: protein  
A;Residues: 1-13 <BRO>  
A;Accession: C61458  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <BR2>  
C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein.  
C;Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPV 9  
|||  
Db 11 LPV 13

## RESULT 38

B56864  
dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
C;Accession: B56864  
R;Plakidou-Dymock, S.; McGivan, J.D.  
Biochim. Biophys. Acta 1145, 105-112, 1993  
A;Title: The oligomeric structure of renal aminopeptidase N from bovine brush-border  
A;Reference number: A56864; MUID:93136203; PMID:8093665  
A;Accession: B56864  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <PLA>  
A;Experimental source: renal brush-border membrane vesicles  
C;Keywords: dipeptidylpeptidase

Query Match 13.6%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7  
|||  
Db 6 KVL 8

## RESULT 39

C61576  
ribosomal protein L30 - Actinomadura malachitica (fragment)  
C;Species: Actinomadura malachitica  
C;Date: 20-Oct-1994 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C;Accession: C61576  
R;Ochi, K.; Miyadoh, S.; Tamura, T.  
Int. J. Syst. Bacteriol. 41, 234-239, 1991  
A;Title: Polyacrylamide gel electrophoresis analysis of ribosomal protein AT-L30 as a  
A;Reference number: A61576; MUID:91307971; PMID:1854638  
A;Accession: C61576  
A;Molecule type: protein  
A;Residues: 1-13 <OCH>  
C;Keywords: protein biosynthesis; ribosome

Query Match 13.6%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14  
|||  
Db 9 KAV 11

## RESULT 40

JN0389  
histamine-releasing peptide I - oriental hornet  
A;Alternate names: venom protein HR-1  
C;Species: Vespa orientalis (oriental hornet)  
C;Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 23-Aug-1997  
C;Accession: JN0389; S06445  
R;Miroshnikov, A.I.; Snezhkova, L.G.; Nazimov, I.V.; Reshetova, O.I.; Rozinov, B.V.; Bioorg. Khim. 7, 1467-1477, 1981  
A;Title: Structure and properties of histamine releasing peptides from the venom of  
A;Reference number: JN0389  
A;Accession: JN0389  
A;Molecule type: protein  
A;Residues: 1-14 <MIR>  
R;Tulichbaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.  
Biochemistry (N.Y.) 53, 183-190, 1988  
A;Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis.  
A;Reference number: S06445  
A;Accession: S06445  
A;Molecule type: protein  
A;Residues: 1-14 <TUI>

C:Superfamily: mastoparan  
 C:Keywords: amidated carboxyl end; venom  
 F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
 |||  
 Db 12 KVL 14

RESULT 41  
 C33098  
 223K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
 C:Species: Plasmodium falciparum  
 C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: C33098  
 R:Nichols, J.H.; Hager, L.P.  
 submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: C33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-14 <NIC>

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8  
 |||  
 Db 1 VLP 3

RESULT 42  
 S45655  
 cathepsin L (EC 3.4.22.15) 2 - liver fluke (fragment)  
 N:Alternate names: cysteine proteinase  
 C:Species: Fasciola hepatica (liver fluke)  
 C:Date: 10-Dec-1994 #sequence\_revision 26-Jul-1996 #text\_change 26-Jul-1996  
 C:Accession: S45655  
 R:Dowd, A.J.; Smith, A.M.; McGonigle, S.; Dalton, J.P.  
 Eur. J. Biochem. 223, 91-98, 1994  
 A:Title: Purification and characterisation of a second cathepsin L proteinase secreted by  
 A:Reference number: S45655; MUID:94307282; PMID:8033913  
 A:Accession: S45655  
 A:Molecule type: protein  
 A:Residues: 1-14 <DOW>  
 C:Keywords: cysteine proteinase; hydrolase

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15  
 |||  
 Db 1 AVP 3

RESULT 43  
 S38307  
 DEB-A protein - fruit fly (Drosophila melanogaster) (fragment)  
 C:Species: Drosophila melanogaster  
 C:Date: 19-May-1994 #sequence\_revision 27-Feb-1997 #text\_change 17-Mar-1999  
 C:Accession: S38307  
 R:Wang, G.L.; Goldstein, E.S.  
 Biochim. Biophys. Acta 1216, 94-104, 1993  
 A:Title: An AP-1 binding site in the upstream region of DEB-A is part of a developmental  
 A:Reference number: S38307; MUID:94032494; PMID:8218421  
 A:Accession: S38307  
 A>Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-14 <WAN>

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21  
 |||  
 Db 1 MPI 3

RESULT 44  
 S14336  
 mastoparan B - hornet (Vespa basalis)  
 C:Species: Vespa basalis  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Apr-1999  
 C:Accession: S14336  
 R:Ho, C.L.; Hwang, L.L.  
 Biochem. J. 274, 453-456, 1991  
 A:Title: Structure and biological activities of a new mastoparan isolated from the ve  
 A:Reference number: S14336; MUID:91174755; PMID:2006909  
 A:Accession: S14336  
 A:Molecule type: protein  
 A:Residues: 1-14 <HOC>  
 A:Experimental source: venom  
 C:Function:  
 A:Description: possesses a potent hemolytic activity which acts in synergy with the le  
 C:Keywords: amidated carboxyl end; mast cell; venom  
 F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
 |||  
 Db 12 KVL 14

RESULT 45  
 A23996  
 beta-granin - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Jun-1993  
 C:Accession: A23996  
 R:Hutton, J.C.; Hansen, F.; Peshavaria, M.  
 FEBS Lett. 188, 336-340, 1985  
 A:Title: Beta-granins: 21 kDa co-secreted peptides of the insulin granule closely rel  
 A:Reference number: A23996; MUID:85285598; PMID:3896848  
 A:Accession: A23996  
 A:Molecule type: protein  
 A:Residues: 1-14 <HUT>

Query Match 13.6%; Score 3; DB 2; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 |||  
 Db 1 LPV 3

RESULT 46  
 I49420  
 placental lactogen I - western wild mouse (fragment)  
 C:Species: Mus spretus (western wild mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 11-Jan-2000  
 C:Accession: I49420  
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau,  
 Mamm. Genome 5, 349-355, 1994  
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
 A:Reference number: I48934; MUID:94319082; PMID:8043949

A/Accession: I49420  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-15 <RES>  
 A/Cross-references: EMBL:U05735; NID:g497071; PIDN:AAB60476.1; PID:g497072  
 C/Superfamily: prolactin

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7  
 |||  
 Db 3 KVL 5

## RESULT 47

PN0117  
 hemoglobin alpha chain - red fox (fragment)  
 C/Species: Vulpes vulpes (red fox)  
 C/Date: 15-Jan-1993 #sequence\_revision 15-Jan-1993 #text\_change 19-May-2000  
 C/Accession: PN0117  
 R/Sukhomlinov, B.F.; Konoshenko, S.V.  
 Mol. Biol. (Mosk.) 5, 415-418, 1971  
 A/Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.  
 A/Reference number: PN0117  
 A/Accession: PN0117  
 A/Molecule type: protein  
 A/Residues: 1-15 <SUK>  
 C/Superfamily: globin; globin homology  
 C/Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14  
 |||  
 Db 7 KAV 9

## RESULT 48

PH0216  
 agarase (EC 3.2.1.81) - Pseudomonas sp. (fragment)  
 N/Alternate names: agarase 4-glycanohydrolase  
 C/Species: Pseudomonas sp.  
 C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 06-Dec-1996  
 C/Accession: PH0216  
 R/Yamaura, I.; Matsumoto, T.; Funatsu, M.; Shigeiri, H.; Shibata, T.  
 Agric. Biol. Chem. 55, 2531-2536, 1991  
 A/Title: Purification and some properties of agarase from Pseudomonas sp. PT-5.  
 A/Reference number: PH0216  
 A/Accession: PH0216  
 A/Molecule type: protein  
 A/Residues: 1-15 <YAM>  
 A/Experimental source: strain PT-5  
 A/Note: the isoelectric point of this enzyme is 3.6  
 C/Comment: This enzyme is stable from pH6 to 9 and has its maximum activity at pH8.5.  
 C/Comment: This enzyme rapidly reduces the viscosity of agarose solution and the activity  
 C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15  
 |||  
 Db 7 AVP 9

## RESULT 49

T09463  
 ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)

C/Species: mitochondrion Pylaiella littoralis  
 C/Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 13-Aug-1999  
 C/Accession: T09463  
 R/Rousvoal, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.  
 J. Mol. Biol. 277, 1047-1057, 1998  
 A/Title: Witnessing the evolution of transcription in mitochondria: The mitochondrial  
 A/Reference number: Z16681; MUID:98239704; PMID:9571021

A/Accession: T09463  
 A/Molecule type: DNA  
 A/Residues: 1-15 <ROU>  
 A/Cross-references: EMBL:AF034976; NID:g3243103; PID:g3243104  
 A/Experimental source: strain Roscoff  
 C/Genetics:  
 A/Gene: rps14  
 A/Genome: mitochondrion  
 C/Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8  
 |||  
 Db 6 VLP 8

## RESULT 50

PA0056  
 protein QP200002 - fungus (Fusarium sporotrichioides) (fragment)  
 C/Species: Fusarium sporotrichioides  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C/Accession: PA0056  
 R/Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
 A/Reference number: PA0051  
 A/Accession: PA0056  
 A/Molecule type: protein  
 A/Residues: 1-15 <CHO>

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14  
 |||  
 Db 3 KAV 5

## RESULT 51

B61457  
 alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)  
 C/Species: Tetrahymena pyriformis  
 C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 07-Dec-1999  
 C/Accession: B61457  
 R/Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.  
 J. Protozool. 36, 562-567, 1989  
 A/Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification  
 A/Reference number: A61457; MUID:90095988; PMID:2689637

A/Accession: B61457  
 A/Molecule type: protein  
 A/Residues: 1-15 <BAN>  
 C/Genetics:  
 A/Genetic code: SGC5

C/Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; mc

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8  
 |||

Db 1 VLP 3

## RESULT 52

PT0090  
 alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)  
 C:Species: Apis mellifera (honeybee)  
 C>Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 07-May-1999  
 C:Accession: PT0090  
 R:Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.  
 Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997  
 A:Title: A catalytic amino acid and primary structure of active site in Aspergillus niger  
 A:Reference number: PT0090; MUID:97399878; PMID:9255970  
 A:Accession: PT0090  
 A:Molecule type: protein  
 A:Residues: 1-15 <KIM>  
 C:Keywords: glycosidase; hydrolase

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15  
 ||||  
 Db 9 AVP 11

## RESULT 53

D46743  
 corneal keratan sulfate proteoglycan core protein 25 - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C:Accession: D46743  
 R:Funderburgh, J.L.; Funderburgh, M.L.; Brown, S.J.; Vergnes, J.P.; Hassell, J.R.; Mann, J. Biol. Chem. 268, 11874-11880, 1993  
 A:Title: Sequence and structural implications of a bovine corneal keratan sulfate proteoglycan  
 A:Reference number: A46743; MUID:93280153; PMID:8099356  
 A:Accession: D46743  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-15 <FUN>

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21  
 ||||  
 Db 2 MPI 4

## RESULT 54

G24417  
 interphotoreceptor retinoid-binding protein - hamster (fragment)  
 N:Alternate names: interstitial retinol-binding protein  
 C:Species: Cricetinae gen. sp. (hamster)  
 C>Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 18-Jun-1993  
 C:Accession: G24417  
 R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.  
 FEBS Lett. 205, 309-312, 1986  
 A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10  
 A:Reference number: A91365; MUID:86301171; PMID:3743780  
 A:Accession: G24417  
 A:Molecule type: protein  
 A:Residues: 1-15 <FON>

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 PIQ 22  
 ||||  
 Db 2 PIQ 4

## RESULT 55

S62675  
 collagen type I - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
 C:Accession: S62675  
 R:Mizuno, M.; Kitafima, T.; Tomita, M.; Kuboki, Y.  
 Biochim. Biophys. Acta 1310, 97-102, 1996  
 A:Title: The osteoblastic MC3T3-E1 cells synthesized C-terminal propeptide of type I  
 A:Reference number: S62675; MUID:97386332; PMID:9244181  
 A:Accession: S62675  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <MTZ>

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 QRD 18  
 ||||  
 Db 8 QRD 10

## RESULT 56

PH1590  
 Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1590  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1590  
 A:Molecule type: DNA  
 A:Residues: 1-15 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 RDM 19  
 ||||  
 Db 3 RDM 5

## RESULT 57

A31902  
 bone acidic glycoprotein-75 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 31-Dec-1993  
 C:Accession: A31902  
 R:Goraki, J.P.; Shimizu, K.  
 J. Biol. Chem. 263, 15938-15945, 1988  
 A:Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone  
 A:Reference number: A31902; MUID:89034045; PMID:2846530  
 A:Accession: A31902  
 A:Molecule type: protein  
 A:Residues: 1-15 <GOR>  
 A>Note: 14-Glu and 15-Glu were also found  
 C:Keywords: glycoprotein

Query Match 13.6%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 ||||



Db 1 LPV 3

RESULT 58  
A27803  
myosin light chain, smooth muscle - turkey (fragment)  
C;Species: Meleagris gallopavo (common turkey)  
C;Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 29-Sep-1999  
C;Accession: A27803  
R;Bengur, A.R.; Robinson, E.A.; Appella, E.; Sellers, J.R.  
J. Biol. Chem. 262, 7613-7617, 1987  
A;Title: Sequence of the sites phosphorylated by protein kinase C in the smooth muscle  
A;Reference number: A27803; MUID:87222380; PMID:3584131  
A;Accession: A27803  
A;Molecule type: protein  
A;Residues: 1-16 <BEN>  
C;Superfamily: calmodulin; calmodulin repeat homology  
C;Keywords: EF hand; muscle; smooth muscle

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQR 17  
|||  
Db 14 PQR 16

RESULT 59  
PA0048  
protein OA100047 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0048; PA0043  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
submitted to JIPID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional  
A;Reference number: PA0001  
A;Accession: PA0048  
A;Molecule type: protein  
A;Residues: 1-16 <KAM>  
A;Experimental source: stem

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 DMP 20  
|||  
Db 5 DMP 7

RESULT 60  
PS0256  
22K protein 4208 - rice (strain Nihonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C;Accession: PS0256  
R;Tsugita, A.; Miyatake, N.  
submitted to JIPID, April 1993  
A;Reference number: PS0208  
A;Accession: PS0256  
A;Molecule type: protein  
A;Residues: 1-16 <TSU>  
A;Experimental source: germ, strain Nihonbare  
C;Comment: molecular weight 22K, pI 6.6.

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14  
|||

Db 2 KAV 4

RESULT 61  
S38292  
30K allergen - rye (fragment)  
C;Species: Secale cereale (rye)  
C;Date: 19-May-1994 #sequence\_revision 27-Feb-1997 #text\_change 07-May-1999  
C;Accession: S38292  
R;Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.  
Bioi. Chem. Hoppe-Seyler 374, 855-861, 1993  
A;Title: Comparison of four grass pollen species concerning their allergens of grass  
A;Reference number: S38288; MUID:94092339; PMID:7505588  
A;Accession: S38292  
A;Molecule type: protein  
A;Residues: 1-16 <PET>

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QPK 5  
|||  
Db 13 QPK 15

RESULT 62  
A23992  
melatin-omochrome-stimulating hormone III - silkworm (fragment)  
N;Alternate names: melanization and reddish coloration hormone III; MRCH III  
C;Species: Bombyx mori (silkworm)  
C;Date: 30-Jan-1988 #sequence\_revision 30-Jan-1988 #text\_change 18-Jun-1993  
C;Accession: A23992  
R;Matsumoto, S.; Isogai, A.; Suzuki, A.  
FEBS Lett. 189, 115-118, 1985  
A;Title: N-terminal amino acid sequence of an insect neurohormone, melanization and  
A;Reference number: A23992; MUID:85285612; PMID:3896851  
A;Accession: A23992  
A;Molecule type: protein  
A;Residues: 1-16 <MAT>  
C;Keywords: hormone

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 DMP 20  
|||  
Db 5 DMP 7

RESULT 63  
S65709  
major allergen Myr p I - bulldog ant (Myrmecia pilosula) (fragment)  
C;Species: Myrmecia pilosula  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C;Accession: S65709  
R;Street, M.D.; Donovan, G.R.; Baldo, B.A.  
Biochim. Biophys. Acta 1305, 87-97, 1996  
A;Title: Molecular cloning and characterization of the major allergen Myr p II from t  
A;Reference number: S65709; MUID:96180991; PMID:8605256  
A;Accession: S65709  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <STR>

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKV 6  
|||  
Db 7 PKV 9

## RESULT 64

S68730  
bleomycin-binding protein - Streptomyces verticillus (fragment)  
C:Species: Streptomyces verticillus  
C>Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 17-Mar-1999  
C:Accession: S68730  
R:Sugiyama, M.; Kunagai, T.; Matsuo, H.; Bhuiyan, M.Z.A.; Ueda, K.; Mochizuki, H.; Nakam  
FBES Lett. 362, 80-84, 1995  
A:Title: Overproduction of the bleomycin-binding proteins from bleomycin-producing Sterp  
al characterisation.  
A:Reference number: S68730; MUID:95212588; PMID:7535252  
A:Accession: S68730  
A:Molecule type: protein  
A:Residues: 1-16 <SUG>  
A:Experimental source: ATCC 15003  
C:Keywords: antibiotic resistance

Query Match 13.6%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15

|||||  
Db 7 AVP 9

## RESULT 65

I65274  
glutathione S-transferase Ya subunit (put.) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 18-Jun-1999  
C:Accession: I65274  
R:Rothkopf, G.S.; Telakowski-Hopkins, C.A.; Scotish, R.L.; Pickett, C.B.  
Biochemistry 25, 993-1002, 1986  
A:Title: Multiplicity of glutathione S-transferase genes in the rat and association with  
A:Reference number: I52395; MUID:86187772; PMID:2421763  
A:Accession: I65274  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-17 <RES>  
A:Cross-references: GB:M12894; NID:G204504; PIDN:AAA41289.1; PID:G204505  
C:Superfamily: glutathione transferase

Query Match 13.6%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9

|||||  
Db 1 LPV 3

## RESULT 66

A29834  
trp leader peptide - Corynebacterium glutamicum  
C:Species: Corynebacterium glutamicum  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Sep-1999  
C:Accession: A29834; A24723; A29458; S13087; A48967  
R:Matsui, K.; Miwa, K.; Sano, K.  
J. Bacteriol. 169, 5330-5332, 1987  
A:Title: Two single-base-pair substitutions causing desensitization to tryptophan feedba  
ntum.

A:Reference number: A29834; MUID:88032866; PMID:3667535  
A:Contents: B. lactofermentum  
A:Accession: A29834  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-17 <MAT>  
A:Cross-references: GB:M17892; NID:G144101; PIDN:AAB59110.1; PID:G1129101  
R:Matsui, K.; Sano, K.; Ohtsubo, E.  
Nucleic Acids Res. 14, 10113-10114, 1986

A:Title: Complete nucleotide and deduced amino acid sequences of the Brevibacterium 1.  
A:Reference number: A93606; MUID:87117512; PMID:3808947  
A:Contents: B. lactofermentum  
A:Accession: A24723  
A:Molecule type: DNA  
A:Residues: 1-17 <MA2>  
A:Cross-references: GB:X04960; NID:G39591; PIDN:CAA28622.1; PID:G580785  
R:Sano, K.; Matsui, K.  
Gene 53, 191-200, 1987  
A:Title: Structure and function of the trp operon control regions of Brevibacterium 1.  
A:Reference number: A91575; MUID:87277409; PMID:3609747  
A:Contents: B. lactofermentum  
A:Accession: A29458  
A:Molecule type: DNA  
A:Residues: 1-17 <SAN>  
R:Heery, D.M.; Dunican, L.K.  
Nucleic Acids Res. 18, 7138, 1990  
A:Title: Nucleotide sequence of the Corynebacterium glutamicum trpE gene.  
A:Reference number: S13087; MUID:91088299; PMID:2263476  
A:Accession: S13087  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <HEE>  
A:Cross-references: EMBL:X55994; NID:G40521; PIDN:CAA39466.1; PID:G580992  
R:Heery, D.M.; Dunican, L.K.  
Appl. Environ. Microbiol. 59, 791-799, 1993  
A:Title: Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of C.  
A:Reference number: A48967; MUID:93243735; PMID:7683184  
A:Accession: A48967  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-13 <HER>  
A:Cross-references: GB:S59299; NID:G299877; PIDN:AAB26395.1; PID:G299878  
A:Experimental source: ATCC 21850  
C:Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBIP:130456)  
C:Genetics:  
A:Gene: trpL  
A:Start codon: GTG  
C:Superfamily: unassigned leader peptides

Query Match 13.6%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQ 3

|||||  
Db 6 LSQ 8

## RESULT 67

A36727  
cytochrome c551 - Methylomonas sp. (fragment)  
C:Species: Methylomonas sp.  
C>Date: 19-Apr-1991 #sequence\_revision 19-Apr-1991 #text\_change 18-Jun-1993  
C:Accession: A36727  
R:DiSpirito, A.A.; Lipscomb, J.D.; Lidstrom, M.E.  
J. Bacteriol. 172, 5360-5367, 1990  
A:Title: Soluble cytochromes from the marine methanotroph Methylomonas sp. strain A4.  
A:Reference number: A36727; MUID:90368596; PMID:2168380  
A:Accession: A36727  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-17 <DIS>

Query Match 13.6%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 OKA 13

|||||  
Db 8 OKA 10

## RESULT 68

A49237  
 45/47K antigen - Mycobacterium bovis (fragment)  
 C:Species: Mycobacterium bovis  
 C>Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
 C:Accession: A49237  
 R:Romain, F.; Laquerriere, A.; Miltzer, P.; Pescher, P.; Chavarot, P.; Lagranderie, M.; Infect. Immun. 61, 742-750, 1993  
 A>Title: Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen complex, a  
 A:Reference number: A49237; MUID:93138802; PMID:8423100  
 A:Contents: BCG  
 A:Accession: A49237  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-17 <ROM>  
 A>Note: sequence extracted from NCBI backbone (NCBIP:123246)

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10  
 |||  
 Db 7 PVP 9

## RESULT 69

S59481  
 hydroxyproline-rich cell wall glycoprotein, 230K - kidney bean (fragment)  
 C:Species: Phaseolus vulgaris (kidney bean)  
 C>Date: 27-Apr-1996 #sequence\_revision 19-Jul-1996 #text\_change 05-Dec-1998  
 C:Accession: S59481  
 R:Wojtaszek, F.; Hethowan, J.; Bolwell, G.P. Plant Mol. Biol. 28, 1075-1087, 1995  
 A>Title: Specificity in the immobilisation of cell wall proteins in response to differ  
 A:Reference number: S59481; MUID:96011753; PMID:7548825  
 A:Accession: S59481  
 A:Molecule type: protein  
 A:Residues: 1-17 <WOJ>  
 C:Keywords: Glycoprotein; hydroxyproline  
 F:6,8,9,10,11/Modified site: hydroxyproline (Pro) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PVP 10  
 |||  
 Db 6 PVP 8

## RESULT 70

S28839  
 RNA-binding protein, 28K - garden pea (fragment)  
 C:Species: Pisum sativum (garden pea)  
 C>Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 05-Dec-1998  
 C:Accession: S28839  
 R:Subbalaiah, C.C.; Tewari, K.K. Eur. J. Biochem. 211, 171-179, 1993  
 A>Title: Purification and characterization of ribonucleoproteins from pea chloroplasts.  
 A:Reference number: S28837; MUID:93145944; PMID:8425527  
 A:Accession: S28839  
 A:Molecule type: protein  
 A:Residues: 1-17 <SUB>  
 A:Experimental source: cv. Arkel  
 C:Function:  
 A>Description: may be involved in post-transcriptional regulation of plastid genes  
 C:Keywords: chloroplast; transcription regulation

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAV 14  
 |||  
 Db 14 KAV 16

## RESULT 71

B22595  
 bombolitin I - American common bumblebee  
 C:Species: Bombus pennsylvanicus (American common bumblebee)  
 C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 08-Dec-1995  
 C:Accession: A22595  
 R:Argiolas, A.; Pisano, J.J. J. Biol. Chem. 260, 1437-1444, 1985  
 A>Title: Bombolitins, a new class of mast cell degranulating peptides from the venom  
 A:Reference number: A92504; MUID:85105003; PMID:2578459  
 A:Molecule type: protein  
 A:Residues: 1-17 <ARG>  
 C:Keywords: amidated carboxyl end; hemolysis; venom  
 F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7  
 |||  
 Db 12 KVL 14

## RESULT 72

B22595  
 bombolitin II - American common bumblebee  
 C:Species: Bombus pennsylvanicus (American common bumblebee)  
 C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 08-Dec-1995  
 C:Accession: B22595  
 R:Argiolas, A.; Pisano, J.J. J. Biol. Chem. 260, 1437-1444, 1985  
 A>Title: Bombolitins, a new class of mast cell degranulating peptides from the venom  
 A:Reference number: A92504; MUID:85105003; PMID:2578459  
 A:Accession: B22595  
 A:Molecule type: protein  
 A:Residues: 1-17 <ARG>  
 C:Keywords: amidated carboxyl end; hemolysis; venom  
 F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7  
 |||  
 Db 12 KVL 14

## RESULT 73

C22595  
 bombolitin III - American common bumblebee  
 C:Species: Bombus pennsylvanicus (American common bumblebee)  
 C>Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 08-Dec-1995  
 C:Accession: C22595  
 R:Argiolas, A.; Pisano, J.J. J. Biol. Chem. 260, 1437-1444, 1985  
 A>Title: Bombolitins, a new class of mast cell degranulating peptides from the venom  
 A:Reference number: A92504; MUID:85105003; PMID:2578459  
 A:Accession: C22595  
 A:Molecule type: protein  
 A:Residues: 1-17 <ARG>  
 C:Keywords: amidated carboxyl end; hemolysis; venom  
 F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
|||  
Db 12 KVL 14

## RESULT 74

D22595  
Bombolitin IV - American common bumblebee  
C:Species: Bombus pennsylvanicus (American common bumblebee)  
C:Date: 29-Aug-1987 #sequence\_revision 29-Aug-1987 #text\_change 08-Dec-1995  
C:Accession: D22595  
R:Argiolas, A.; Pisano, J.J.  
J. Biol. Chem. 260, 1437-1444, 1985  
A:Title: Bombolitins, a new class of mast cell degranulating peptides from the venom of  
A:Reference number: A92504; MUID:85105003; PMID:2578459  
A:Accession: D22595  
A:Molecule type: protein  
A:Residues: 1-17 <ARG>  
A:Keywords: amidated carboxyl end; hemolysis; venom  
F:17/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 13.6%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
|||  
Db 12 KVL 14

## RESULT 75

PT0234  
IG heavy chain CRD3 region (clone 1-130) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0234  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0234  
A:Molecule type: DNA  
A:Residues: 1-17 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 13.6%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
|||  
Db 5 KVL 7

Search completed: November 25, 2003, 19:36:11  
Job time : 16.093 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 7.80233 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22  
Sequence: 1 LSQPKVLVPQKAVPQDRMPIQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	22.7	10	UPA5 HUMAN	P30091 homo sapien
2	4	18.2	14	TKN1_SCHGR	P82470 schistocerc
3	4	18.2	19	COOT_SARBU	Q09148 sarcophaga
4	4	18.2	20	YOA4 KLEAE	P56506 klebsiella
5	3	13.6	8	NPB_BOVIN	P15507 bos taurus
6	3	13.6	9	FAR4 PENMO	P83319 penaeus mon
7	3	13.6	10	BPP_VIPAS	P31351 vipera aspi
8	3	13.6	10	UPA8 HUMAN	P30094 homo sapien
9	3	13.6	12	LMT1_LOCMI	P22395 locusta mig
10	3	13.6	12	TM2A_METMA	P80652 methanosarc
11	3	13.6	13	EP65 HUMAN	P54963 homo sapien
12	3	13.6	13	FIBB_RABIT	P14478 oryctolagus
13	3	13.6	13	HPA1_RANES	P32415 rana escul
14	3	13.6	13	PED1_HVDAT	P80578 hydra atten
15	3	13.6	13	TEME_RANTE	P56920 rana tempor
16	3	13.6	13	TEME_RANTE	P56921 rana tempor
17	3	13.6	14	CAT2_FASHE	P80342 fasciola he
18	3	13.6	14	MAST_VESBA	P21654 vespa basal
19	3	13.6	14	MAST_VESOR	P17238 vespa orien
20	3	13.6	14	TAT_HVIW2	P12509 human immun
21	3	13.6	14	TAT_HVIW2	P12511 human immun
22	3	13.6	14	UC15_MAIZE	P80621 zea mays (m
23	3	13.6	15	AFP3_MALPA	P83137 malva parvi
24	3	13.6	15	IRBP_CRISP	P12665 cricetidae
25	3	13.6	15	MCA2_RHOOP	P56870 rhodococcus
26	3	13.6	15	RBS_EHYPA	P80657 physcomitre
27	3	13.6	15	UC29_MAIZE	P80635 zea mays (m
28	3	13.6	16	AF25_MALPA	P83142 malva parvi
29	3	13.6	17	A45K_MYCBO	P80069 mycobacteri
30	3	13.6	17	BOL1_MEGPE	P10521 megabombus
31	3	13.6	17	BOL2_MEGPE	P07493 megabombus
32	3	13.6	17	BOL3_MEGPE	P07494 megabombus
33	3	13.6	17	BOL4_MEGPE	P07495 megabombus

RESULT 1

#### ALIGNMENTS

34	13.6	1	H2B3 ICTPU	P81904 ictalurus p
35	13.6	1	LEW_CORGL	P06556 corynebacte
36	13.6	17	UP34_UPEMJ	P82041 uperoleia m
37	13.6	17	UP35_UPEMJ	P82042 uperoleia m
38	13.6	18	AL13_CARMA	P81816 carcinus ma
39	13.6	18	ALL2_CVDPO	P82153 cydia pomon
40	13.6	18	D7AL_ACASC	P83402 acanthopagr
41	13.6	18	DRPH_UCAPU	P08871 uca pugiliat
42	13.6	18	LCTN_LAMGL	P83315 lama glama
43	13.6	18	NPA_BOVIN	P15506 bos taurus
44	13.6	19	FIBB_PIG	P14477 sus scrofa
45	13.6	19	IRBP_CAVPO	P12666 cavia porce
46	13.6	20	ABP_FIG	Q98rc7 sus scrofa
47	13.6	20	AF2L_MALPA	P81443 malva parvi
48	13.6	20	BIP_PHAVU	P80089 phaseolus v
49	13.6	20	CAT1_FASHE	Q05093 fasciola he
50	13.6	20	CD4_SHEEP	P05542 ovis aries
51	13.6	20	FIBB_ELEMA	P14538 elephas max
52	13.6	20	H2B1 ICTPU	P81903 ictalurus p
53	13.6	20	OAR_PROPHY	P14803 photinus py
54	9.1	4	DCWS_PSECH	P19918 pseudomonas
55	9.1	4	FFKA_ATEHL	P58705 anthopleura
56	9.1	5	BPP7_BOTIN	P30425 bothrops in
57	9.1	5	PRCT_PERAM	P01373 periplaneta
58	9.1	6	ACPH_RABIT	P25154 oryctolagus
59	9.1	6	E101_LITRU	P82096 litorea rub
60	9.1	6	TRPI_PSEPU	P36414 pseudomonas
61	9.1	7	CARP_MYTED	P10420 mytilus edu
62	9.1	7	LANC_CARUI	P36960 carnobacter
63	9.1	7	TPFY_PACDA	P83455 pachymedusa
64	9.1	7	UF04_MOUSE	P83642 mus musculu
65	9.1	7	UN06_PINPS	P81675 pinus pinas
66	9.1	8	AL12_CARMA	P81815 carcinus ma
67	9.1	8	AL18_CARMA	P81821 carcinus ma
68	9.1	8	ALI6_CVDPO	P82157 cydia pomon
69	9.1	8	B44K_PORGI	P81886 porphyromon
70	9.1	8	CAD1_ENTFA	P13268 enterococcu
71	9.1	8	CLP_THICU	P80488 thiobacillu
72	9.1	8	COM2_CONPU	P58785 conus purpu
73	9.1	8	CPD1_ENTFA	P13269 enterococcu
74	9.1	8	FUSS_FUSSO	P81010 fusarium so
75	9.1	8	PK3_PERAM	P82618 periplaneta
76	9.1	8	RS7_WYCIT	P33564 mycobacteri
77	9.1	8	UC26_MAIZE	P80632 zea mays (m
78	9.1	8	UPA1_HUMAN	P30087 homo sapien
79	9.1	8	VGLG_HSV2B	P81780 herpes simp
80	9.1	9	AL10_CARMA	P81813 carcinus ma
81	9.1	9	ALC_CHLRE	P82678 chlamydomon
82	9.1	9	BS43_SERPL	P83375 serratia pl
83	9.1	9	CONO_CONGE	P05486 conus geogr
84	9.1	9	COXE_THUOB	P80975 thunnus obe
85	9.1	9	FAR1_CALVO	P41856 calliphora
86	9.1	9	FAR2_CALVO	P41857 calliphora
87	9.1	9	FAR3_CALVO	P41858 calliphora
88	9.1	9	FAR3_PENMO	P83320 penaeus mon
89	9.1	9	FAR5_PENMO	P83318 penaeus mon
90	9.1	9	FARA_CALVO	P41865 calliphora
91	9.1	9	FIBB_EHYPA	P19346 erythrocebu
92	9.1	9	FLA2_TREHY	P80159 treponema h
93	9.1	9	FRF1_SARBU	P83350 sarcophaga
94	9.1	9	HUTU_KLEAE	P12381 klebsiella
95	9.1	9	ISOT_CYPCA	P42993 cyprinus ca
96	9.1	9	LITO_LITRU	P08945 litorea aur
97	9.1	9	LMT3_LOCMI	P41489 locusta mig
98	9.1	9	MGMT_BOVIN	P29177 bos taurus
99	9.1	9	OXYA_SCYCA	P42996 scyllorhinu
100	9.1	9	OXYF_SCYCA	P42997 scyllorhinu

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UPAS_HUMAN
ID UPAS_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1450907;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tisot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.95, ITS MW IS: 40 kDa.
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON TER 1 1 G -> Y.
FT VARIANT 9 9 /FTID=VAR_000002.
FT NON TER 10 10
FT SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 22.2%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPKVL 7
Db 3 QPKVL 7

RESULT 2
TKN1 SCHGR STANDARD; PRT; 14 AA.
AC P82470;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tachykinin-1 (Scg-midgut-TK).
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Midgut;
RX MEDLINE=20050081; PubMed=10581195;
RA Veelaert D., Baggerman G., Derua R., Waalkens E., Meeusen T.,
RA Vande Water G., De Loof A., Schoofs L.;
RT "Identification of a new tachykinin from the midgut of the desert
locust, Schistocerca gregaria, by ESI-Qq-TOF mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 266:237-242(1999).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.
CC -1- SIMILARITY: SIMILAR TO THE COCKROACH LEMTRP 3, A TACHYKININ-
CC RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1496 MW; CA4C578C0169FCT2 CRC64;

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Query Match 18.2%; Score 4; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVP 15
Db 5 KAVP 8

RESULT 3
COOT_SARBU STANDARD; PRT; 19 AA.
AC Q09148;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NEB-colloostatatin (Folliculoestatatin).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga.
OX NCBI_TaxID=7385;
RN [1]
RP SEQUENCE.
RX MEDLINE=95188911; PubMed=7883009;
RA Bylemans D., Proost P., Samijn B., Borovsky D., Grauwels L.,
RA Huybrechts R., van Damme J., van Beeumen J., de Loof A.;
RT "Neob-colloostatatin, a second folliculoestatatin of the grey fleshfly,
Neobellieria bullata.";
RL Eur. J. Biochem. 228:45-49(1995).
CC -1- FUNCTION: HAS AN OOSTATIC ACTIVITY. IT INHIBITS YOLK SYNTHESIS SO
CC INHIBITING THE SUBSEQUENT YOLK DEPOSITION IN PREVITELLOGENIC
CC FOLLICLES.
CC -1- SIMILARITY: TO THE NONHELICAL REGIONS OF THE COLLAGEN FAMILY.
CC -1- CAUTION: NEB-COLLOOSTATIN MAY BE PROTEOLYTICALLY CLEAVED FROM
CC COLLAGEN IV.
DR PIR; S69153; S69153.
SQ SEQUENCE 19 AA; 1880 MW; 41B6AF5F0CEB8251 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 7 LPVP 10

RESULT 4
YOA_H KLEAE STANDARD; PRT; 20 AA.
AC P56506;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yoaH (Fragment).
GN YOA_H.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=28451;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89056707; PubMed=3057324;
RA Goncharoff P., Nichols B.P.;
RT "Evolution of aminobenzoate synthases: nucleotide sequences of
Salmonella typhimurium and Klebsiella aerogenes pabB.";
RL Mol. Biol. Evol. 5:531-548(1988).
RN [2]
RP IDENTIFICATION.
RX MEDLINE=98248213; PubMed=9588799;
RA Rudd K.E., Humphery-Smith I., Wasinger V.C., Bairoch A.;

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RT "Low molecular weight proteins: a challenge for post-genomic
RL research.";
RL Electrophoresis 19:536-544(1998).
CC -!- SIMILARITY: BELONGS TO THE UPF0181 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M22078; -; NOT ANNOTATED_CDS.
DR HAWAP; MF_00507; -; 1.
DR InterPro; IPR005371; UPF0181.
DR Pfam; PF03701; UPF0181; 1.
KW Hypothetical protein.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2270 MW; E8AF6425DD9BC88 CRC64;

Query Match 18.2%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QKAV 14
Db 14 QKAV 17

RESULT 5
NPB_BOVIN
ID NPB_BOVIN STANDARD; PRT; 8 AA.
AC P15507;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; B24749; B24749.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
Db 5 PQR 7

RESULT 6
FAR4_PENMO
ID FAR4_PENMO STANDARD; PRT; 9 AA.
AC P8319;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP4 (SQPSMKLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S.,
RA Chaivathangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1119.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 1121 MW; DA0B07340685A776 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
Db 1 SQP 3

RESULT 7
BPP_VIPAS
ID BPP_VIPAS STANDARD; PRT; 10 AA.
AC P31351;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90382616; PubMed=2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
RT enzyme from the venom of Vipera aspis aspis.";
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
CC PIR; A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db 6 PKV 8

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RESULT 8  
UPAB HUMAN  
ID UPAB HUMAN STANDARD; PRT; 10 AA.  
AC P30094;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 34) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RA MEDLINE=93092937; PubMed=145097;  
RX Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714 (1992).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 7.2, ITS MW IS: 16 kDa.  
DR SWISS-2DPAGE; P30094; HUMAN.  
FT NON TER 1 10  
FT VARIANT 4 4 S -> H.  
FT NON TER 1 10 /FTID=VAR\_000003.  
FT SEQUENCE 10 AA; 977 MW; 2EA6E0C77AE325B8 CRC64;  
Query Match 13.6%; Score 3; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 13 AVP 15  
Db 8 AVP 10  
ID LMT1 LOCOMI STANDARD; PRT; 12 AA.  
AC P22395;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-AUG-1991 (Rel. 19, Last annotation update)  
DE Locustamytropin 1 (LOM-MT-1).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RA MEDLINE=90341077; PubMed=1974346;  
RX Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,  
RA Vandesande F., de Loof A.;  
RT "Isolation, identification and synthesis of locustamytropin  
RT (LOM-MT), a novel biologically active insect peptide.";  
RL Peptides 11:427-433 (1990).  
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
CC (MYOTROPIC ACTIVITY).  
CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A43975; A43975.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD RES 12 12 AMIDATION.  
FT SEQUENCE 12 AA; 1213 MW; D766C92722D6DDDD CRC64;  
Query Match 13.6%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 13 AVP 15  
Db 2 AVP 4  
RESULT 10  
TM2A METMA  
ID TM2A METMA STANDARD; PRT; 12 AA.  
AC P80652;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Alternative tetrahydromethanopterin S-methyltransferase 28 kDa subunit  
DE (SC 2.1.1.86) (N5-methyltetrahydromethanopterin-coenzyme M  
DE methyltransferase 28 kDa subunit) (Fragment).  
OS Methanobacteria; Methanobacteria; Methanobacteria; Methanobacteria;  
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;  
OC Methanobacteriales; Methanobacteriales; Methanobacteriales;  
OX NCBI\_TaxID=2209;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;  
RX MEDLINE=96370840; PubMed=8774736;  
RA Lienard T., Becher B., Marschall M., Bowien S., Gottschalk G.;  
RT "Sodium ion translocation by N5-methyltetrahydromethanopterin:  
RT coenzyme M methyltransferase from Methanobacteriales mazel Go1  
RT reconstituted in ether lipid liposomes.";  
RL Eur. J. Biochem. 239:857-864 (1996).  
CC -!- FUNCTION: THIS ENZYME COMPLEX CATALYZES AN INTERMEDIATE STEP IN  
CC METHANOGENESIS, THE FORMATION OF METHYL-COENZYME M AND  
CC TETRAHYDROMETHANOPTERIN FROM COENZYME M AND N5-METHYL-  
CC TETRAHYDROMETHANOPTERIN.  
CC -!- CATALYTIC ACTIVITY: 5-methyl-5,6,7,8-tetrahydromethanopterin + 2-  
CC mercaptoethanesulfonate = 5,6,7,8-tetrahydromethanopterin + 2-  
CC (methylthio)ethanesulfonate.  
CC -!- SUBUNIT: COMPOSED OF SIX DIFFERENT SUBUNITS.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
KW Transferase; Methyltransferase; Transmembrane; Methanogenesis.  
FT NON TER 12 12  
FT SEQUENCE 12 AA; 1321 MW; 6DB4A5766232D76B CRC64;  
Query Match 13.6%; Score 3; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 VLP 8  
Db 7 VLP 9  
RESULT 11  
EP65 HUMAN  
ID EP65 HUMAN STANDARD; PRT; 13 AA.  
AC P54963;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Erythrocyte 65 kDa protein (P65) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.  
RX MEDLINE=90004678; PubMed=2507249;  
RA Hart G.W., Haltiwanger R.S., Holt G.D., Kelly W.G.;  
RT "Nucleoplasmic and cytoplasmic glycoproteins.";  
RL Ciba Found. Symp. 145:102-118 (1989).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC GO; GO:0005737; Cytoplasm; NAS.  
DR Glycoprotein.  
KW Glycoprotein.



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FT NON_TER 1 1
FT CARBOHYD 2 2
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; DOB873344C61A776 CRC64;
    Query Match 13.6%; Score 3; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 2.2e+03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
Db |||
5 SQP 7

RESULT 12
ID FIBB RABIT STANDARD; PRT; 13 AA.
AC P14478;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen C.
DR PROSITE: PS00514; FIBRIN_AG_C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 13 FIBRINOPEPTIDE B.
FT MOD_RES 4 4 SULFATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1493 MW; 9417F3B76337CB1A CRC64;

    Query Match 13.6%; Score 3; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 2.2e+03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
8 VLP 10

RESULT 13
ID HPAL PANES STANDARD; PRT; 13 AA.
AC P32415;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein A1 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;

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RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR FIR; S09018; S09018.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD_RES 13 13 AMIDATION.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1390 MW; C6BA768B9DFE587D CRC64;

    Query Match 13.6%; Score 3; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 2.2e+03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQ 3
Db |||
9 LSQ 11

RESULT 14
ID PEDI HYDAT STANDARD; PRT; 13 AA.
AC P80578;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Pedin.
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
OC Hydridae; Hydra.
OX NCBI_TaxID=6087;
RN [1]
RP SEQUENCE.
RA MEDLINE=96232307; PubMed=8674432;
RA Hoffmeister S.A.H.;
RT "Isolation and characterization of two new morphogenetically active
RT peptides from Hydra vulgaris.";
RL Development 122:1941-1948(1996).
CC -!- FUNCTION: MORPHOGENETICALLY ACTIVE PEPTIDE. ACTIVE IN FOOT
CC DEVELOPMENT.
KW Morphogen.
SQ SEQUENCE 13 AA; 1512 MW; 6F5266E3F37632CB CRC64;

    Query Match 13.6%; Score 3; DB 1; Length 13;
    Best Local Similarity 100.0%; Pred. No. 2.2e+03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db |||
7 VLP 9

RESULT 15
ID TEME RANTE STANDARD; PRT; 13 AA.
AC P56920;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Temporin E.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;

```

RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
RT temporaria";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -1- FUNCTION: Has antibacterial activity against Gram-positive  
CC bacteria.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD\_RES 13 13 AMIDATION  
SQ SEQUENCE 13 AA; 1379 MW; 26505DFA79A92448 CRC64;  
  
Query Match 13.6%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 6 VLP 8  
DB 1 VLP 3  
  
RESULT 16  
TEMP\_RANTE STANDARD; PRT; 13 AA.  
ID TEMP\_RANTE  
AC P56921;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Temporin F.  
OS Rana temporaria (European common frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
OX NCBI\_TaxID=8407;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97175050; PubMed=9022710;  
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
RA Barra D.;  
RT "Temporins, antimicrobial peptides from the European red frog Rana  
RT temporaria";  
RL Eur. J. Biochem. 242:788-792(1996).  
CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-NEGATIVE AND  
CC GRAM-POSITIVE BACTERIA.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
CC -1- SIMILARITY: Belongs to the brevinin family.  
KW Amphibian defense peptide; Antibiotic; Amidation.  
FT MOD\_RES 13 13 AMIDATION.  
FT MOD\_RES 13 13  
SQ SEQUENCE 13 AA; 1370 MW; 2653612B9DECC338 CRC64;  
  
Query Match 13.6%; Score 3; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 KVL 7  
DB 7 KVL 9  
  
RESULT 17  
CAT2\_FASHE STANDARD; PRT; 14 AA.  
ID CAT2\_FASHE  
AC P80342;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cathepsin L2 (EC 3.4.22.15) (Fragment).  
OS Fasciola hepatica (Liver fluke).  
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Fasciola.  
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.

OX NCBI\_TaxID=6192;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94307282; PubMed=8033913;  
RA Dowd A.J., Smith A.M., McGonicle S., Dalton J.P.;  
RT "Purification and characterisation of a second cathepsin L proteinase  
RT secreted by the parasitic trematode Fasciola hepatica";  
RL Eur. J. Biochem. 223:91-98(1994).  
CC -1- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING  
CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.  
CC -1- CATALYTIC ACTIVITY: Specificity close to that of papain. As  
CC compared to cathepsin B, cathepsin L exhibits higher activity  
CC towards protein substrates, but has little activity on Z-Arg-Arg-  
CC NMeac, and no peptidyl-dipeptidase activity.  
CC -1- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE  
CC BONDS.  
CC -1- SUBCELLULAR LOCATION: Lysosomal.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.  
DR PIR; S45655; S45655.  
DR MEROPS; C01.033; --  
DR InterPro; IPR000169; SHprot acsite.  
DR PROSITE; PS00139; THIOL\_PROTEASE\_CYS; PARTIAL.  
DR PROSITE; PS00639; THIOL\_PROTEASE\_HIS; PARTIAL.  
DR PROSITE; PS00640; THIOL\_PROTEASE\_ASN; PARTIAL.  
KW Hydrolase; Thiol protease; Lysosome.  
FT NON\_TER 14 14  
SQ SEQUENCE 14 AA; 1605 MW; 9CAEAB74E9DA110A CRC64;  
  
Query Match 13.6%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 13 AVP 15  
DB 1 AVP 3  
  
RESULT 18  
MAST\_VESBA STANDARD; PRT; 14 AA.  
ID MAST\_VESBA  
AC P21654;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Mastoparan B.  
OS Vespa basalis (Hornet).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7444;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=91174755; PubMed=2006909;  
RA Lo C.-L., Hwang L.-L.;  
RT "Structure and biological activities of a new mastoparan isolated  
RT from the venom of the hornet Vespa basalis";  
RL Biochem. J. 274:453-456(1991).  
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins  
CC that couple to phospholipase C.  
DR PIR; S14336; S14336.  
KW Mast cell degranulation; Amidation.  
FT MOD\_RES 14 14 AMIDATION.  
FT MOD\_RES 14 14  
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;  
  
Query Match 13.6%; Score 3; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 KVL 7  
DB 12 KVL 14

```

RESULT 19
MAST VESOR
ID MAST VESOR STANDARD; PRT; 14 AA.
AC P17238;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan (Histamine releasing peptide I) (HR-I).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; JN0389; JN0389
KW Mast cell degranulation; Amidation.
FT MOD RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1494 MW; C94F9ECA026B00DD CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 20
TAT_HV128
ID TAT HV128 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553 (1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
DR EMBL; J03653; AAA44685.1; -.
DR HIV; J03653; TAT$JY1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 3 SQP 5

RESULT 21
TAT_HV128
ID TAT HV128 STANDARD; PRT; 14 AA.
AC P12511;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11681;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88281278; PubMed=3395517;
RA Yourho J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
RA Gallo R.C.;
RT "Nucleotide sequence analysis of the env gene of a new Zairian
RT isolate of HIV-1.";
RL AIDS Res. Hum. Retroviruses 4:165-173(1988).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR-OLD
CC ZAIREAN MALE.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; J03653; AAA44685.1; -.
DR HIV; J03653; TAT$JY1.
KW Transcription regulation; Activator; RNA-binding; Nuclear protein;
KW AIDS.
FT NON TER 1 1
SQ SEQUENCE 14 AA; 1453 MW; 37CC737BF82D7AA8 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
DB 3 SQP 5

RESULT 22

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RESULT 19
MAST VESOR
ID MAST VESOR STANDARD; PRT; 14 AA.
AC P17238;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan (Histamine releasing peptide I) (HR-I).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Miroshnikov A.I., Snezhkova L.G., Nazimov I.V., Reshetova O.I.,
RA Rozynov B.V., Gushchin I.S.;
RT "Structure and properties of histamine releasing peptides from the
RT venom of Vespa orientalis hornet.";
RL Bioorg. Khim. 7:1467-1477(1981).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR; JN0389; JN0389
KW Mast cell degranulation; Amidation.
FT MOD RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA; 1494 MW; C94F9ECA026B00DD CRC64;

Query Match 13.6%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 2.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 20
TAT_HV128
ID TAT HV128 STANDARD; PRT; 14 AA.
AC P12509;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TAT protein (Transactivating regulatory protein) (Fragment).
GN TAT.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11705;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salahuddin S.Z., Wong-Staal F., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-III/LAV over time in patients with AIDS or
RT at risk for AIDS.";
RL Science 232:1548-1553 (1986).
CC -!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE
CC TRANS-ACTIVATING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND
CC ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
CC PROMOTER.
CC -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM
CC BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO
CC WAS PERINATALLY INFECTED BY HER MOTHER.
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Qy		15 POR 17	
Dd		4 POR 6	
 RESULT 24			
IRBP CRISP			
ID	_IRBP_CRISP	STANDARD;	PRT; 15 AA.
AC	P12655;		
DT	01-OCT-1989	(Rel. 12, Created)	
DT	01-OCT-1989	(Rel. 12, Last sequence update)	
DT	01-FEB-1996	(Rel. 33, Last annotation update)	
DE	Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial retinol-binding protein) (Fragment).		
GN	RBP3		
OS	Cricetidae sp. (Hamster).		
OC	Rukaryotca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae.		
NCBI_TaxID=36483;	[1]		
RN	SEQUENCE.		
RX	MEDLINE=86301171; PubMed=3743780;		
RA	Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A., Bridges C.D.B.;		
RT	"N-terminal sequence homologies in interstitial retinol-binding proteins from 10 vertebrate species.";		
RL	FEBS Lett. 205:309-312(1986).		
CC -I-	FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.		
CC	-I- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT EPITHELIUM CELLS.		
CC	PIR; G24417; G24417.		
KW	Vitamin A; Transport.		
FT	NON_TER 15 15		
SQ	SEQUENCE 15 AA; 1752 MW; CSIA8780C85DSC1E CRC64;		
 Query Match 13.6%; Score 3; DB 1; Length 15; Best Local Similarity 100.0%; Pred.No. 2.5e+03; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps			
Qy		20 PIQ 22	
Dd		2 PIQ 4	
 RESULT 25			
MCA2_RHOOP			
ID	_MCA2_RHOOP	STANDARD;	PRT; 15 AA.
AC	P56870;		
DT	30-MAY-2000	(Rel. 39, Created)	
DT	30-MAY-2000	(Rel. 39, Last sequence update)	
DT	16-OCT-2001	(Rel. 40, Last annotation update)	
DE	Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).		
OS	Rhodococcus opacus (Nocardia opaca).		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Corynebacterineae; Nocardiaceae; Rhodococcus.		
NCBI_TaxID=37919;	[1]		
RN	SEQUENCE.		
RC	STRAIN=ICP;		
RX	MEDLINE=98324954; PubMed=9657989;		
RA	Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;		
RT	"Characterization of a maleylacetate reductase encoding region from Rhodococcus opacus ICP.";		
RL	J. Bacteriol. 180:3503-3508(1998).		
CC -I-	CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate + NAD(P)H.		
CC	-I- PATHWAY: 3-chlorocatechol degradation (beta-ketoadiopate pathway)		
CC	THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL PRODUCTS AND AS INDUSTRIAL EFFLUENT.		

CC -!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE  
 CC FAMILY;  
 DR InterPro; IPR001670; Fe-ADH.  
 DR PROSITE; PS00913; ADH IRON 1; PARTIAL.  
 DR PROSITE; PS00060; ADH IRON 2; PARTIAL.  
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1884 MW; 59DA90DD038F025E CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PQR 17  
 DB 9 PQR 11  
 RESULT 26  
 RBS\_PHYPA STANDARD; PRT; 15 AA.  
 AC P80657;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Ribulose biphosphate carboxylase small chain (EC 4.1.1.39) (RuBisCO  
 DE small subunit) (Fragment).  
 GN RBGS.  
 OS Physcomitrella patens (Moss).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
 CC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.  
 OX NCBI\_TaxID=3218;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Protonema;  
 RX MEDLINE=97275459; PubMed=9129336;  
 RA Kaestn B., Buck F., Nuske J., Reski R.;  
 RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
 RT plastid enzymes.";  
 RL Planta 201:261-272(1997).  
 CC -!- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-  
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic  
 CC carbon dioxide fixation, as well as the oxidative fragmentation of  
 CC the pentose substrate in the photorespiration process. Both  
 CC reactions occur simultaneously and in competition at the same  
 CC active site.  
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) = 2 3-  
 CC phospho-D-glycerate.  
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) =  
 CC 3-phospho-D-glycerate + 2-phosphoglycolate.  
 CC -!- SUBUNIT: 8 large chains + 8 small chains.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast.  
 CC -!- SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.  
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration;  
 KW Lyase; Oxidoreductase; Monooxygenase; Chloroplast.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1801 MW; 28B9E7AC4AED6C80 CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QPK 5  
 DB 9 QPK 11  
 RESULT 27  
 UC29\_MAIZE STANDARD; PRT; 15 AA.  
 ID UC29\_MAIZE  
 AC P80635;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 45)  
 DE (Fragment).  
 OC Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9 ITS MW IS: 37.6 kDa.  
 CC Maize-2DPAGE; P80635; COLEOPTILE.  
 DR MaizedB; 123960; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1679 MW; 3D53086B16018BC1 CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PVP 10  
 DB 4 PVP 6  
 RESULT 28  
 AF2S\_MALPA STANDARD; PRT; 16 AA.  
 ID AF2S\_MALPA  
 AC P83142;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 small subunit (CW-2) (Fragment).  
 OS Malva parviflora (Little mallow) (Cheeseweed).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosid II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RT parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 CC GO: GO:0003799; P:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 2027 MW; 9998D9EB8FB7E65 CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 POK 12  
 DB 10 POK 12

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RESULT 29
A45K MYCBO
ID BOLA_MEGPE STANDARD; PRT; 17 AA.
AC P80069;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 45/47 kDa antigen (Fragment).
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE.
RC STRAIN=BCG / Paris 1173 P2;
RX MEDLINE=93138802; PubMed=8423100;
RA Romain F., Laquerrie A., Militzer P., Pescher P., Chavarot P.,
RA Lagranderie M., Auregan G., Gheorghiu M., Marchal G.A.;
RT "Identification of a Mycobacterium bovis BCG 45/47-kilodalton antigen
RT complex, an immunodominant target for antibody response after
RT immunization with living bacteria.";
RL Infect. Immun. 61:742-750(1993).
CC -/- SUBCELLULAR LOCATION: Secreted.
CC -/- SIMILARITY: TO M.LEPRAE NL43, AND M.TUBERCULOSIS MPT32.
DR PIR; A49237; A49237.
KW Antigen.
FT NON TER 17 17
SQ SEQUENCE 17 AA; 1521 MW; 4492CC389D9D9893 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10
DB 7 PVP 9

RESULT 30
BOLA_MEGPE
ID BOLA_MEGPE STANDARD; PRT; 17 AA.
AC P10521;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin I.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -/- FUNCTION: Mast cell degranulating peptide.
DR PIR; A22595; A22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1836 MW; D5FA46F44B876602 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 31
BOLA_MEGPE
ID BOLA_MEGPE STANDARD; PRT; 17 AA.
AC P07493;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin II.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -/- FUNCTION: Mast cell degranulating peptide.
DR PIR; B22595; B22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1806 MW; C52026F14BD76602 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 32
BOLA_MEGPE
ID BOLA_MEGPE STANDARD; PRT; 17 AA.
AC P07494;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin III.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
CC -/- FUNCTION: Mast cell degranulating peptide.
DR PIR; C22595; C22595.
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1862 MW; D5FA46F14BC85B02 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 33
BOLA_MEGPE
ID BOLA_MEGPE STANDARD; PRT; 17 AA.

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AC P07495;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bombolitin IV.
OS Megabombus pennsylvanicus (American common bumblebee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Apidae; Bombus.
OX NCBI_TaxID=28643;
RN [1]_SEQUENCE.
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=85105003; PubMed=2578459;
RA Argiolas A., Pisano J.J.;
RT "Bombolitins, a new class of mast cell degranulating peptides from
RT the venom of the bumblebee Megabombus pennsylvanicus.";
RL J. Biol. Chem. 260:1437-1444(1985).
RC -!- FUNCTION: Mast cell degranulating peptide.
DR PIR; D22595;
KW Mast cell degranulation.
SQ SEQUENCE 17 AA; 1873 MW; A34A43514BCDFB6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 12 KVL 14

RESULT 34
H2B3 ICTPU STANDARD; PRT; 17 AA.
ID H2B3 ICTPU STANDARD; PRT; 17 AA.
AC P81904;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B-3 (Antibacterial histone-like protein 3) (HLP-3)
DE (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]_SEQUENCE, AND FUNCTION.
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Skin;
RX MEDLINE=98309109; PubMed=9645227;
RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;
RT "Antimicrobial activity in the skin of the channel catfish Ictalurus
RT punctatus: characterization of broad-spectrum histone-like
RT antimicrobial proteins.";
RL Cell. Mol. Life Sci. 54:467-475(1998).
CC -!- FUNCTION: Has antimicrobial activity. Possesses strong activity
CC against saprolegnia, the most common fungal infection in fish.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- MASS SPECTROMETRY: MW=13506; METHOD=WALDI.
CC -!- SIMILARITY: Belongs to the histone H2B family.
DR InterPro; IPR000558; Histone H2B.
DR PROSITE; PS00357; HISTONE H2B; PARTIAL.
KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
KW Antibiotic; Fungicide.
FT NON TER 17
SQ SEQUENCE 17 AA; 1795 MW; 44FB8D966FD2F377 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 12 KAV 14
DB 14 KAV 16

RESULT 35
LPW CORGL
ID LPW CORGL STANDARD; PRT; 17 AA.
AC P06556;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR CGL3028.1.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=87117512; PubMed=3808947;
RA Matsui K., Sano K., Ohtsubo E.;
RT "Complete nucleotide and deduced amino acid sequences of the
RT Brevibacterium lactofermentum tryptophan operon.";
RL Nucleic Acids Res. 14:10113-10114(1986).
RN [2]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=88032866; PubMed=3667535;
RA Matsui K., Miwa K., Sano K.;
RT "Two single-base-pair substitutions causing desensitization to
RT tryptophan feedback inhibition of anthranilate synthase and enhanced
RT expression of tryptophan genes of Brevibacterium lactofermentum.";
RL J. Bacteriol. 169:5330-5332(1987).
RN [3]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RX MEDLINE=87277409; PubMed=3609747;
RA Sano K., Matsui K.;
RT "Structure and function of the trp operon control regions of
RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
RL Gene 53:191-200(1987).
RN [4]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13059 / AS019;
RX MEDLINE=91088299; PubMed=2263476;
RA Heery D.M., Dunican L.K.;
RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
RL Nucleic Acids Res. 18:7138-7138(1990).
RN [5]_SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X04960; CAA28622.1; -
CC EMBL; M17892; AAB59110.1; -
CC EMBL; M16663; -; NOT_ANNOTATED_CDS.
CC EMBL; X55994; CAA39466.1; -
CC EMBL; AP005283; -; NOT_ANNOTATED_CDS.
CC PIR; A29834; A29834.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 17 AA; 2112 MW; 74C7E7924DAE56B CRC64;

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Query Match      13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQ 3
Db 6 LSQ 8

RESULT 36
UP34_UPEMJ
ID UP34_UPEMJ STANDARD; PRT; 17 AA.
AC P82041;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 3.4.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
  Australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1735; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 17 17
SQ SEQUENCE 17 AA; 1737 MW; 6F61E4834375DE1B CRC64;

Query Match      13.6%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 8 KAV 10

RESULT 37
UP35_UPEMJ
ID UP35_UPEMJ STANDARD; PRT; 17 AA.
AC P82042;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 3.5.
OS Uperoleia mjobergii (Australian toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104954;
RN [1]
SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RA Bradford A.M., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "New antibiotic uperin peptides from the dorsal glands of the
  Australian toadlet Uperoleia mjobergii.";
RL Aust. J. Chem. 49:1325-1331(1996).
CC -!- FUNCTION: SHOWS ANTIBACTERIAL ACTIVITY AGAINST B.CEREUS, L.LACTIS,
  L.INNOCCUA, M.LUTEUS, S.AUREUS, P.MULTOCI, S.EPIDERMIS AND
  S.UBERIS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1779; METHOD=FAB.
KW Amphibian defense peptide; Antibiotic; Amidation.

Query Match      13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db 11 PKV 13

RESULT 39
ALL2_CYPDPO
ID ALL2_CYPDPO STANDARD; PRT; 18 AA.
AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 2.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
SEQUENCE.
RP TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
  Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db 11 PKV 13

RESULT 38
AL13_CARMA
ID AL13_CARMA STANDARD; PRT; 18 AA.
AC P81816;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 13.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
SEQUENCE.
RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
  Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
  allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

Query Match      13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db 11 PKV 13

RESULT 39
ALL2_CYPDPO
ID ALL2_CYPDPO STANDARD; PRT; 18 AA.
AC P82153;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaastatin 2.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
SEQUENCE.
RP TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
  Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 18 18
SQ SEQUENCE 18 AA; 2225 MW; 3531112C8160AE27 CRC64;

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SQ SEQUENCE 18 AA; 2169 MW; 8B66679C0CDF175C CRC64;
Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
   |||
DB 11 LPV 13

RESULT 40
D7A1 ACASC STANDARD; PRT; 18 AA.
AC P83402;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)
DE (Fragment).
OS Acanthopagrus schlegelii (Black porgy).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Acanthopagrus.
OX NCBI_TaxID=72011;
RN SEQUENCE 18 AA; 2059 MW; BFF8C3EFA9B4047 CRC64;
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.
RC TISSUE=Liver;
EX MEDLINE=21956475; PubMed=11959129;
RA Tang W.-K.; Cheng C.H.K.; Fong W.-P.;
RT "First purification of the antiquitin protein and demonstration of its
  enzymatic activity."
RL FEBS Lett. 516:183-186(2002).
CC -|- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid +
  NADH.
CC -|- SUBUNIT: Homotetramer.
CC -|- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is
  2.0 mM and Vmax is 1.3 micromol/min x mg enzyme.
CC -|- SIMILARITY: Belongs to the aldehyde dehydrogenase family.
DR GO; GO:0004029; P:aldehyde dehydrogenase (NAD+) activity; IDA.
DR GO; GO:0006081; P:aldehyde metabolism; IDA.
DR InterPro; IPR002086; Aldehyde dehydr.
DR PROSITE; PS00070; ALDEHYDE DEHYDR. CYS; PARTIAL.
DR KOWAT; K00687; ALDEHYDE DEHYDR. GLU; PARTIAL.
DR OXidoreductase; NAD.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EFA9B4047 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPK 5
   |||
DB 7 QPK 9

RESULT 41
DRPH UCAPU STANDARD; PRT; 18 AA.
ID P08871;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Pigment-dispersing hormone (PDH) (light adapting distal retinal
  pigment hormone) (DRPH).
OS Uca pugnator (Atlantic sand fiddler crab) (Celuca pugnator).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Ocypodidae; Ocypodinae; Ocypodinae; Ocypodinae;
OC Celuca.
OX NCBI_TaxID=6772;
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RN SEQUENCE.
RP Rao K.R.; Riehm J.P.; Zahnow C.A.; Kleinholz L.H.; Tarr G.E.;
RA Johnson L.; Norton S.; Landau M.; Semmes O.J.; Sattelberg R.M.;
RA Jorenby W.H.; Hintz M.F.;
RT "Characterization of a pigment-dispersing hormone in eyestalks of the
  fiddler crab Uca pugnator."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5319-5322 (1985).
RN SEQUENCE.
RP MEDLINE=93230895; PubMed=8472537;
RA Leehr J.; Klein J.; Webster S.G.; Dirksen H.;
RT "Quantification, immunoaffinity purification and sequence analysis of
  a pigment-dispersing hormone of the shore crab, Carcinus maenas
  (L.)."
RL Comp. Biochem. Physiol. 104B:699-706(1993).
CC -|- FUNCTION: CAUSES THE MIGRATION OF THE DISTAL RETINAL PIGMENT
  INTO THE PROXIMAL END OF THE PIGMENT CHROMATOPHORE CELLS AND
  THUS DECREASES THE AMOUNT OF LIGHT ENTERING THE RETINULAS.
CC -|- SIMILARITY: TO THE PDH OF OTHER ARTHROPODS.
DR PIR; A25144; DRUPPD.
KW Hormone; Amidation.
FT DOMAIN 6 9 IMPORTANT FOR DRPH ACTIVITY.
FT MOD_RES 18 18 AMIDATION.
SQ SEQUENCE 18 AA; 1928 MW; 25D5CE8D016F544E CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
   |||
DB 12 PKV 14

RESULT 42
LCFN LAMGL STANDARD; PRT; 18 AA.
ID AC P8315;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lactophorin (Whey protein) (Fragment).
OS Lama glama (llama).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX NCBI_TaxID=9844;
RN SEQUENCE.
RP MEDLINE=20000588; PubMed=10531593;
RA Kappeler S.; Farah Z.; Puhan Z.;
RT "Alternative splicing of lactophorin mRNA from lactating mammary gland
  of the camel (Camelus dromedarius).";
RL J. Dairy Sci. 82:1-10(1999).
CC -|- SIMILARITY: BELONGS TO THE PP3 / GLYCAM-1 FAMILY.
DR GO; GO:0005576; C:extracellular; ISS.
DR Pfam; PF05242; GLYCAM-1; 1.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2079 MW; CDS96165B236AC6 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQP 4
   |||
DB 16 SQP 18

RESULT 43
NPA BOVIN STANDARD; PRT; 18 AA.
ID NP4 BOVIN
AC P15506;
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DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuropeptide A.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Brain;
RX MEDLINE=86067985; PubMed=3865193;
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
RT "Isolation, sequencing, synthesis, and pharmacological
RT characterization of two brain neuropeptides that modulate the action
RT of morphine.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
DR PIR; A24749; A24749.
KW Neuropeptide; Amidation.
FT MOD RES 18 18
SQ SEQUENCE 18 AA; 1921 MW; EC52DAE1F45CFPCB CRC64;

Query Match 13.6%; Score 3; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 POR 17
DB 15 POR 17

RESULT 44
FIBB_PIG
ID FIBB_PIG STANDARD; PRT; 19 AA.
AC P14477;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IP002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AGC_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 19
FT MOD RES 4 4
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2200 MW; 09F87B4F4F3863D CRC64;

Query Match 13.6%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4' PKV 6

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DB 12 PKV 14

RESULT 45
IRBP_CAVPO
ID IRBP_CAVPO STANDARD; PRT; 19 AA.
AC P12666;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Interphotoreceptor retinoid-binding protein (IRBP) (Interstitial
DE retinoid-binding protein) (Fragment).
GN RBP.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RX MEDLINE=86301171; PubMed=3743780;
RA Fong S.L., Cook R.G., Alvarez R.A., Liou G.I., Landers R.A.,
RA Bridges C.D.B.;
RT "N-terminal sequence homologies in interstitial retinoid-binding
RT proteins from 10 vertebrate species.";
RL FEBS Lett. 205:309-312(1986).
CC -!- FUNCTION: IRBP SHUTTLES 11-CIS AND ALL TRANS RETINOIDS BETWEEN
CC THE RETINOL ISOMERASE IN THE PIGMENT EPITHELIUM AND THE VISUAL
CC PIGMENTS IN THE PHOTORECEPTOR CELLS OF THE RETINA.
CC -!- SUBCELLULAR LOCATION: INTERPHOTORECEPTOR MATRIX THAT PERMEATES
CC THE SPACE BETWEEN THE RETINA AND THE CONTIGUOUS LAYER OF PIGMENT
CC EPITHELIUM CELLS.
DR PIR; D24417; D24417.
KW Vitamin A; Transport.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2155 MW; 7172B271C85969D5 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
DB 14 KVL 16

RESULT 46
ABP_PIG
ID ABP_PIG STANDARD; PRT; 20 AA.
AC Q9TRC7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Amiloride-sensitive amine oxidase [copper-containing] (EC 1.4.3.6)
DE (Diamine oxidase) (DAO) (Amiloride-binding protein) (ABP)
DE (Histaminase) (PK-DAO) (Fragment).
GN ABPL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=94193685; PubMed=8144586;
RA Novotny W.F., Chassande O., Baker M., Lazdunski M., Barbry P.;
RT "Diamine oxidase is the amiloride-binding protein and is inhibited by
RT amiloride analogues.";
RL J. Biol. Chem. 269:9921-9925(1994).
CC -!- FUNCTION: Catalyzes the degradation of compounds such as
CC putrescine, histamine, spermine, and spermidine, substances
CC involved in allergic and immune responses, cell proliferation,
CC tissue differentiation, tumor formation, and possibly apoptosis.
CC

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CC (By similarity).  
 CC -!- CATALYTIC ACTIVITY: RCH(2)NH(2) + H(2)O + O(2) = RCHO + NH(3) +  
 CC H(2)O(2).  
 CC -!- COPACTOR: Binds 1 copper ion and 1 topaquinone per subunit (By  
 CC similarity).  
 CC -!- SUBUNIT: HOMODIMER; Disulfide-linked (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).  
 CC -!- PTM: Topaquinone (TPO) is generated by copper-dependent  
 CC autooxidation of a specific tyrosyl residue (By similarity).  
 CC -!- SIMILARITY: BELONGS TO THE COPPER/TOPAQUINONE OXIDASE FAMILY.  
 DR PIR; B54410; B54410.  
 DR GlycoSuiteDB; O9TRC7; -.  
 DR InterPro; IPR000269; CUNH oxidase.  
 DR PROSITE; PS01164; COPPER AMINE OXID 1; PARTIAL.  
 DR PROSITE; PS01165; COPPER AMINE OXID 2; PARTIAL.  
 KW Oxidoreductase; Copper; Heparin-binding; TPQ.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 1898 MW; 4A0E3133B0B2D69F CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 12 KAV 14  
 Db ||||  
 18 KAV 20  
 RESULT 47  
 AF2L MALPA ID AF2L MALPA STANDARD; PRT; 20 AA.  
 AC P83143;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Antifungal protein 2 large subunit (CW-2) (fragment).  
 OS Malva parviflora (Littie mallow) (Cheeseweed).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RL parviflora).";  
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 PQR 17  
 Db ||||  
 4 PQR 6  
 RESULT 48  
 BIP\_PHAVU ID BIP\_PHAVU STANDARD; PRT; 20 AA.  
 AC P80089;  
 DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Luminal binding protein (78 kDa glucose-regulated protein homolog)  
 DE (GRP 78) (fragment).  
 OS Phaseolus vulgaris (Kidney bean) (French bean).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.  
 OX NCBI\_TaxID=3885;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Greensleeves; TISSUE=Cotyledon;  
 RX MEDLINE=94221064; PubMed=1344885;  
 RA D'Amico L., Valsasina B., Daminati M.G., Fabbri M.S., Nitti G.,  
 RA Bollini R., Ceriotti A., Vitale A.;  
 RT "Bean homologs of the mammalian glucose-regulated proteins: induction  
 RT by tunicamycin and interaction with newly synthesized seed storage  
 RT proteins in the endoplasmic reticulum.";  
 RL Plant J. 2:443-455(1992).  
 CC -!- FUNCTION: PROBABLY PLAYS A ROLE IN FACILITATING THE ASSEMBLY OF  
 CC MULTIMERIC PROTEIN COMPLEXES INSIDE THE ER.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
 CC -!- INDUCTION: By tunicamycin.  
 CC -!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.  
 DR InterPro; IPR001023; Hsp70.  
 DR PROSITE; PS00297; HSP70\_1; PARTIAL.  
 DR PROSITE; PS00329; HSP70\_2; PARTIAL.  
 DR PROSITE; PS01036; HSP70\_3; PARTIAL.  
 KW ATP-binding; Endoplasmic reticulum.  
 FT UNSURE 4 4 OR T.  
 FT NON\_TER 18 18 OR T.  
 FT NON\_TER 20 20  
 SQ SEQUENCE 20 AA; 2147 MW; 809D43AF21A21476 CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 KVL 7  
 Db ||||  
 5 KVL 7  
 RESULT 49  
 CAT1\_PASHE ID CAT1\_PASHE STANDARD; PRT; 20 AA.  
 AC Q09093;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cathepsin L1 (EC 3.4.22.15) (fragment).  
 OS Fasciola hepatica (liver fluke).  
 CC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 CC Echinostomida; Echinostomata; Fasciolidae; Fasciola.  
 OX NCBI\_TaxID=6192;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94158959; PubMed=8114809;  
 RA Smith A.M., Dowd A.J., McConigle S., Keegan P.S., Brennan G.,  
 RA Trudgett A., Dalton J.P.;  
 RT "Purification of a cathepsin L-like proteinase secreted by adult  
 RT Fasciola hepatica.";  
 RL Mol. Biochem. Parasitol. 62:1-8(1993).  
 CC -!- FUNCTION: THIOL PROTEASE THAT ASSISTS THE PARASITE IN BURROWING  
 CC THROUGH THE GUT WALL AND LIVER OF ITS MAMMALIAN HOST.  
 CC -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As  
 CC compared to cathepsin B, cathepsin L exhibits higher activity  
 CC towards protein substrates, but has little activity on Z-Arg-Arg-  
 CC NHMeC, and no peptidyl-diesterase activity.  
 CC -!- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE  
 CC BONDS.  
 CC -!- SUBCELLULAR LOCATION: Lysosomal.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.

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DR PIR; S68785; S68785.
DR MEROPS; COL033; -.
DR InterPro; IPR000668; Peptidase C1.
DR InterPro; IPR000169; SHProt acsite.
DR Pfam; PF00112; Peptidase C1; 1.
DR PROSITE; PS00139; THIOLESTERASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOLESTERASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOLESTERASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease; Lysosome.
FT NON TER 20
SQ SEQUENCE 20 AA; 2174 MW; 97CDEDB33055BCAE CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 1 AVP 3

RESULT 50
CD4 SHEEP STANDARD; PRT; 20 AA.
AC P05542;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD4 (T-cell surface antigen T4/Leu-3)
DE (Fragment).
GN CD4.

Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]_TaxID=9940;
RP SEQUENCE.
RX MEDLINE=86166694; PubMed=3082751;
RA Claesson B.J., Tsagaratos J., Kirsbaum L., Maddox J., McKay C.R.,
RA Brandon M., McKenzie I.F.C., Walker I.D.;
RT "The L3T4 antigen in mouse and the sheep equivalent are
RT immunoglobulin-like."
RL Immunogenetics 23:129-132(1986).
CC -!- FUNCTION: ACCESSORY PROTEIN FOR MHC CLASS-II ANTIGEN/T-CELL
CC RECEPTOR INTERACTION. MAY REGULATE T-CELL ACTIVATION.
CC -!- SUBUNIT: ASSOCIATES WITH P56-LCK (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
DR PIR; B47642; B47642.
DR GO; GO:0042101; C-T-cell receptor complex; ISS.
DR GO; GO:0015026; F:coreceptor activity; ISS.
DR GO; GO:0042289; F:MHC class II protein binding activity; ISS.
DR GO; GO:0006955; P:immune response; ISS.
DR GO; GO:0045086; P:positive regulation of interleukin-2 biosyn. . .; ISS.
DR GO; GO:0030217; P:T-cell differentiation; ISS.
DR GO; GO:0045058; P:T-cell selection; ISS.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; ISS.
KW Immunoglobulin domain; T-cell; Immune response.
FT NON TER 20
SQ SEQUENCE 20 AA; 1928 MW; 421F09570FEA97EE CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
DB 1 KAV 3

RESULT 51
FIBB ELEMA STANDARD; PRT; 20 AA.
ID FIBB_ELEMA

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AC P14538;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]_TaxID=9783;
RP SEQUENCE.
RA O'Neill P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma; Sulfation.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT MOD RES 4 4 SULFATION.
FT NON TER 20
SQ SEQUENCE 20 AA; 2107 MW; B4F52B959933273 CRC64;

Query Match 13.6%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVP 15
DB 12 AVP 14

RESULT 52
H2B1 ICTPU STANDARD; PRT; 20 AA.
ID H2B1 ICTPU
AC F81903;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B-1 (Antibacterial histone-like protein 1) (HLP-1)
DE (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]_TaxID=7998;
RP SEQUENCE, AND FUNCTION.
RP TISSUE=Skin;
RX MEDLINE=98309109; PubMed=9645227;
RA Robinette D., Wada S., Arroll T., Levy M.G., Miller W.L., Noga E.J.;
RT "Antimicrobial activity in the skin of the channel catfish Ictalurus
RT punctatus: characterization of broad-spectrum histone-like
RT antimicrobial proteins."
RL Cell. Mol. Life Sci. 54:467-475(1998).
CC -!- FUNCTION: Has broad-spectrum antimicrobial and antibacterial
CC activity. It is important in the antimicrobial defenses of fish
CC skin and possesses strong activity against saprolegnia, the most
CC common fungal infection in fish. It is also inhibitory to fish
CC bacterial pathogens, such as aeromonas hydrophila, vibrio
CC alginolyticus and E.coli D31.
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC BP of DNA.

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CC -!- SUBCELLULAR LOCATION: Nuclear.  
 CC -!- MASS SPECTROMETRY: MW=13459; METHOD=WALDI.  
 CC -!- SIMILARITY: Belongs to the histone H2B family.  
 DR InterPro; IPR000558; Histone\_H2B.  
 DR PROSITE; PS00357; HISTONE\_H2B; PARTIAL.  
 KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;  
 KW Antibiotic; Fungicide.  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2033 MW; C13E4A04FB8D966F CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 KAV 14  
 DB 14 KAV 16  
 RESULT 53  
 OAR\_PROPHY STANDARD; PRT; 20 AA.  
 AC P14803;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-JUL-1993 (Rel. 26, Last annotation update)  
 DE Octopamine receptor (Octopamine binding protein) (Fragment).  
 OS Phocinus pyralis (North American firefly).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Coleoptera; Polyphaga; Elateriformia;  
 CC Cantharoidea; Lampyridae; Photinus.  
 OX NCBI\_TaxID=7054;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Light organ;  
 RX MEDLINE=90092510; PubMed=2513233;  
 RA Nathanson J.A., Kantham L., Hunnicutt E.J.;  
 RT "Isolation and N-terminal amino acid sequence of an octopamine ligand  
 RT binding protein.";  
 RL FEBS Lett. 259:117-120 (1989).  
 CC -!- FUNCTION: PUTATIVE RECEPTOR FOR OCTOPAMINE. OCTOPAMINE (OA) IS A  
 CC NEUROTRANSMITTER, NEUROHORMONE, AND NEUROMODULATOR IN  
 CC INVERTEBRATES. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G  
 CC PROTEINS WHICH ACTIVATE ADENYL CYCLASE.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 DR PIR; S28779; S28779.  
 DR InterPro; IPR00276; GPCR\_Rhodpsn.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; PARTIAL.  
 KW G-protein coupled receptor.  
 FT UNSURE 2 2  
 FT UNSURE 9 9  
 FT UNSURE 19 19  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2500 MW; ACBC81A11BB8D4AB CRC64;  
 Query Match 13.6%; Score 3; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LSQ 3  
 DB 5 LSQ 7  
 RESULT 54  
 DCMS\_PSECH STANDARD; PRT; 4 AA.  
 AC P19918;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO

DE dehydrogenase subunit S) (CO-DH S) (Fragment).  
 GN CUS.  
 OS Pseudomonas carboxydohydrogena.  
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 CC Bradyrhizobiaceae.  
 OX NCBI\_TaxID=290;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90055678; PubMed=2818128;  
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;  
 RT "Homology and distribution of CO dehydrogenase structural genes in  
 RT carboxydohydrogenic bacteria.";  
 RL Arch. Microbiol. 152:335-341 (1989).  
 CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
 CC dioxide.  
 CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced  
 CC acceptor.  
 CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.  
 CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND  
 CC SMALL.  
 DR PIR; P10146; P10146.  
 KW Oxidoreductase; Metal-binding; Iron-sulfur; Iron; 2Fe-2S.  
 FT NON TER 4 4  
 SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;  
 Query Match 9.1%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 KA 13  
 DB 3 KA 4  
 RESULT 55  
 FFKA\_ANTEL STANDARD; PRT; 4 AA.  
 ID FFKA\_ANTEL  
 AC P58705;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antho-Kaamide.  
 OS Anthopleura elegantissima (Sea anemone).  
 CC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 CC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92028852; PubMed=1681803;  
 RA Nothacker H.-P., Rinehart K.L., Jr., Grimmelikhuijzen C.J.P.;  
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kaamide), a  
 RT novel neuropeptide from sea anemones.";  
 RL Biochem. Biophys. Res. Commun. 179:1205-1211 (1991).  
 RN [2]  
 RP FUNCTION.  
 RX MEDLINE=93391436; PubMed=8397415;  
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
 RT "The expansion behaviour of sea anemones may be coordinated by two  
 RT inhibitory neuropeptides, Antho-Kaamide and Antho-Riamide.";  
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188 (1993).  
 CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
 CC groups. May be involved in the expansion phase of feeding  
 CC behaviour in sea anemones.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron-specific.  
 DR PIR; JQ1273; JQ1273.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 1 1  
 FT MOD RES 4 4  
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;  
 Query Match 9.1%; Score 2; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KA 13  
||  
Db 3 KA 4

RESULT 56  
BPP7 BOTIN  
ID BPP7 BOTIN STANDARD; PRT; 5 AA.  
AC P30425;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting  
enzyme inhibitor).  
OS Bothrops insularis (Island jararaca) (Queimada jararaca).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
NCBI\_TaxID=8723;  
[1]  
RN  
RP  
SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990).  
CC  
CC -1- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
DR PIR; G37196; G37196.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QK 12  
||  
Db 1 QK 2

RESULT 57  
PRCT\_PREAM  
ID PRCT\_PREAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.  
OS Periplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
NCBI\_TaxID=6978, 6850, 6759;  
[1]  
RN  
RP  
SEQUENCE.  
RC SPECIES=P. americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Starratt A.N., Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
in insects.";  
RL Life Sci. 17:1253-1256(1975).  
[2]  
RN  
RP  
BIOLOGICAL SOURCE.  
RC SPECIES=P. americana;

RX MEDLINE=81225865; PubMed=6113690;  
RA O'Shea M., Adams M.E.;  
RT "Pentapeptide (proctolin) associated with an identified neuron.";  
RL Science 213:567-569(1981).  
[3]  
RN  
RP  
SEQUENCE.  
RC SPECIES=L.polyphemus;  
RX MEDLINE=90287800; PubMed=236151;  
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
RA Shabanowitz J.;  
RT "Identification of proctolin in the central nervous system of the  
horseshoe crab, Limulus polyphemus.";  
RL Peptides 11:205-211(1990).  
[4]  
RN  
RP  
SEQUENCE.  
RC SPECIES=C.maenas;  
RX MEDLINE=86232789; PubMed=2872661;  
RA Stangler J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
pericardial organs of the shore crab, Carcinus maenas.";  
RL Peptides 7:67-72(1986).  
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
THE CRAB PERICARDIAL ORGANS.  
DR PIR; A01644; HOROHA.  
DR PIR; A60411; A60411.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LP 8  
||  
Db 3 LP 4

RESULT 58  
ACPH\_RABIT  
ID ACPH\_RABIT STANDARD; PRT; 6 AA.  
AC P25154;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase)  
DE (APH) (Acylaminoacyl-peptidase) (Fragment).  
GN APEH.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
NCBI\_TaxID=9986;  
[1]  
RN  
RP  
SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=92222120; PubMed=1807161;  
RA Krishna R.G., Chin C.C.Q., Wold F.;  
RT "N-terminal sequence analysis of N alpha-acetylated proteins after  
unblocking with N-acylaminoacyl-peptide hydrolase.";  
RL Anal. Biochem. 199:45-50(1991).  
CC  
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-  
TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE  
AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.  
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.  
CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
+ peptide.  
CC  
CC -1- SUBUNIT: Homotrimer.  
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.  
DR PIR; A49792; A49792.  
DR MEROPS; S09.004; -;  
DR InterPro; IPR002471; Prol\_endopep\_ser.

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DR PROSITE; PS00708; PRO ENDOPEP_SER; PARTIAL.
KW Hydrolase; Acetylation.
FT MOD_RES 1 ACETYLATION.
FT NON_TER 6
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VL 7
Db 5 VL 6

RESULT 59
EI01 LITRU
ID EI01 LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUPCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VP 10
Db 2 VP 3

RESULT 60
TRPI PSEPU
ID TRPI PSEPU STANDARD; PRT; 6 AA.
AC P36414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TrpA operon transcriptional activator (Fragment).
GN TRPI.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPG1 C18;
RX MEDLINE=89335826; PubMed=2503057;
RT Eberly L., Crawford I.P.;
RT "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT putida.";
RL Biochimie 71:521-531(1999).
CC -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING

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CC THE TWO TRYPTOPHAN SYNTHASE SUBUNITS, IN THE ABSENCE OF THE
CC INDUCER (INDOLEGLYCEROL PHOSPHATE), TRP1 BINDS UPSTREAM OF THE
CC TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC -!- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13299; CAA31660.1; -.
DR InterPro; IPR000847; HTH_LysR.
DR PROSITE; PS00044; HTH_LYSR FAMILY; PARTIAL.
KW Tryptophan biosynthesis; Transcription regulation; Activator;
KW DNA-binding.
FT NON_TER 6
SQ SEQUENCE 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LP 8
Db 5 LP 6

RESULT 61
CARP MYTED
ID CARP MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987)
CC -!- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)
CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RETRACTOR MUSCLE.
DR PIR; A29342; ECMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 MP 20
Db 2 MP 3

RESULT 62
LANC CARUI
ID LANC CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lantibiotic carnocin UI49 (Fragment).  
 OS Carnobacterium sp. (strain UI49).  
 OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
 OC Carnobacterium  
 OX NCBI\_TaxID=35782;  
 RN [1]  
 RN SEQUENCE.  
 RP MEDLINE=92321768; PubMed=1622206;  
 RX Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
 RA Nes I.F.;  
 RT "Purification and characterization of a new bacteriocin isolated from  
 RT a Carnobacterium sp.";  
 RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
 CC -1- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
 CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
 KW Antibiotic; Bacteriocin; Lantibiotic.  
 FT NON\_TER 7  
 FT SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;  
 SQ  
 Query Match 9.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 QP 4  
 DB 5 QP 6  
 RESULT 63  
 TPFY\_PACDA  
 ID TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyllin-1 (PdT-1).  
 OS Pachymedusa dactinolor (Giant Mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=15988;  
 RN [1]  
 RN SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RP TISSUE=Skin secretion;  
 RC Chen T.B., Orr D.F., Shaw C.;  
 RA "Pachymedusa dactinolor tryptophyllin-1 (PdT-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA";  
 RL Submitted (SEP-2002) to the SWISS-PROT data bank.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.  
 KW Amphibian defense peptide; Amidation; Hydroxylation.  
 FT MOD\_RES 3 7  
 FT SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;  
 SQ  
 Query Match 9.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VP 10  
 DB 6 VP 7  
 RESULT 64  
 AL12\_CARMA  
 ID AL12\_CARMA STANDARD; PRT; 8 AA.  
 AC P81815;

UF04\_MOUSE  
 ID UF04\_MOUSE STANDARD; PRT; 7 AA.  
 AC P38642;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-FEB-1995 (Rel. 31, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Fibroblast;  
 RC MEDLINE=9500907; PubMed=7523108;  
 RX Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RA "Separation and sequencing of familial and novel murine proteins  
 RT using preparative two-dimensional gel electrophoresis";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.  
 FT NON\_TER 7  
 FT SEQUENCE 7 AA; 766 MW; 68640AB77632700 CRC64;  
 SQ  
 Query Match 9.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 PK 5  
 DB 1 PK 2  
 RESULT 65  
 UN06\_PINPS  
 ID UN06\_PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime pine)  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RN SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 FT SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;  
 SQ  
 Query Match 9.1%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LP 8  
 DB 5 LP 6  
 RESULT 66  
 AL12\_CARMA  
 ID AL12\_CARMA STANDARD; PRT; 8 AA.  
 AC P81815;



DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 12.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas";  
EL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
SQ SEQUENCE 8 AA; 913 MW; 672879DCDB569AB7 CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 18 DM 19  
Db 2 DM 3  
RESULT 67  
AL18 CARMA STANDARD; PRT; 8 AA.  
AC P81821;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 18.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas";  
EL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 919 MW; C82879DSAB569AB5 CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 18 DM 19  
Db 2 DM 3  
RESULT 68  
ALL6\_CVDPO STANDARD; PRT; 8 AA.  
ID ALL6\_CVDPO  
AC P82157;  
DE Sex pheromone CAD1.  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAD1.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
EL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 7 LP 8  
Db 1 LP 2  
RESULT 69  
B44K\_PORGI STANDARD; PRT; 8 AA.  
AC P81836;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE 44 kDa immunogenic protein (Fragment).  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteri; Bacteroidetes; Bacteroides (class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE.  
RC STEAIN=VPB 3492;  
RX MEDLINE=20198497; PubMed=10731616;  
RA Norris J.M., Love D.N.;  
RT "Serum antibody responses of cats to soluble whole cell antigens of  
RT feline Porphyromonas gingivalis";  
RL Vet. Microbiol. 73:37-49(2000).  
CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.  
KW Antigen.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 QK 12  
Db 4 QK 5  
RESULT 70  
CAD1\_ENTFA STANDARD; PRT; 8 AA.  
ID CAD1\_ENTFA  
AC P13258;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAD1.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
EL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 QK 12  
Db 4 QK 5  
RESULT 70  
CAD1\_ENTFA STANDARD; PRT; 8 AA.  
ID CAD1\_ENTFA  
AC P13258;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAD1.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
EL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8  
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
Query Match 9.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 QK 12  
Db 4 QK 5  
RESULT 70  
CAD1\_ENTFA STANDARD; PRT; 8 AA.  
ID CAD1\_ENTFA  
AC P13258;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAD1.  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 6.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily";  
EL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLAT

OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=8501889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, cAD1, that  
 RT induces plasmid transfer in Streptococcus faecalis.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC -1- FUNCTION: cAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PADI.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VL 7  
 Db ||  
 3 VL 6

RESULT 71  
 CLP\_THICU STANDARD; PRT; 8 AA.  
 AC P80488;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE Chemolithotroph-specific protein (Fragment).  
 OS Thiobacillus cuprinus.  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Comenadaceae; Thiomonas.  
 OX NCBI\_TaxID=36860;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=DSM 5494;  
 RA Marin I., Amaro A.M., Jerez C.A., Amils R., Abad J.P.;  
 RL Submitted (SEP-1995) to the SWISS-PROT data bank.  
 CC -1- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED  
 CC NON TER 8  
 FT SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 PV 9  
 Db ||  
 2 PV 3

RESULT 72  
 COW2\_CONPU STANDARD; PRT; 8 AA.  
 AC P58785;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Leu-contryphan-P.  
 OS Conus purpurascens (Purple cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=41690;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC STRAIN=Ciidderton Island; TISSUE=Venom;  
 RX MEDLINE=99388839; PubMed=10461743;

RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
 RA Olivera B.M.;  
 RT "A novel D-leucine-containing Conus peptide: diverse conformational  
 RT dynamics in the contryphan family.";  
 RL J. Pept. Res. 54:93-99(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.  
 CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.  
 KW Toxin; Hydroxylation; D-amino acid.  
 RL DISULFID 2 8  
 FT MOD\_RES 4 4 D-LEUCINE.  
 SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 VL 7  
 Db ||  
 3 VL 4

RESULT 73  
 CPDI\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13269;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CPD1.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=85040388; PubMed=6436978;  
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B.;  
 RT "Isolation and structure of bacterial sex pheromone, cPD1.";  
 RL Science 226:849-850(1984).  
 CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC BACTERIOCIN PLASMID PPDI.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 913 MW; 8655B729C682C729 CRC64;

Query Match 9.1%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LS 2  
 Db ||  
 6 LS 7

RESULT 74  
 FUSO\_FUSSO STANDARD; PRT; 8 AA.  
 AC P81010;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Allergen Fus s I3596\* (Fragment).  
 OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=70751;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=IARI 3596; TISSUE=Mycelium;  
 RA Verma J., Gengal S.V.;  
 RL Submitted (JUL-1997) to the SWISS-PROT data bank.  
 KW Allergen.

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FT  NON TER      8      8      C372C441F5B69041 CRC64;
SQ  SEQUENCE    8 AA;  898 MW;
Query Match      9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VP 10
      ||
Db      7 VP 8

RESULT 75
PK3 PERAM
ID  PPK3 PERAM  STANDARD;  PRT;  8 AA.
AC  P82618;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
OS  Periplaneta americana (American cockroach).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC  Blattidae; Periplaneta.
OX  NCBI_TaxID=6978;
RN  [1]
RN  [1]
RP  SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC  TISSUE=Retrocerebral complex;
RX  MEDLINE=99212469; PubMed=10196736;
RA  Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT  "Differential distribution of pyrokinin-isoforms in cerebral and
RT  abdominal neurohemal organs of the American cockroach.";
RL  Insect Biochem. Mol. Biol. 29:139-144 (1999).
RN  [2]
RP  TISSUE SPECIFICITY.
RX  MEDLINE=20189894; PubMed=10723010;
RA  Predel R., Eckert M.;
RT  "Tagma-specific distribution of FXPRLamides in the nervous system of
RT  the American cockroach.";
RL  J. Comp. Neurol. 419:352-363 (2000).
CC  -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC  (MYOTROPIC ACTIVITY).
CC  -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
CC  -!- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
CC  -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
KW  Neuropeptide; Amidation; Pyrokinin.
FT  MOD RES      8
SQ  SEQUENCE    8 AA;  997 MW;  0B34177409D772C7 CRC64;

Query Match      9.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 VP 10
      ||
Db      2 VP 3

Search completed: November 25, 2003, 19:28:24
Job time : 7.87375 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 25, 2003, 18:25:50 ; Search time 41.314 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-27  
Perfect score: 22  
Sequence: 1 LSQPKVLPQKAVPQRDMPIQ 22

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3  
Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SPTREMBL 23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacterioph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	22.7	20	5 Q9TWX2	Q9twx2 physarum po
2	4	18.2	11	6 Q9TQSO	Q9tqso bos taurus
3	4	18.2	12	6 Q8WNW9	Q8wnw9 ovis aries
4	4	18.2	17	12 Q65373	Q65373 orgyia pseu
5	4	18.2	18	4 Q16173	Q16173 homo sapien
6	4	18.2	18	6 Q9SMB1	Q9smb1 equus caball
7	4	18.2	19	12 Q11338	Q11338 molluscum c
8	4	18.2	19	13 Q9PRT0	Q9prt0 gallus gall
9	4	18.2	20	2 Q8KUI9	Q8kui9 neisseria m
10	4	18.2	20	5 Q9TWP4	Q9twp4 physarum po
11	4	18.2	20	15 Q9INA9	Q9ina9 human immun
12	3	13.6	7	2 Q50556	Q50556 actinobacil
13	3	13.6	8	2 Q45615	Q45615 bacillus su
14	3	13.6	8	2 Q56759	Q56759 xanthobacte
15	3	13.6	8	4 Q9UHK1	Q9uhk1 homo sapien
16	3	13.6	8	6 Q9TRX8	Q9trx8 bos taurus

17	3	13.6	9	2 P72345	P72345 pseudomonas
18	3	13.6	9	2 P82568	P82568 streptococc
19	3	13.6	9	3 Q9P8ES	Q9p8es kluyveromyc
20	3	13.6	9	12 Q84333	Q84333 simian viru
21	3	13.6	9	15 Q64972	Q64972 avian rous-
22	3	13.6	10	2 Q9R5N2	Q9r5n2 clostridium
23	3	13.6	10	2 Q9R5N1	Q9r5n1 clostridium
24	3	13.6	10	2 Q9R5N3	Q9r5n3 clostridium
25	3	13.6	10	5 Q26093	Q26093 pisaster oc
26	3	13.6	10	5 P82223	P82223 bombyx mori
27	3	13.6	10	8 P82224	P82224 bombyx mori
28	3	13.6	10	8 Q8WBR7	Q8wbr7 chaetophoru
29	3	13.6	10	8 Q9SDS3	Q9sds3 magnolia me
30	3	13.6	10	11 Q9JLI5	Q9jli5 mus musculu
31	3	13.6	10	11 Q9ESU5	Q9esu5 mus musculu
32	3	13.6	10	11 Q8CJEO	Q8cjeo rattus norv
33	3	13.6	10	12 Q39957	Q39957 hepatitis g
34	3	13.6	10	13 Q9TWX9	Q9twx9 eptaretus
35	3	13.6	10	13 Q8JFE7	Q8jfe7 ficedula al
36	3	13.6	10	13 Q8JF33	Q8jf33 ficedula hy
37	3	13.6	11	2 Q9EUZ3	Q9euz3 escherichia
38	3	13.6	11	12 Q86864	Q86864 lymphocytic
39	3	13.6	12	2 Q312U8	Q312u8 acinetobact
40	3	13.6	12	2 Q52112	Q52112 acinetobact
41	3	13.6	12	2 Q8GMV1	Q8gmv1 acinetobact
42	3	13.6	12	2 Q8GMT8	Q8gmt8 acinetobact
43	3	13.6	12	2 Q8GML2	Q8gml2 acinetobact
44	3	13.6	12	2 Q8GBY8	Q8gby8 planktothri
45	3	13.6	12	4 Q9H4F4	Q9h4f4 homo sapien
46	3	13.6	12	4 Q9CP98	Q9cp98 homo sapien
47	3	13.6	12	8 Q31851	Q31851 arabidopsis
48	3	13.6	12	10 Q8SAS2	Q8sas2 pinus sylve
49	3	13.6	12	10 Q8SAS3	Q8sas3 pinus sylve
50	3	13.6	12	10 P82441	P82441 nicotiana t
51	3	13.6	12	12 Q83139	Q83139 barley stri
52	3	13.6	12	13 Q902L3	Q902l3 xenopus lae
53	3	13.6	13	2 Q312S5	Q312s5 buchnera ap
54	3	13.6	13	6 Q8WNS4	Q8wns4 bos taurus
55	3	13.6	13	8 Q9THS0	Q9ths0 bryopsis sp
56	3	13.6	13	11 Q88176	Q88176 mus musculu
57	3	13.6	13	11 Q9QVK6	Q9qv6 rattus sp.
58	3	13.6	13	12 Q81761	Q81761 hepatitis c
59	3	13.6	13	12 Q81794	Q81794 hepatitis c
60	3	13.6	13	12 Q81784	Q81784 hepatitis c
61	3	13.6	13	12 Q81778	Q81778 hepatitis c
62	3	13.6	13	12 Q81787	Q81787 hepatitis c
63	3	13.6	13	12 Q81775	Q81775 hepatitis c
64	3	13.6	13	12 Q81767	Q81767 hepatitis c
65	3	13.6	13	12 Q81798	Q81798 hepatitis c
66	3	13.6	13	12 Q81774	Q81774 hepatitis c
67	3	13.6	13	12 Q81766	Q81766 hepatitis c
68	3	13.6	13	12 Q81793	Q81793 hepatitis c
69	3	13.6	13	12 Q81768	Q81768 hepatitis c
70	3	13.6	13	12 Q81785	Q81785 hepatitis c
71	3	13.6	13	12 Q81800	Q81800 hepatitis c
72	3	13.6	13	12 Q81765	Q81765 hepatitis c
73	3	13.6	13	12 Q81781	Q81781 hepatitis c
74	3	13.6	13	12 Q81769	Q81769 hepatitis c
75	3	13.6	13	12 Q81773	Q81773 hepatitis c
76	3	13.6	13	12 Q81799	Q81799 hepatitis c
77	3	13.6	13	12 Q9WNG5	Q9wng5 sigma virus
78	3	13.6	13	12 Q81786	Q81786 hepatitis c
79	3	13.6	13	12 Q81788	Q81788 hepatitis c
80	3	13.6	13	12 Q81763	Q81763 hepatitis c
81	3	13.6	13	12 Q81764	Q81764 hepatitis c
82	3	13.6	13	12 Q81796	Q81796 hepatitis c
83	3	13.6	13	12 Q81791	Q81791 hepatitis c
84	3	13.6	13	12 Q81770	Q81770 hepatitis c
85	3	13.6	13	12 Q81762	Q81762 hepatitis c
86	3	13.6	13	12 Q81790	Q81790 hepatitis c
87	3	13.6	13	12 Q81783	Q81783 hepatitis c
88	3	13.6	13	12 Q81789	Q81789 hepatitis c
89	3	13.6	13	12 Q81797	Q81797 hepatitis c

90 Q81795 hepatitis c  
 91 Q81782 hepatitis c  
 92 Q81780 hepatitis c  
 93 Q81771 hepatitis c  
 94 Q81779 hepatitis c  
 95 Q81772 hepatitis c  
 96 Q81792 hepatitis c  
 97 Q81777 hepatitis c  
 98 P82882 rana clamit  
 99 P82883 rana clamit  
 100 P82884 rana clamit

## ALIGNMENTS

RESULT 1  
 Q9TWX2 ID Q9TWX2 PRELIMINARY; PRT; 20 AA.  
 AC Q9TWX2  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Vitronectin-like protein (Fragment).  
 OS Physarum polycephalum (Slime mold).  
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
 OC Physarum.  
 OX NCBI\_TaxID=5791;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92137326; PubMed=1370938;  
 RA Miyazaki K., Hamano T., Hayashi M.;  
 RT "Physarum vitronectin-like protein: an Arg-Gly-Asp-dependent cell-  
 spreading protein with a distinct NH2-terminal sequence.";  
 RL Exp. Cell Res. 199;106-110(1992).  
 FT NON TER 1 1  
 FT NON TER 20 20  
 SQ SEQUENCE 20 AA; 2173 MW; 7DA5DAC504E7177F CRC64;

Query Match 22.7%; Score 5; DB 5; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQK 12  
 DB 4 PVPQK 8

RESULT 2  
 Q9TQSO ID Q9TQSO PRELIMINARY; PRT; 11 AA.  
 AC Q9TQSO  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE C-KIT (Fragment).  
 GN KIT.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;  
 RT "A polymorphism in the bovine c-kit gene.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ243424; CAB60775.1; -.  
 DR EMBL; AJ243060; CAB60774.1; -.  
 FT NON TER 1 1  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVP 15  
 DB 2 KAVP 5

RESULT 3  
 Q8WNW9 ID Q8WNW9 PRELIMINARY; PRT; 12 AA.  
 AC Q8WNW9  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Estrogen receptor alpha (Fragment).  
 GN ER.  
 OS Ovis aries (Sheep).  
 OC Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Endometrium;  
 RA Ing N.H.;  
 RT "Estradiol Stabilizes Estrogen Receptor mRNA in Ovine Endometrium Via  
 Discrete Sequence Elements in its 4000 Base Long 3'Untranslated  
 Region." (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY059388; AAL31379.1; -.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1301 MW; 419C0B96EA21A1E7 CRC64;

Query Match 18.2%; Score 4; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVP 15  
 DB 8 KAVP 11

RESULT 4  
 Q65373 ID Q65373 PRELIMINARY; PRT; 17 AA.  
 AC Q65373  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
 DE ORF 2 minigene.  
 OS Orgyia pseudotsugata single capsid nuclear polyhedrosis virus  
 OS (OpSNPV).  
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;  
 OC Nucleopolyhedrovirus.  
 OX NCBI\_TaxID=10450;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93286576; PubMed=8389803;  
 RA Russell R.L., Rohrmann G.F.;  
 RT "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyia  
 pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome.";  
 RL J. Gen. Virol. 74;1191-1195(1993).  
 DR EMBL; D13375; BAA02640.1; -.  
 SQ SEQUENCE 17 AA; 1882 MW; BFEC2A959495FE6A CRC64;

Query Match 18.2%; Score 4; DB 12; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9

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Db          2 VLPV 5
|||||
PRT;      18 AA.
RESULT 5
Q16173
ID Q16173      PRELIMINARY;      PRT;      18 AA.
AC Q16173;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94258162; PubMed=8199594;
RA Wilton S.D., Chandler D.C., Kakulas B.A., Laing N.G.;
RT "Identification of a point mutation and germinal mosaicism in a
RT Duchenne muscular dystrophy family.";
RL Hum. Mutat. 3:133-140(1994).
DR EMBL; S71486; AAD14085.1; -.
FT NON TER 1
SQ SEQUENCE 18 AA; 2159 MW; C33D41084760ED6E CRC64;

Query Match      18.2%; Score 4; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          11 QKAV 14
|||||
PRT;      18 AA.
RESULT 6
Q95MB1
ID Q95MB1      PRELIMINARY;      PRT;      18 AA.
AC Q95MB1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Desmocollin 2 (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21314992; PubMed=11421942;
RA Shubitowski D.M., Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.;
RT "Polymorphism identification within 50 equine gene-specific sequence
RT tagged sites.";
RL Anim. Genet. 32:78-78(2001).
DR EMBL; AY08781; AAG39473.1; -.
FT NON TER 1
SQ SEQUENCE 18 AA; 1992 MW; B67FE953ECF19196 CRC64;

Query Match      18.2%; Score 4; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          3 QPKV 6
|||||
PRT;      19 AA.
RESULT 7
O11338
ID O11338      PRELIMINARY;      PRT;      19 AA.
AC O11338;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE H1-7-1 protein (Fragment).
GN H1-7-1.
OS Molluscum contagiosum virus subtype 1 (MCV1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Molluscipoxvirus.
OX NCBI_TaxID=10280;
RN [1]
RP SEQUENCE FROM N.A.
RA Moratilla M., Agromayor M., Nunez A., Funes J.M., Varas A.J.,
RA Lopez-Esteban J.L., Esteban M., Martin-Gallardo A.;
RT "A Random DNA Sequencing, Computer-Based Approach for the Generation
RT of a Gene Map of Molluscum Contagiosum Virus.";
RL Virus Genes 0:0-0(1997).
DR EMBL; U86916; AAB57971.1; -.
DR InterPro; IPR004900; Pox_P35.
DR Pfam; PF03213; Pox_P35; 1.
FT NON TER 19
SQ SEQUENCE 19 AA; 2018 MW; 1ECAF8E98F95ED65 CRC64;

Query Match      18.2%; Score 4; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 VLPV 9
|||||
PRT;      19 AA.
RESULT 8
Q9PRT0
ID Q9PRT0      PRELIMINARY;      PRT;      19 AA.
AC Q9PRT0;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE 23A7 antigen (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=95332492; PubMed=7608337;
RA Denburg J.L., Caldwell R.T., Marner J.M.;
RT "Developmental changes in epitope accessibility as an indicator of
RT multiple states of an immunoglobulin-like neural cell adhesion
RT molecule.";
RL J. Comp. Neurol. 354:533-550(1995).
SQ SEQUENCE 19 AA; 2051 MW; 83E67BEE484EBD03 CRC64;

Query Match      18.2%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 LSQP 4
|||||
PRT;      20 AA.
RESULT 9
Q8KUI9
ID Q8KUI9      PRELIMINARY;      PRT;      20 AA.
AC Q8KUI9;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nitrogen regulatory protein P-II (Fragment).
OS Neisseria meningitidis.

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OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OC Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=C11;  
 RC MEDLINE=22040572; PubMed=12045242;  
 RA Comanducci M., Bambini S., Brunelli B., Adu-Bobie J., Arico B.,  
 RA Capecechi B., Giuliani M.M., Massignani V., Santini L., Savino S.,  
 RA Granoff D.M., Caugant D.A., Pizzo M., Rappuoli R., Mora M.;  
 RT "Nada, a novel vaccine candidate of Neisseria meningitidis";  
 RL J. Exp. Med. 195;1445-1454(2002).  
 DR EMBL: AF452480; AM53107.1;  
 DR InterPro; IPR002187; PII\_glnB.  
 DR Pfam; PF00543; P-II; 1.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2165 MW; 5CE529B59D995B5C CRC64;

Query Match 18.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
 Db 1 VLPV 4

## RESULT 10

Q9TWP4 PRELIMINARY; PRT; 20 AA.  
 ID Q9TWP4  
 AC Q9TWP4  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Vitronectin homolog (Fragment).  
 OS Physarum polycephalum (Slime mold).  
 OC Eukaryota; Mycetozoa; Myxogastria; Myxogastromycetidae; Physarida;  
 OC Physarum.  
 OX NCBI\_TaxID=5791;  
 [1]  
 RN SEQUENCE.  
 RP MEDLINE=94221676; PubMed=8168157;  
 RA Miyazaki K., Miyata T., Sawada H., Matuda S., Hayashi M.;  
 RT "Physarum vitronectin-like protein has extensive homology to  
 RT dihydrolipamide acetyltransferase";  
 RL Cell Struct. Funct. 18:323-331(1993).  
 SQ SEQUENCE 20 AA; 2116 MW; EDB10130972831EA CRC64;

Query Match 18.2%; Score 4; DB 5; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPQ 16  
 Db 1 AVPQ 4

## RESULT 11

Q9INA9 PRELIMINARY; PRT; 20 AA.  
 ID Q9INA9  
 AC Q9INA9  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag protein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=DRCM23;  
 RC MEDLINE=39260287; PubMed=10331444;  
 RX

RA Mokili J.L., Wade C.M., Burns S.M., Cutting W.A., Bopopi J.M.,  
 RA Green S.D., Peutherer J.F., Simmonds P.;  
 RT "Genetic heterogeneity of HIV type 1 subtypes in Kimpese, rural  
 RT Democratic Republic of Congo";  
 RL AIDS Res. Hum. Retroviruses 15:655-664(1999).  
 DR EMBL: AF144840; AAF69066.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2271 MW; B39B8CB9B53ABCF8 CRC64;

Query Match 18.2%; Score 4; DB 15; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QKAV 14  
 Db 15 QKAV 18

## RESULT 12

O50556 PRELIMINARY; PRT; 7 AA.  
 ID O50556  
 AC O50556  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE GlyA (Fragment).  
 GN GLYA.  
 OS Actinobacillus actinomycetemcomitans (Haemophilus  
 OS actinomycetemcomitans).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OX NCBI\_TaxID=714;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=ATCC 33384;  
 RC MEDLINE=96355846; PubMed=8751884;  
 RA Kolodrubetz D., Spitznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
 RA Kraig E.;  
 RT "cis Elements and trans factors are both important in strain-specific  
 RT regulation of the leukotoxin gene in Actinobacillus  
 RT actinomycetemcomitans";  
 RL Infect. Immun. 64:3451-3460(1996).  
 DR EMBL: U51862; AAB88721.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db 3 LPV 5

## RESULT 13

Q45615 PRELIMINARY; PRT; 8 AA.  
 ID Q45615  
 AC Q45615  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE GutB protein (Fragment).  
 GN GUTB.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=168;  
 RC MEDLINE=94253000; PubMed=8195086;  
 RX Ye R., Wong S.L.;  
 RA "Transcriptional regulation of the Bacillus subtilis glucitol  
 RT

RT dehydrogenase gene.";  
 RL J. Bacteriol. 176:3314-3320(1994).  
 DR EMBL; L16626; AAA20875.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;  
 Query Match 13.6%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VPO 11  
 Db |||  
 5 VPO 7  
 RESULT 14  
 Q56759 PRELIMINARY; PRT; 8 AA.  
 ID Q56759;  
 AC Q56759;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Haloacid dehalogenase (Fragment).  
 GN DHLB.  
 OS Xanthobacter autotrophicus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
 OC Hyphomicrobiaceae; Xanthobacter.  
 OX NCBI\_TaxID=280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=GJ10, and CV. M50;  
 RX MEDLINE=95173113; PubMed=7868610;  
 RA Van der Ploeg J., Willemse M., van Hall G., Janssen D.B.;  
 RT "Adaptation of Xanthobacter autotrophicus GJ10 to bronacetate due to  
 RT activation and mobilization of the haloacetate dehalogenase gene by  
 RT insertion element IS1247.";  
 RL J. Bacteriol. 177:1348-1356(1995).  
 DR EMBL; X84038; CAA58857.1; -.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CRC64;  
 Query Match 13.6%; Score 3; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 KAV 14  
 Db |||  
 3 KAV 5  
 RESULT 15  
 Q9UHK1 PRELIMINARY; PRT; 8 AA.  
 ID Q9UHK1  
 AC Q9UHK1;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Alpha-1-antitrypsin M-variant (Fragment).  
 GN A1A.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC Ambrose H.J., Chambers S., Miel-Vergani G., Robertson N.H.,  
 RA Newton C.R., Ferrie R.M.;  
 RT "Molecular characterization of a new alpha-1-antitrypsin M variant  
 RT allele, Mm15tstable: implications for DNA-based diagnosis.";  
 RL Diagn. Mol. Pathol. 0:0-0(2000).  
 DR EMBL; AF159454; AAF15128.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 1  
 NON\_TER 8

SQ SEQUENCE 8 AA; 838 MW; 84A732CDD331F2CD CRC64;  
 Query Match 13.6%; Score 3; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 KAV 14  
 Db |||  
 4 KAV 6  
 RESULT 16  
 Q9TRX8 PRELIMINARY; PRT; 8 AA.  
 ID Q9TRX8;  
 AC Q9TRX8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Osteopontin (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91282766; PubMed=1676261;  
 RA Prince C.W., Dickie D., Krundieck C.L.;  
 RT "Osteopontin, a substrate for transglutaminase and factor XIII  
 RT activity.";  
 RL Biochem. Biophys. Res. Commun. 177:1205-1210(1991).  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 920 MW; 05DAFAF76322D767 CRC64;  
 Query Match 13.6%; Score 3; DB 6; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LPV 9  
 Db |||  
 1 LPV 3  
 RESULT 17  
 P72345 PRELIMINARY; PRT; 9 AA.  
 ID P72345  
 AC P72345;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE TabA (Fragment).  
 GN TABA.  
 OS Pseudomonas syringae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=317;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR2R;  
 RX MEDLINE=93167809; PubMed=7679566;  
 RA Barta T.M., Kinscherf T.G., Uchytel T.F., Willis D.K.;  
 RT "DNA sequence and transcriptional analysis of the tbaA gene required  
 RT for tabtoxin biosynthesis by Pseudomonas syringae.";  
 RL Appl. Environ. Microbiol. 59:458-466(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BR2R;  
 RA Kinscherf T.G., Willis D.K.;  
 RT "Sequence analysis of the tabtoxin biosynthetic region.";  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF519896; AAB25381.2; -.  
 FT NON\_TER 9



SQ SEQUENCE 9 AA; 1037 MW; 2B34D9D5BB05B047 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21  
 Db 1 MPI 3

RESULT 18

P82568 PRELIMINARY; PRT; 9 AA.

AC P82568; 9 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE Unknown protein from 2D-page (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=1314;

RN [1]

RC SEQUENCE AND MASS SPECTROMETRY.

RP STRAIN=JRS4;

RA Hogan D.A.; Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J., VanBogelen R.A.;

RA "Two-dimensional gel electrophoresis map of Streptococcus pyogenes proteins.";

RT Submitted (MAY-2000) to the SWISS-PROT data bank.

RL -1- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.

CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.

FT NON\_TER 1 1

FT NON\_TER 9 9

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1069 MW; 2A771042CBIAB2D7 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db 1 LPV 3

RESULT 19

Q9P8E5 PRELIMINARY; PRT; 9 AA.

AC Q9P8E5; 9 AA.

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE HIS4 protein (Fragment).

OS Kluyveromyces fragilis (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetes; Saccharomycetaceae; Kluyveromyces.

OX NCBI\_TaxID=28985;

RN [1]

RC SEQUENCE FROM N.A.

RP STRAIN=NRL-Y1140;

RA Lamas-Macielas M., Esperanza Cerdan E., Freire-Picos M.A.;

RA "Kluyveromyces fragilis HIS4 transcriptional regulation: similarities and differences to Saccharomyces cerevisiae HIS4 gene.";

RL FEBS Lett. 458:72-76(1999).

DR EMBL; AJ238494; CAB87125.1; -.

FT NON\_TER 9 9

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1015 MW; 5770D272D2D767 CRC64;

Query Match 13.6%; Score 3; DB 3; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db 2 LPV 4

RESULT 20

Q84333 PRELIMINARY; PRT; 9 AA.

AC Q84333; 9 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE (Defective variant in 1449) with monkey alu-type insert (Fragment).

OS Simian virus 40 (SV40).

OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.

OX NCBI\_TaxID=10633;

RN [1]

RC SEQUENCE FROM N.A.

RP MEDLINE=81054804; PubMed=6254029;

RA Dhruva B.R., Shenk T., Subramanian K.N.;

RT "Integration in vivo into Simian virus 40 DNA of a sequence that resembles a certain family of genomic interspersed repeated sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 77:4514-4518(1980).

DR EMBL; K01001; AAA47875.1; -.

FT NON\_TER 9 9

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1133 MW; 802204044732C33A CRC64;

Query Match 13.6%; Score 3; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7  
 Db 3 KVL 5

RESULT 21

Q64972 PRELIMINARY; PRT; 9 AA.

AC Q64972; 9 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Rous associated virus type 1 (RAV-1) ml protein, 3' end, and env protein (Fragment).

OS Avian rous-associated virus type 1.

OC Viruses; Retroviridae; Retroviridae; Alpharetrovirus.

OX NCBI\_TaxID=11950;

RN [1]

RC SEQUENCE FROM N.A.

RP MEDLINE=89037349; PubMed=2846875;

RA Marx M., Crisanti P., Eychene A., Bechade C., Laugier D., Chysdael J., Pessac B., Calothy G.;

RT "Activation and transduction of c-mil sequences in chicken neuroretina cells induced to proliferate by infection with avian lymphomatosis virus.";

RL J. Virol. 62:4627-4633(1988).

DR EMBL; M25399; AAA42548.1; -.

FT NON\_TER 1 1

FT NON\_TER 1 1

SQ SEQUENCE 9 AA; 1033 MW; 83AED7673411B5A1 CRC64;

Query Match 13.6%; Score 3; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9  
 Db 6 LPV 8

RESULT 22  
Q9RSN2 PRELIMINARY; PRT; 10 AA.  
AC Q9RSN2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Neurotoxin type A HN+ 57 kDa SUBUNIT=SAMPLE 2 (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1] \_SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E.; DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";  
RT J. Protein Chem. 10:415-425(1991).  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1225 MW; EC3DB932D366C1BA CRC64;  
Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 VLP 8  
Db 7 VLP 9  
RESULT 23  
Q9RSN1 PRELIMINARY; PRT; 10 AA.  
AC Q9RSN1;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Neurotoxin type A HN+ 57 kDa subunit (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1] \_SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E.; DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";  
RT J. Protein Chem. 10:415-425(1991).  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1172 MW; B5DAE932D416C1BA CRC64;  
Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 VLP 8  
Db 7 VLP 9  
RESULT 24  
Q9RSN3 PRELIMINARY; PRT; 10 AA.  
AC Q9RSN3;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Neurotoxin type B HN+ 57 kDa subunit (Fragment).  
OS Clostridium botulinum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1491;  
RN [1] \_SEQUENCE.  
RX MEDLINE=92143938; PubMed=1781887;  
RA Somers E.; DasGupta B.R.;  
RT "Clostridium botulinum types A, B, C1, and E produce proteins with or without hemagglutinating activity: do they share common amino acid sequences and genes?";  
RT J. Protein Chem. 10:415-425(1991).  
RL J. Protein Chem. 10:415-425(1991).  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1221 MW; C3DBE932D416C1B2 CRC64;  
Query Match 13.6%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 VLP 8  
Db 7 VLP 9  
RESULT 25  
Q26093 PRELIMINARY; PRT; 10 AA.  
ID Q26093;  
AC Q26093;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE H2B (10 AA) (Fragment).  
OS Pisaster ochraceus (Sea star).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;  
OC Asteroidea; Forcipulatacea; Forcipulata; Asteriidae; Pisaster.  
OX NCBI\_TaxID=7612;  
RN [1] \_SEQUENCE FROM N.A.  
RP TISSUE=SpERM;  
RA Howell A.M.; Cool D.; Hewitt J.; Ydenberg B.; Smith M.J.; Honda B.M.;  
RT "Organization and Unusual Expression of Histone Genes in the Sea Star Pisaster ochraceus";  
RL J. Mol. Evol. 25:29-36(1987).  
DR EMEL; X05620; CAA29107.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1126 MW; DD7806B1BB5321B2 CRC64;  
Query Match 13.6%; Score 3; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 KAV 14  
Db 1 KAV 3  
RESULT 26  
P82223 PRELIMINARY; PRT; 10 AA.  
ID P82223;  
AC P82223;  
DT 01-OCT-2001 (TREMBLrel. 18, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE Unknown protein from 2D-page (Fragment).  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;  
OC Bombycidae; Bombyx.  
OX NCBI\_TaxID=7091;  
RN [1] \_SEQUENCE.

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RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
  silkworm.";
RL I Chuan Hsueh Pao 28:217-224 (2001).
FT NON TER 10
SQ SEQUENCE 10 AA; 1054 MW; D0F722C325B1F1B2 CRC64;

Query Match      13.6%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db 7 KVL 9

RESULT 27
P82224 PRELIMINARY; PRT; 10 AA.
AC P82224;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Unknown protein from 2D-page (Fragment).
OS Bombyx mori (Silk moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC Bombycidae; Bombyx.
OX NCBI_TaxID=7091;
RN [1]
RP SEQUENCE
RC STRAIN=XINHANG X KEMING; TISSUE=Body wall, and Fat body;
RX MEDLINE=21177481; PubMed=11280994;
RA Zhong B.X.;
RT "Protein database for several tissues derived from five instar of
  silkworm.";
RL I Chuan Hsueh Pao 28:217-224 (2001).
FT NON TER 10
SQ SEQUENCE 10 AA; 1064 MW; D77CBF25B1F1B2CD CRC64;

Query Match      13.6%; Score 3; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db 8 KVL 10

RESULT 28
Q8WB7 PRELIMINARY; PRT; 10 AA.
AC Q8WB7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
OC COI.
OS Chaitophorus leucomelas.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
OC Aphidoidea; Drepanosiphidae; Chaitophorus.
OX NCBI_TaxID=136351;
RN [1]
RP SEQUENCE FROM N.A.
RA Shingleton A.W.; Stern D.L.;
RT "Molecular phylogenetic evidence for multiple origins of ant mutualism
  within the aphid genus Chaitophorus.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF44288; AAL38565.1; -

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KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 10 AA; 1194 MW; 6E553D5042D7672B CRC64;

Query Match      13.6%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPV 9
Db 4 LPV 6

RESULT 29
Q95DS3 PRELIMINARY; PRT; 10 AA.
AC Q95DS3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Rbcl protein (Fragment).
OC Rbcl.
GN Rbcl.
OS Magnolia mexicana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Magnoliales; Magnoliaceae; Magnolia.
OX NCBI_TaxID=111569;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H.; Garcia-Franco J.G.; Rico-Gray V.; Thien L.B.;
RT "Molecular phylogeny of Magnoliaceae.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055580; BAB69572.1; -
KW Chloroplast.
FT NON TER 10
SQ SEQUENCE 10 AA; 1091 MW; 344DEA21AB01A327 CRC64;

Query Match      13.6%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 8 KAV 10

RESULT 30
Q9JLI5 PRELIMINARY; PRT; 10 AA.
AC Q9JLI5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MC1R (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=20090876; PubMed=10623832;
RA Adachi S.; Morii E.; Kim D.-k.; Ogiwara H.; Jippo T.; Ito A.; Lee Y.M.;
RA Kitamura Y.;
RT "Involvement of ml-transcription factor in expression of alpha-
  melanocyte-stimulating hormone receptor in cultured mast cells of
  mice.";
RL J. Immunol. 164:855-860 (2000).
DR EMBL; AF176016; AAF37323.1; -
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

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Query Match 13.6%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 POK 12  
 Db 6 POK 8

RESULT 31  
 Q9ESU5 PRELIMINARY; PRT; 10 AA.  
 AC Q9ESU5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Fas death receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He;  
 RX MEDLINE=20127858; PubMed=10660538;  
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,  
 RA Yonish-Rouach E., Reisdorf P.;  
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a  
 RT p53-responsive element that is activated by p53 mutants unable to  
 RT induce apoptosis.";  
 RL J. Biol. Chem. 275:3867-3872(2000).  
 DR EMBL; AF282865; AAC02410.1; -.  
 KW Receptor.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLP 8  
 Db 7 VLP 9

RESULT 32  
 Q8CJEO PRELIMINARY; PRT; 10 AA.  
 AC Q8CJEO;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Resistin (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Nobita T., Hisatomi H.;  
 RA "Rattus norvegicus resistin DNA, intron2.";  
 RL Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB093559; BAC21195.1; -.  
 FT NON TER 1  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1079 MW; 34EA46D32DDC777 CRC64;

Query Match 13.6%; Score 3; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 QKA 13

Db 6 QKA 8

RESULT 33  
 O39957 PRELIMINARY; PRT; 10 AA.  
 ID O39957;  
 AC O39957;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE E1 protein (Fragment).  
 OS Hepatitis GB virus C.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC GBV-C/HGV group.  
 OX NCBI\_TaxID=39839;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Edinburgh haemophilic;  
 RX MEDLINE=97368412; PubMed=9225026;  
 RA Smith D.B., Cuccaneu N., Davidson P., Jarvis L.M., Mokili J.L.,  
 RA Hamid S., Ludlam C.A., Simmonds P.;  
 RT "Discrimination of hepatitis G virus (GBV-C) geographical variants by  
 RT analysis of the 5' non-coding region.";  
 RL J. Gen. Virol. 78:1533-1542(1997).  
 DR EMBL; AF003175; AAC57986.1; -.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1067 MW; CC89FE2727273772 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVP 15  
 Db 2 AVP 4

RESULT 34  
 Q9TWX9 PRELIMINARY; PRT; 10 AA.  
 ID Q9TWX9;  
 AC Q9TWX9;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE HX-C3 homolog.  
 OS Eptatretus burgeri (Inshore hagfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;  
 OC Myxiniidae; Eptatretinae; Eptatretus.  
 OX NCBI\_TaxID=7764;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92091759; PubMed=1727859;  
 RA Fujii T., Nakamura T., Sekizawa A., Tomonaga S.;  
 RA "Isolation and characterization of a protein from hagfish serum that  
 RA is homologous to the third component of the mammalian complement  
 RA system.";  
 RL J. Immunol. 148:117-123(1992).  
 SQ SEQUENCE 10 AA; 968 MW; DB3C186DD042C732 CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL 7  
 Db 2 KVL 4

RESULT 35  
 Q8JFE7 PRELIMINARY; PRT; 10 AA.  
 ID Q8JFE7  
 AC Q8JFE7;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula albicollis. Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bg5; and Bg8;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454217; AAM22903.1; -.
DR EMBL; AF454218; AAM22904.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 5 VLP 7

RESULT 36
Q8JU33 PRELIMINARY; PRT; 10 AA.
AC Q8JU33;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myelin proteolipid protein (Fragment).
OS Ficedula hypoleuca. Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=46689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Op86;
RX MEDLINE=21918460; PubMed=11918793;
RA Primer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454216; AAM22902.1; -.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 1FAAC9676732C86B CRC64;

Query Match 13.6%; Score 3; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLP 8
Db 5 VLP 7

RESULT 37
Q9EUZ3 PRELIMINARY; PRT; 11 AA.
AC Q9EUZ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ribosome binding factor A (Fragment).
GN RBFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IQ490;
RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
RA Mortensen K.K.;
RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
RT IQ490.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ132862; CAC20133.1; -.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 13.6%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 POR 17
Db 8 POR 10

RESULT 38
Q86864 PRELIMINARY; PRT; 11 AA.
AC Q86864;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LCMV viral protein (Fragment).
GN LCMV VIRAL PROTEIN.
OC Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
OX NCBI_TaxID=11623;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL; S75739; AAB33665.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1186 MW; D6235C80D9C45B42 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAV 14
Db 2 KAV 4

RESULT 39
Q932U8 PRELIMINARY; PRT; 12 AA.
AC Q932U8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Urf-2X protein.
GN URF-2X.
OS Acinetobacter sp.
OX Plasmid pKLH205, and plasmid pKLH204.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.

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OX NCB1_TaxID=472;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ED45-25; PLASMID=pKLH205, and pKLH204;
RX MEDLINE=21272500; PubMed=11376944;
RA Kholodii G.;
RT "The shuffling function of resolvases.";
RL Gene 269:121-130(2001).
DR EMBL; AJ251707; CAC39413.1; -.
DR EMBL; AJ250851; CAC39402.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3B821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db |||
4 SQP 6

RESULT 40
Q52112
ID Q52112 PRELIMINARY; PRT; 12 AA.
AC Q52112; O08093; O08128; O08132; Q56909;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE URF2X protein (Fragment).
GN URF-2X OR URF2X.
OS Acinetobacter calcoaceticus,
OS Pantoea agglomerans,
OS Alcaligenes sp.,
OS Enterobacter cloacae,
OS Escherichia coli,
OS Yersinia enterocolitica, and
OS mercury resistant bacterium '96 SE13.
OG Plasmid pKLH2, Plasmid pKLH256, Plasmid pKLH210, Plasmid pCh17, and
OG Plasmid pKLH201.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCB1_TaxID=471, 549, 512, 550, 562, 630, 93601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=A.calcoaceticus; PLASMID=pKLH2;
RX MEDLINE=94134837; PubMed=8302940;
RA Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
RA Yurieva O.V., Nikiforov V.G.;
RT "Molecular characterization of an aberrant mercury resistance
transposable element from an environmental Acinetobacter strain.";
RL Plasmid 30:303-308(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=P.agglomerans, Alcaligenes sp., E.cloacae, and E.coli;
RX MEDLINE=97303088; PubMed=9159519;
RA Nikiforov V., Kholodii G., Minakhin L., Gorlenko Z., Kalyaeva E.,
RA Mindlin S., Nikiforov V.;
RT "Intercontinental spread of promiscuous mercury-resistance transposons
in environmental bacteria.";
RL Mol. Microbiol. 24:321-329(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Y.enterocolitica; STRAIN=Various strains;
RX MEDLINE=95273477; PubMed=7753910;
RA Osbourn S.E.V., Turner A.K., Grinstead J.;
RT "Nucleotide sequence within Tn3926 confirms this as a Tn21-like
transposable element and provides evidence for the origin of the mer
operon carried by plasmid pKLH2.";
RL Plasmid 33:65-69(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=mercury resistant bacterium '96 SE13;

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RA Holt R.J., Bruce K.D., Strike P.;
RT "Conservation of transposon structures in soil bacteria.";
RL FEMS Microbiol. Ecol. 0:0-0(1999).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=A.calcoaceticus; STRAIN=KHW14; PLASMID=pKLH201;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
dissemination.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213017; AAA19685.1; -.
DR EMBL; Y08992; CAA70180.1; -.
DR EMBL; Y08993; CAA70193.1; -.
DR EMBL; Y09025; CAA70234.1; -.
DR EMBL; Y10102; CAA71186.1; -.
DR EMBL; X78059; CAA54979.1; -.
DR EMBL; AF134211; AAD34400.1; -.
DR EMBL; AJ251307; CAC80877.1; -.
KW Plasmid.
FT NON TER 12
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db |||
4 SQP 6

RESULT 41
Q8GMV1
ID Q8GMV1 PRELIMINARY; PRT; 12 AA.
AC Q8GMV1
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Urf-2X protein.
GN Urf-2X.
OS Acinetobacter lwoffii.
OG Plasmid pKLH202.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCB1_TaxID=28090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TC108;
RA Kholodii G.Y., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKLH2-like aberrant transposons and possible mechanisms of their
dissemination.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250245; CAC80792.1; -.
KW Plasmid.
SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQP 4
Db |||
4 SQP 6

RESULT 42
Q8GMT8
ID Q8GMT8 PRELIMINARY; PRT; 12 AA.
AC Q8GMT8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)

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DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Urf-2X protein.  
 GN URF-2X.  
 OS Acinetobacter junii.  
 OG Plasmid pKLH203.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=40215;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=NC13-1;  
 RC Kholodii G.Y.; Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
 RA Nikiforov V.G.;  
 RT "pKLH2-like aberrant transposons and possible mechanisms of their  
 RT dissemination.";  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ250494; CAC80763.1; -.  
 KW Plasmid.  
 SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;  
  
 Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 SQP 4  
 DB 4 SQP 6  
  
 RESULT 43  
 Q8GML2 ID Q8GML2 PRELIMINARY; PRT; 12 AA.  
 AC Q8GML2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Urf-2X protein.  
 GN URF-2X.  
 OS Acinetobacter sp. ED23-35.  
 OG Plasmid pKLH208.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=109250;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=ED23-35;  
 RC Kholodii G.Y.; Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,  
 RA Nikiforov V.G.;  
 RT "pKLH2-like aberrant transposons and possible mechanisms of their  
 RT dissemination.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ251272; CAC80895.1; -.  
 KW Plasmid.  
 SQ SEQUENCE 12 AA; 1219 MW; D4B99D3E821DC776 CRC64;  
  
 Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 2 SQP 4  
 DB 4 SQP 6  
  
 RESULT 44  
 Q8GBY8 ID Q8GBY8 PRELIMINARY; PRT; 12 AA.  
 AC Q8GBY8;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Gas vesicle protein Gvpa (Fragment).  
 GN GVPA.

OS Planktothrix agardhii.  
 OC Bacteria; Cyanobacteria; Oscillatoriales; Planktothrix.  
 OX NCBI\_TaxID=54305;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=CYA 29;  
 RC Beard S.J., Handley B.A., Walsby A.E.;  
 RA "Spontaneous mutations in gas vesicle genes of Planktothrix spp.  
 RT affect gas vesicle production and critical pressure."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ494992; CAD41965.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1112 MW; C78F8CAB43DDC6DD CRC64;  
  
 Query Match 13.6%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 13 AVP 15  
 DB 8 AVP 10  
  
 RESULT 45  
 Q9H4F4 ID Q9H4F4 PRELIMINARY; PRT; 12 AA.  
 AC Q9H4F4;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE Survival interacting protein 1 (Fragment).  
 GN SIp1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Helmsken C., Wetter A., Rudnik-Schoneborn S., Liehr T., Zerres K.,  
 RA Wirth B.;  
 RT "An essential SMN interacting protein (SIP1) is not involved in the  
 RT phenotypic variability of spinal muscular atrophy (SMA).";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ250939; CAC16171.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 12 AA; 1455 MW; 6BA6698AD0D72AB4 CRC64;  
  
 Query Match 13.6%; Score 3; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 16 QRD 18  
 DB 4 QRD 6  
  
 RESULT 46  
 Q96P98 ID Q96P98 PRELIMINARY; PRT; 12 AA.  
 AC Q96P98;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE CD27-binding protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RP Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;  
 RA "Characterization of TPA-responsive genes in U937 cells using ordered  
 RT differential display PCR.";

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RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF401214; AAL02171.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1333 MW; 977A27103ADEA5A1 CRC64;
  Query Match      13.6%; Score 3; DB 4; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.4e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db |||
  1 KVL 3

RESULT 47
ID Q31851 PRELIMINARY; PRT; 12 AA.
AC Q31851;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia; TISSUE=Leaf;
RX MEDLINE=94187724; PubMed=8133955;
RA Conley T.R., Park S.-C., Kwon H.-B., Peng H.-S., Shih M.-C.;
RT "Characterization of cis-acting elements in light regulation of the
RT nuclear gene encoding the A subunit of chloroplast isozymes
RT glyceraldehyde-3-phosphate dehydrogenase from Arabidopsis thaliana.";
RL Mol. Cell. Biol. 14:2525-2533(1994).
DR EMBL; L14743; AAA31640.1; -.
KW Chloroplast.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1263 MW; 81BA4C7D4BD5B9D1 CRC64;

  Query Match      13.6%; Score 3; DB 8; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.4e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6
Db |||
  9 PKV 11

RESULT 48
ID Q8SAS2 PRELIMINARY; PRT; 12 AA.
AC Q8SAS2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative fructokinase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=plus tree E1101;
RX MEDLINE=21660210; PubMed=11801746;
RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low Nucleotide Diversity at the pall Locus in the Widely Distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359120; AAL74388.1; -.
KW Kinase.

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FT NON_TER 1
SQ SEQUENCE 12 AA; 1228 MW; C6FE739330A72DDD CRC64;

  Query Match      13.6%; Score 3; DB 10; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.4e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db |||
  9 KVL 11

RESULT 49
ID Q8SAS3 PRELIMINARY; PRT; 12 AA.
AC Q8SAS3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative fructokinase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=plus tree E635C;
RX MEDLINE=21660210; PubMed=11801746;
RA Dvornyk V., Sirvio A., Mikkonen M., Savolainen O.;
RT "Low Nucleotide Diversity at the pall Locus in the Widely Distributed
RT Pinus sylvestris.";
RL Mol. Biol. Evol. 19:179-188(2002).
DR EMBL; AF359119; AAL74387.1; -.
KW Kinase.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1198 MW; C6E9EC9330A72DDD CRC64;

  Query Match      13.6%; Score 3; DB 10; Length 12;
  Best Local Similarity 100.0%; Pred. No. 1.4e+04;
  Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL 7
Db |||
  9 KVL 11

RESULT 50
ID P82441 PRELIMINARY; PRT; 12 AA.
AC P82441;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE 26 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
KW Cell wall.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1234 MW; 340012240872C9D7 CRC64;

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Query Match 13.6%; Score 3; DB 10; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10  
 DB 8 PVP 10

## RESULT 51

ID Q83139 PRELIMINARY; PRT; 12 AA.  
 AC Q83139;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE (Strain CV17) genomic RNA-gamma, 5' leader.  
 OS Barley stripe mosaic virus (BSMV).  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hordeivirus.  
 OX NCBI\_TaxID=12327;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CV17;  
 RX MEDLINE=91062385; PubMed=2247462;  
 RA Petty I.T., Edwards M.C., Jackson A.O.;  
 RT "Systemic movement of an RNA plant virus determined by a point  
 substitution in a 5' leader sequence."  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8894-8897 (1990).  
 DR EMBL; M38633; AAA75527.1; -.  
 SQ SEQUENCE 12 AA; 1416 MW; 36A281207BC05047 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21  
 DB 4 MPI 6

## RESULT 52

ID Q90ZL3 PRELIMINARY; PRT; 12 AA.  
 AC Q90ZL3;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE Casein kinase 2 alpha subunit (Fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wilhelm V., Neckelman G., Allende C.C., Allende J.E.;  
 RT "The Genomic Structure of Two Protein Kinase CK2 alpha Genes of  
 RT Xenopus laevis and Features of the Putative Promoter Region."  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY032954; AAK50341.1; -.  
 KW Kinase.  
 FT NON TER 12 12  
 SQ SEQUENCE 12 AA; 1320 MW; D005098DFD15A772 CRC64;

Query Match 13.6%; Score 3; DB 13; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVP 10  
 DB 4 PVP 6

## RESULT 53

ID O31295 PRELIMINARY; PRT; 13 AA.  
 AC O31295;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).  
 GN LEUA.  
 OS Buchnera aphidicola.  
 OC Plasmid pBTet.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OX NCBI\_TaxID=9;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97386415; PubMed=9244264;  
 RA Van Ham R.C.H.J., Moya A., Latorre A.;  
 RT "Putative origin of plasmids carrying the genes involved in leucine  
 biosynthesis in Buchnera aphidicola (endosymbiont of aphids)."  
 RL J. Bacteriol. 179:4768-4777 (1997).  
 DR EMBL; Y11966; CAA72696.1; -.  
 KW Lyase; Plasmid.  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1487 MW; 1BD1D3E72A9E2050 CRC64;

Query Match 13.6%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKV 6  
 DB 3 PKV 5

## RESULT 54

ID Q8WNS4 PRELIMINARY; PRT; 13 AA.  
 AC Q8WNS4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE X-linked zinc finger protein (Fragment).  
 GN ZFX.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poloumienko A., Blecher S.;  
 RT "Comparison between intron-exon structures in ZFX and ZFY genes."  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF032363; AAL58189.1; -.  
 FT NON TER 1 1  
 FT NON TER 13 13  
 SQ SEQUENCE 13 AA; 1366 MW; C32F1B202464DDDD CRC64;

Query Match 13.6%; Score 3; DB 6; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 MPI 21  
 DB 1 MPI 3

## RESULT 55

Q9THS0 PRELIMINARY; PRT; 13 AA.  
 ID Q9THS0  
 AC Q9THS0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE PSSH (Fragment).  
 GN PSSH.  
 OS Bryopsis sp. B.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;  
 OC Bryopsidaceae; Bryopsis.  
 OX NCBI\_TaxID=103785;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96-15-06;  
 RA Krellwitz E.C., Kowalik K.V., Manos P.S.;  
 RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North  
 RT Atlantic and Caribbean based on Coding and Non-coding sequences of the  
 RT Chloroplast psbB Operon."  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AF170406; AAD56844.1; --  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1351 MW; 2C316AF02E93A338 CRC64;  
  
 Query Match 13.6%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 19 MPI 21  
 DB 1 MPI 3  
  
 RESULT 56  
 ID 088176 PRELIMINARY; PRT; 13 AA.  
 AC 088176;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM1 OR NCAM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb-c; TISSUE=Liver;  
 RX MEDLINE=98250618; PubMed=9582442;  
 RA Kawahigashi H., Harada Y., Asano A., Nakamura M.;  
 RT "A cis-acting regulatory element that affects the alternative splicing  
 RT of a muscle-specific exon in the mouse NCAM gene."  
 RL Biochim. Biophys. Acta 1397:305-315(1998).  
 DR EMBL; AB001873; BAA31275.1; --  
 DR MGD; MGI:97281; Ncam1.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1496 MW; CC6098E54C72D732 CRC64;  
  
 Query Match 13.6%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 LPV 9  
 DB 4 LPV 6  
  
 RESULT 57  
 ID Q9QVK6 PRELIMINARY; PRT; 13 AA.  
 AC Q9QVK6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE Phosphoglycerate mutase P29 (EC 2.7.5.3) (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=91373341; PubMed=1832670;  
 RA Hoppner W., Becker L., Buck F., Seitz H.J.;  
 RT "Is the p29 protein involved in the rapid regulation of  
 RT phosphoenolpyruvate carboxykinase (GTP)?";  
 RL J. Biol. Chem. 266:17257-17260(1991).  
 SQ SEQUENCE 13 AA; 1456 MW; 39099D8C8BA6D2D7 CRC64;  
  
 Query Match 13.6%; Score 3; DB 11; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 LPV 9  
 DB 5 LPV 7  
  
 RESULT 58  
 ID Q81761 PRELIMINARY; PRT; 13 AA.  
 AC Q81761;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.  
 OS Hepatitis C virus.  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D3;  
 RX MEDLINE=92279243; PubMed=1317578;  
 RA Bukh J., Purcell R.H., Miller R.H.;  
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 DR EMBL; M84842; AAA45679.1; --  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON TER  
 FT NON TER  
 SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;  
  
 Query Match 13.6%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 15 POR 17  
 DB 7 POR 9  
  
 RESULT 59  
 ID Q81794 PRELIMINARY; PRT; 13 AA.  
 AC Q81794;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.

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OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=INDS;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84854; AAA45701.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 60
Q81784
ID Q81784 PRELIMINARY; PRT; 13 AA.
AC Q81784;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=21;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84845; AAA45701.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 61
Q81778
ID Q81778 PRELIMINARY; PRT; 13 AA.
AC Q81778;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=SW3;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84850; AAA45695.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 62
Q81787
ID Q81787 PRELIMINARY; PRT; 13 AA.
AC Q81787;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=26;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84862; AAA45704.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 61
Q81778
ID Q81778 PRELIMINARY; PRT; 13 AA.
AC Q81778;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=26;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84862; AAA45704.1; -.
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

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QY      15 POR 17
DB      |||
        7 POR 9

RESULT 63
Q81775 PRELIMINARY; PRT; 13 AA.
ID Q81775
AC Q81775;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=SA7;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND MRNA (BY SIMILARITY).
CC EMBL; M84852; AAA45693.1; -
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 POR 17
DB      |||
        7 POR 9

RESULT 64
Q81767 PRELIMINARY; PRT; 13 AA.
ID Q81767
AC Q81767;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=HK5;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND MRNA (BY SIMILARITY).
CC EMBL; M84849; AAA45685.1; -
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
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FT NON TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 POR 17
DB      |||
        7 POR 9

RESULT 65
Q81798 PRELIMINARY; PRT; 13 AA.
ID Q81798
AC Q81798;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=SA11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND MRNA (BY SIMILARITY).
CC EMBL; M84868; AAA45715.1; -
DR InterPro; IPR002522; HCV_capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER 13
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 POR 17
DB      |||
        7 POR 9

RESULT 66
Q81774 PRELIMINARY; PRT; 13 AA.
ID Q81774
AC Q81774;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]_TaxID=11103;
RP SEQUENCE FROM N.A.
RC STRAIN=SA1;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 DR EMBL; M84860; AAA45692.1; -.  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;  
 Query Match 13.6%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PQR 17  
 Db 7 PQR 9  
 RESULT 67  
 Q81766 PRELIMINARY; PRT; 13 AA.  
 AC Q81766;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.  
 OS Hepatitis C virus.  
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HK2;  
 RX MEDLINE=92279243; PubMed=1317578;  
 RA Bukh J., Purcell R.H., Miller R.H.;  
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 CC EMBL; M84827; AAA45684.1; -.  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1571 MW; 464D1DE1A42FC763 CRC64;  
 Query Match 13.6%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PQR 17  
 Db 7 PQR 9  
 RESULT 68  
 Q81793 PRELIMINARY; PRT; 13 AA.  
 AC Q81793;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.  
 OS Hepatitis C virus.  
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=IND3;  
 RX MEDLINE=92279243; PubMed=1317578;  
 RA Bukh J., Purcell R.H., Miller R.H.;  
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 CC EMBL; M84861; AAA45710.1; -.  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;  
 Query Match 13.6%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PQR 17  
 Db 7 PQR 9  
 RESULT 69  
 Q81768 PRELIMINARY; PRT; 13 AA.  
 AC Q81768;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Genome polyprotein (Fragment).  
 GN POLYPROTEIN.  
 OS Hepatitis C virus.  
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
 OC Hepacivirus.  
 OX NCBI\_TaxID=11103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P10;  
 RX MEDLINE=92279243; PubMed=1317578;  
 RA Bukh J., Purcell R.H., Miller R.H.;  
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
 CC PROTEIN C AND MRNA (BY SIMILARITY).  
 CC EMBL; M84855; AAA45686.1; -.  
 DR InterPro; IPR002522; HCV\_capsid.  
 DR Pfam; PF01543; HCV\_capsid; 1.  
 KW Polyprotein.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;  
 Query Match 13.6%; Score 3; DB 12; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PQR 17  
 Db 7 PQR 9  
 RESULT 70  
 Q81785 PRELIMINARY; PRT; 13 AA.  
 AC Q81785;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

```

DE Genome polyprotein (Fragment).
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=24;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946 (1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84848; AAA45702.1; -.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 71
Q81800 PRELIMINARY; PRT; 13 AA.
AC Q81800;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-US11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946 (1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84865; AAA45717.1; -.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 72
Q81765 PRELIMINARY; PRT; 13 AA.
AC Q81765;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DR4;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946 (1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84859; AAA45683.1; -.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

RESULT 73
Q81781 PRELIMINARY; PRT; 13 AA.
AC Q81781;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946 (1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL; M84846; AAA45698.1; -.
DR InterPro; IPR002522; HCV capsid.
DR Pfam; PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON TER
SQ SEQUENCE 13 AA; 1557 MW; 464CF7E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17
DB 7 PQR 9

```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 PQR 17  
Db |||  
7 PQR 9

## RESULT 74

ID Q81769 PRELIMINARY; PRT; 13 AA.  
AC Q81769;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Genome polyprotein (Fragment).  
GN POLYPROTEIN.  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P8;  
RX MEDLINE=92279243; PubMed=1317578;  
RA Bukh J., Purcell R.H., Miller R.H.;  
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
PROTEIN C AND MRNA (BY SIMILARITY).  
DR EMBL: M84856; AAA45687.1; -.  
DR InterPro: IPR002522; HCV\_capsid.  
DR Pfam: PF01543; HCV\_capsid; 1.  
KW Polyprotein.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1559 MW; 465365E1A42FC763 CRC64;

Query Match 13.6%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQR 17  
Db |||  
7 PQR 9

## RESULT 75

ID Q81773 PRELIMINARY; PRT; 13 AA.  
AC Q81773;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Genome polyprotein (Fragment).  
GN POLYPROTEIN.  
OS Hepatitis C virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;  
OC Hepacivirus.  
OX NCBI\_TaxID=11103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=S9;  
RX MEDLINE=92279243; PubMed=1317578;  
RA Bukh J., Purcell R.H., Miller R.H.;  
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).  
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A  
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:  
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF  
PROTEIN C AND MRNA (BY SIMILARITY).  
DR EMBL: M84838; AAA45691.1; -.  
DR InterPro: IPR002522; HCV\_capsid.

DR Pfam: PF01543; HCV\_capsid; 1.  
KW Polyprotein.  
FT NON\_TER 13 13  
SQ SEQUENCE 13 AA; 1572 MW; 464F97E1A42FC763 CRC64;  
Query Match 13.6%; Score 3; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 PQR 17  
Db |||  
7 PQR 9  
Search completed: November 25, 2003, 19:34:06  
Job time : 42.314 secs





83 5 22.7 20 16 AAR81712 C.albicans enolase  
 84 4 18.2 5 23 ABB84011 Transglutaminase i  
 85 4 18.2 5 24 ABU12265 Chymotrypsin inhib  
 86 4 18.2 5 24 ABU12267 Chymotrypsin inhib  
 87 4 18.2 6 23 AAU83283 Antiviral composi  
 88 4 18.2 7 15 AAR58327 Hypotensive polype  
 89 4 18.2 7 17 AAW05076 Proline-rich SH3 b  
 90 4 18.2 7 18 AAW25906 Beta-2-microglobul  
 91 4 18.2 7 18 AAW25922 Beta-2-microglobul  
 92 4 18.2 7 22 AAM47044 H11 binding site c  
 93 4 18.2 7 22 AAM47107 H11 binding site c  
 94 4 18.2 7 23 ABG57831 Human ADPI tryptic  
 95 4 18.2 7 23 ABB05245 Tumour necrosis fa  
 96 4 18.2 8 16 AAR84463 Hepatitis C virus  
 97 4 18.2 8 17 AAR95795 Alpha-4Beta-1 inte  
 98 4 18.2 8 22 ABP14017 HIV A02 super moti  
 99 4 18.2 8 22 ABP21946 HIV A03 motif tat  
 100 4 18.2 8 23 ABB07551 A localisation dom

## ALIGNMENTS

RESULT 1  
 AAU83308  
 ID AAU83308 standard; Peptide; 14 AA.  
 AC AAU83308;  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #26.  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 OS Synthetic.  
 XX US2002004579-A1.  
 FN 10-JAN-2002.  
 PD 17-JAN-2001; 2001US-0764017.  
 PF 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 FI Friedland B, Hirschman SZ, Taraporewala IB;  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 14 AA;  
 Query Match 50.0%; Score 11; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 KVLVPVQKAVP 15  
 Db 1 KVLVPVQKAVP 11  
 RESULT 2  
 AAU83331  
 ID AAU83331 standard; Peptide; 16 AA.  
 AC AAU83331;  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #49.  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 OS Synthetic.  
 XX US2002004579-A1.  
 FN 10-JAN-2002.  
 PD 17-JAN-2001; 2001US-0764017.  
 PF 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 FI Friedland B, Hirschman SZ, Taraporewala IB;  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 16 AA;  
 Query Match 50.0%; Score 11; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 KVLVPVQKAVP 15  
 Db 1 KVLVPVQKAVP 11  
 RESULT 3  
 AAU83340  
 ID AAU83340 standard; Peptide; 19 AA.  
 AC AAU83340;  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #58.

XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 DR  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 19 AA;  
 Query Match 50.0%; Score 11; DB 23; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.0002;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KVLVPQKAVP 15  
 DB 1 KVLVPQKAVP 11  
 |||||  
 RESULT 4  
 AAU83287  
 ID AAU83287 standard; Peptide; 10 AA.  
 XX  
 AC AAU83287;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #5.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX

XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 DR  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 45.5%; Score 10; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0011;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KVLVPQKAV 14  
 DB 1 KVLVPQKAV 10  
 |||||  
 RESULT 5  
 AAU83311  
 ID AAU83311 standard; Peptide; 14 AA.  
 XX  
 AC AAU83311;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #29.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 OS  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 DR  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.

XX  
SQ Sequence 14 AA;

Query Match 45.5%; Score 10; DB 23; Length 14;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVPQKAVP 15  
||| |||||  
Db 1 VLPVPQKAVP 10

## RESULT 6

AAU83334  
ID AAU83334 standard; Peptide; 17 AA.

XX  
AC AAU83334;

XX  
DT 23-APR-2002 (first entry)

XX  
DE Antiviral composition peptide-A, fragment #52.

XX  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.

XX  
OS Synthetic.

XX  
PN US2002004579-A1.

XX  
PD 10-JAN-2002.

XX  
PF 17-JAN-2001; 2001US-0764017.

PR 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.

XX  
PA (ADVI-) ADVANCED VIRAL RES CORP.

XX  
PI Friedland B, Hirschman SZ, Taraporewala IB;

XX  
WPI; 2002-163727/21.

XX  
PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -

XX  
PS Disclosure; Page 8; 37pp; English.

XX  
CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.

XX  
SQ Sequence 17 AA;

Query Match 45.5%; Score 10; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.0018;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVPQKAVP 15  
||| |||||  
Db 1 VLPVPQKAVP 10

## RESULT 7

AAE07191

ID AAE07191 standard; peptide; 9 AA.

XX  
AC AAE07191;

XX  
DT 06-NOV-2001 (first entry)

XX  
DE Colostrinin peptide 7.

XX  
KW Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
KW central nervous system disorder; neurodegenerative disorder; weight loss;  
KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
KW acquired immunological deficiency; neurological disorder; dementia;  
KW antiviral.

XX  
OS Unidentified.

XX  
PN WO200155199-A1.

XX  
PD 02-AUG-2001.

XX  
PF 26-JAN-2001; 2001WO-GB00329.

XX  
PR 26-JAN-2000; 2000GB-0001825.

XX  
PA (REG-) REGEN THERAPEUTICS PLC.

XX  
PI Georgiades JA;

XX  
DR WPI; 2001-488775/53.

XX  
PT Peptide useful as an inter alia in the treatment of e.g. disorders of  
PT the immune system and the central nervous system comprises ten  
PT amino-terminal amino acid sequence derived from peptides present in  
PT colostrinin -

XX  
PS Claim 1; Page 15; 40pp; English.

XX  
CC The invention relates to colostrinin peptide fragments which are useful,  
CC inter alia, in the treatment of chronic disorders of the immune system  
CC and the central nervous system. Colostrinin peptides are used as a  
CC medicament in the treatment of neurological disorders e.g., dementia,  
CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
CC viral infections and diseases characterised by the presence of beta-  
CC amyloid plaques and as a dietary supplement for babies, small children,  
CC adults and senile persons, who have been subjected to chemotherapy or  
CC have suffered from cachexia or weight loss due to the chronic disease.  
CC Colostrinin peptides are also used as food additives and as an auxiliary  
CC withdrawal treatment for drug addicts, after a period of detoxification  
CC and in persons dependent on stimulants. Colostrinin peptides are used to  
CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
CC disturbances of psychiatric patients in a state of depression. These  
CC colostrinin peptides improves the development of immune system in a new  
CC born child and to correct the immunological deficiencies in a child.  
CC The present sequence is colostrinin peptide 7 related to the invention.  
CC Colostrinin peptide 7 corresponds to position 182-200 of beta-caesin.

XX  
SQ Sequence 9 AA;

Query Match 40.9%; Score 9; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 QPKVLPVPQ 11  
||| |||||  
Db 1 QPKVLPVPQ 9

## RESULT 8

AAE07201	
ID	AAE07201 standard; peptide; 10 AA.
XX	
AC	AAE07201;
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Modified colostrinin cyclic peptide #7.
XX	
KW	Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;
KW	Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KW	central nervous system disorder; neurodegenerative disorder; weight loss;
KW	beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;
KW	acquired immunological deficiency; neurological disorder; dementia;
KW	antiviral; cyclic.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Modified-site 1
FT	/note= "N-terminal acetyl; this residue forms a cyclic
FT	linkage with Gln found at the C-terminal end"
XX	
PN	WO200155199-A1.
XX	
PD	02-AUG-2001.
XX	
XX	26-JAN-2001; 2001WO-GB00329.
PF	
XX	26-JAN-2000; 2000GB-0001825.
PR	
XX	(REGG-) REGEN THERAPEUTICS PLC.
PA	
XX	Georgiades JA;
PI	
XX	WPI; 2001-488775/53.
DR	
XX	
PT	Peptide useful as an inter alia in the treatment of e.g. disorders of
PT	the immune system and the central nervous system comprises ten
PT	amino-terminal amino acid sequence derived from peptides present in
PT	colostrinin -
XX	
PS	Example 2; Page 9; 40pp; English.
XX	
CC	The invention relates to colostrinin peptide fragments which are useful,
CC	inter alia, in the treatment of chronic disorders of the immune system
CC	and the central nervous system. Colostrinin peptides are used as a
CC	medicament in the treatment of neurological disorders e.g., dementia,
CC	neurodegenerative disorders e.g., Alzheimer's disease, motor neuron
CC	disease e.g., Parkinson's disease, mental disorders e.g. psychosis and
CC	neurosis, in acquired immunological deficiencies, chronic bacterial and
CC	viral infections and diseases characterised by the presence of beta-
CC	amyloid plaques and as a dietary supplement for babies, small children,
CC	adults and senile persons, who have been subjected to chemotherapy or
CC	have suffered from cachexia or weight loss due to the chronic disease.
CC	Colostrinin peptides are also used as food additives and as an auxiliary
CC	withdrawal treatment for drug addicts, after a period of detoxification
CC	and in persons dependent on stimulants. Colostrinin peptides are used to
CC	prepare antibodies and to treat emotional disturbances, e.g. emotional
CC	disturbances of psychiatric patients in a state of depression. These
CC	colostrinin peptides improves the development of immune system in a new
CC	born child and to correct the immunological deficiencies in a child.
CC	The present sequence is modified colostrinin cyclic peptide #7 related to
CC	the invention.
XX	
SQ	Sequence 10 AA;
XX	
Query Match	40.9%; Score 9; DB 22;
Best Local Similarity	100.0%; Pred. No. 0.011;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	3 QPKYLPVPEQ 11



```

XX SQ Sequence 9 AA;
Query Match 36.4%; Score 8; DB 23; Length 9;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PORDMPIQ 22
DB 2 PORDMPIQ 9

RESULT 13
AAU83301
ID AAU83301 standard; Peptide; 13 AA.
XX
AC AAU83301;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #19.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
KW WPI; 2002-163727/21.
XX
PT New peptides compositions, useful for treating viral infections and
stimulating the immune system -
XX
PS Disclosure; Page 7; 37pp; English.
XX
CC The invention relates to a new peptide composition comprising a specified
peptide sequence. The composition comprises nucleotide-peptide comprising
a peptide linked through a serine residue and diphosphodiester to a
nucleotide; or peptides with about 31 amino acid residues capable of
stimulating production of interleukin-8 in cultured cells; or peptides
with about 31 amino acid residues capable of stimulating production of
monocyte chemotactic protein 1 in cultured cells. The peptides are useful
for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
invention.
XX
SQ Sequence 13 AA;
Query Match 36.4%; Score 8; DB 23; Length 13;
Best Local Similarity 100.0%; Pred.No. 0.14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PORDMPIQ 22
DB 6 PORDMPIQ 13

RESULT 15
AAU83304
ID AAU83304 standard; Peptide; 13 AA.
XX
AC AAU83304;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #22.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
PN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.

```



QY 15 PORDMPIQ 22  
 Db 4 PORDMPIQ 11

RESULT 18  
 AAU83310  
 ID AAU83310 standard; Peptide; 14 AA.  
 XX  
 AC AAU83310;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #28.  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 14 AA;  
 XX

Query Match 36.4%; Score 8; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PORDMPIQ 22  
 Db 4 PORDMPIQ 11

RESULT 19  
 AAU83315  
 ID AAU83315 standard; Peptide; 14 AA.  
 XX  
 AC AAU83315;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #33.  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 14 AA;  
 XX

Query Match 36.4%; Score 8; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 0.15;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PORDMPIQ 22  
 Db 5 PORDMPIQ 12

RESULT 20  
 AAU83317  
 ID AAU83317 standard; Peptide; 14 AA.  
 XX  
 AC AAU83317;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #35.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;







XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

SQ Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22

Db 7 PQRDMPIQ 14

RESULT 26

AAU83324

ID AAU83324 standard; Peptide; 15 AA.

XX AC AAU83324;

DT 23-APR-2002 (first entry)

DE Antiviral composition peptide-A, fragment #42.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

OS Synthetic.

XX US2002004579-A1.

PN 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

PF 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA Friedland B, Hirschman SZ, Taraporewala IB;

PI WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and  
 CC stimulating the immune system -

PS Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22

Db 5 PQRDMPIQ 12

RESULT 27

AAU83326

ID AAU83326 standard; Peptide; 15 AA.

XX AC AAU83326;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #44.

XX Virucide; Immunostimulant; interleukin-8; viral infection;

KW monocyte chemotactic protein 1; immune system.

OS Synthetic.

XX US2002004579-A1.

PN 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

PF 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

PA Friedland B, Hirschman SZ, Taraporewala IB;

PI WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and  
 CC stimulating the immune system -

PS Disclosure; Page 8; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

SQ Sequence 15 AA;

Query Match 36.4%; Score 8; DB 23; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PQRDMPIQ 22

Db 4 PQRDMPIQ 11

RESULT 28

AAU83332

ID AAU83332 standard; Peptide; 15 AA.

XX AC AAU83332;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #50.

XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocytic chemotactic protein 1; immune system.  
 XX Synthetic.  
 XX US2002004579-A1.  
 XX 10-JAN-2002.  
 XX 17-JAN-2001; 2001US-0764017.  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX Disclosure; Page 8; 37pp; English.  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocytic chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX Sequence 15 AA;  
 XX  
 XX Query Match 36.4%; Score 8; DB 23; Length 15;  
 XX Best Local Similarity 100.0%; Pred. No. 0.16;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 PORDMPIQ 22  
 Db |||||  
 2 PORDMPIQ 9  
 RESULT 29  
 AAU83330  
 ID AAU83330 standard; Peptide; 16 AA.  
 XX AC AAU83330;  
 XX 23-APR-2002 (first entry)  
 XX Antiviral composition peptide-A, fragment #48.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocytic chemotactic protein 1; immune system.  
 XX Synthetic.  
 XX US2002004579-A1.  
 XX 10-JAN-2002.  
 XX 17-JAN-2001; 2001US-0764017.  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX Disclosure; Page 8; 37pp; English.  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocytic chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX Sequence 16 AA;  
 XX  
 XX Query Match 36.4%; Score 8; DB 23; Length 16;  
 XX Best Local Similarity 100.0%; Pred. No. 0.17;  
 XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 KVLVPVQK 12  
 Db |||||  
 1 KVLVPVQK 8  
 RESULT 30  
 AAU83333  
 ID AAU83333 standard; Peptide; 16 AA.  
 XX AC AAU83333;  
 XX 23-APR-2002 (first entry)  
 XX Antiviral composition peptide-A, fragment #51.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocytic chemotactic protein 1; immune system.  
 XX Synthetic.  
 XX US2002004579-A1.  
 XX 10-JAN-2002.  
 XX 17-JAN-2001; 2001US-0764017.  
 XX 22-OCT-1996; 96US-0735236.  
 XX 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX Disclosure; Page 8; 37pp; English.  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocytic chemotactic protein 1 in cultured cells; or peptides  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of

CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPQ 22  
 |||||  
 Db 7 PQDMPQ 14

RESULT 31

AAU83336  
 ID AAU83336 standard; Peptide; 16 AA.

XX AC AAU83336;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #54.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX EN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and

XX stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPQ 22  
 |||||  
 Db 1 PQDMPQ 8

RESULT 32

AAU83337

ID AAU83337 standard; Peptide; 16 AA.

XX AC AAU83337;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #55.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX EN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and  
 XX stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX SQ Sequence 16 AA;

Query Match 36.4%; Score 8; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 0.17;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PQDMPQ 22  
 |||||  
 Db 4 PQDMPQ 11

RESULT 33

AAU83339

ID AAU83339 standard; Peptide; 16 AA.

XX AC AAU83339;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #57.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;

XX KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX EN US2002004579-A1.

XX PD

XX 10-JAN-2002.  
XX  
XX 17-JAN-2001; 2001US-0764017.  
XX  
XX 22-OCT-1996; 96US-0735236.  
PR  
XX 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX  
XX New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
XX Disclosure; Page 8; 37pp; English.  
XX  
XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
XX Sequence 16 AA;  
SQ  
Query Match 36.4%; Score 8; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 PQRDMPPIQ 22  
Db 3 PQRDMPPIQ 10  
RESULT 34  
AAU83338  
ID AAU83338 standard; Peptide; 17 AA.  
XX  
XX AC AAU83338;  
XX  
XX 23-APR-2002 (first entry)  
DE Antiviral composition peptide-A, fragment #56.  
XX  
XX Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
XX Synthetic.  
XX  
XX US2002004579-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX PF 17-JAN-2001; 2001US-0764017.  
XX  
XX PR 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX  
XX New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -

XX Disclosure; Page 8; 37pp; English.  
XX  
XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
XX Sequence 17 AA;  
SQ  
Query Match 36.4%; Score 8; DB 23; Length 17;  
Best Local Similarity 100.0%; Pred. No. 0.18;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 PQRDMPPIQ 22  
Db 7 PQRDMPPIQ 14  
RESULT 35  
AAU83341  
ID AAU83341 standard; Peptide; 19 AA.  
XX  
XX AC AAU83341;  
XX  
XX 23-APR-2002 (first entry)  
DE Antiviral composition peptide-A, fragment #59.  
XX  
XX Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
XX Synthetic.  
XX  
XX US2002004579-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX PF 17-JAN-2001; 2001US-0764017.  
XX  
XX PR 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX  
XX New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
XX Disclosure; Page 8; 37pp; English.  
XX  
XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
XX Sequence 19 AA;  
SQ

Query Match 36.4%; Score 8; DB 23; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 0.2;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PORDMPTQ 22  
 |||||  
 Db 5 PORDMPTQ 12

RESULT 36  
 AAW04273  
 ID AAW04273 standard; peptide; 7 AA.  
 XX  
 AC AAW04273;  
 XX  
 DT 06-JUN-1997 (first entry)  
 XX  
 DE Milk derived anti-hypertensive peptide.  
 XX  
 KW Anti-hypertensive; fermentation; animal milk; Lactobacillus;  
 KW microorganism; digestion; protease; reduction; blood pressure.  
 XX  
 OS Mammalian spp.  
 XX  
 PN EP737690-A2.  
 XX  
 PD 16-OCT-1996.  
 XX  
 PF 10-APR-1996; 96EP-0302522.  
 XX  
 PR 10-APR-1995; 95JP-0084247.  
 XX  
 PA (CALV ) CALPIS FOOD IND CO LTD.  
 XX  
 PI Maeno M;  
 XX  
 DR WPI; 1996-457284/46.  
 XX

XX Antihypertensive compans. derived from milk - by fermentation or  
 PT protease digestion  
 PT  
 XX Claim 1; Page 9; 10pp; English.  
 PS  
 CC The present anti-hypertensive (AH) peptide was prepared by  
 CC fermenting an animal milk starting material with a Lactobacillus  
 CC microorganism, especially L. helveticus, L. delbrueckii subspecies  
 CC bulgaricus or L. acidophilus, or digesting it with a protease at  
 CC 20-50 degrees C for 3-30 hours, obtaining an eluent by  
 CC ultrafiltration and then fractionating the eluent by reverse phase  
 CC HPLC. An AH composition comprising the peptide is safe and reduces  
 CC blood pressure at low oral doses, e.g. 0.2-10, preferably  
 CC 1 mg/kg/day or 5-20 ml/kg/day when ingested as a yogurt. The change  
 CC in the systolic blood pressure of spontaneously hypertensive rats  
 CC treated intragastrically with 1 mg/kg of body weight of the present  
 CC AH peptide was minus 24 +/- 7.8 mmHg.  
 XX

SQ Sequence 7 AA;  
 Query Match 31.8%; Score 7; DB 17; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLFPVQ 11  
 |||||  
 Db 1 KVLFPVQ 7

RESULT 37  
 AAU83284  
 ID AAU83284 standard; Peptide; 8 AA.  
 XX  
 AC AAU83284;  
 XX

DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #2.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 FI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX  
 DR WPI; 2002-163727/21.  
 XX  
 PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 PS Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 8 AA;

Query Match 31.8%; Score 7; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPQKAVP 15  
 |||||  
 Db 1 VPQKAVP 7

RESULT 38  
 AAU83295  
 ID AAU83295 standard; Peptide; 11 AA.  
 XX  
 AC AAU83295;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #13.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PR 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.

PR 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 XX Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 11 AA;  
 SQ  
 Query Match 31.8%; Score 7; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VPQKAVP 15  
 Db |||||  
 1 VPQKAVP 7  
 RESULT 39  
 AAU83312  
 ID AAU83312 standard; Peptide; 12 AA.  
 XX  
 AC AAU83312;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #30.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 XX Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a

CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 12 AA;  
 SQ  
 Query Match 31.8%; Score 7; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 16 QRDMPFIQ 22  
 Db |||||  
 1 QRDMPFIQ 7  
 RESULT 40  
 AAU83298  
 ID AAU83298 standard; Peptide; 13 AA.  
 XX  
 AC AAU83298;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #16.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX  
 XX Disclosure; Page 7; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 31.8%; Score 7; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 9 VPQKAVP 15  
 Db |||||



Db 1 VPQKAVP 7

RESULT 41  
AAU83314  
ID AAU83314 standard; Peptide; 13 AA.  
AC AAU83314;  
XX  
XX 23-APR-2002 (first entry)  
XX  
XX Antiviral composition peptide-A, fragment #32.  
XX  
XX Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
XX Synthetic.  
XX  
XX US2002004579-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 17-JAN-2001; 2001US-0764017.  
XX  
XX 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX  
XX New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
XX Disclosure; Page 8; 37pp; English.  
XX  
XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
XX Sequence 13 AA;  
SQ  
Query Match 31.8%; Score 7; DB 23; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.5;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 QRDWPIQ 22  
Db 1 QRDWPIQ 7

RESULT 42  
AAU83325  
ID AAU83325 standard; Peptide; 14 AA.  
XX  
XX AAU83325;  
XX  
XX 23-APR-2002 (first entry)  
XX  
XX Antiviral composition peptide-A, fragment #43.  
DE Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX

OS Synthetic.  
XX US2002004579-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 17-JAN-2001; 2001US-0764017.  
XX  
XX 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX  
XX New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
XX Disclosure; Page 8; 37pp; English.  
XX  
XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
XX Sequence 14 AA;  
SQ  
Query Match 31.8%; Score 7; DB 23; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 16 QRDWPIQ 22  
Db 1 QRDWPIQ 7

RESULT 43  
AAU83328  
ID AAU83328 standard; Peptide; 14 AA.  
XX  
XX AAU83328;  
XX  
XX 23-APR-2002 (first entry)  
XX  
XX Antiviral composition peptide-A, fragment #46.  
DE Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
XX Synthetic.  
XX  
XX US2002004579-A1.  
XX  
XX 10-JAN-2002.  
XX  
XX 17-JAN-2001; 2001US-0764017.  
XX  
XX 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
XX (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX Friedland B, Hirschman SZ, Taraporewala IB;  
XX WPI; 2002-163727/21.  
XX



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XX 04-MAR-1992; 92JP-0047340.
XX (CALV ) CALPIS SHOKUJIN KOGYO KK.
XX WPI; 1994-089332/11.
XX New polypeptide - used in physiologically active agents having
PT e.g. hypotensive antioxidative and calcium absorption promoting
PT activity
XX
XX Claim 1-2; Page 8; 10pp; Japanese.
XX
XX Sequences (AAR58319-341) are used in conjunction with
CC physiologically active agents showing a property such as
CC hypotensive activity, calcium absorption promoting activity and
CC antioxidative activity. The peptides are non-toxic and can be
CC used in physiologically active agents.
XX
XX Sequence 8 AA;
XX
XX Query Match 27.3%; Score 6; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10
Db 2 KVLVPV 7

RESULT 47
AAR58338
ID AAR58338 standard; peptide; 8 AA.
XX
XX AAR58338;
XX
XX 22-SEP-1994 (first entry)
XX
XX Hypotensive polypeptide.
XX
XX Hypotensive; antioxidative; calcium absorption; salt; food;
XX pharmaceuticals; physiologically active agents.
XX
XX Lactobacillus helveticus.
XX
XX JP06041191-A.
XX
XX 15-FEB-1994.
XX
XX 03-MAR-1993; 93JP-0043047.
XX
XX 04-MAR-1992; 92JP-0047340.
XX
XX (CALV ) CALPIS SHOKUJIN KOGYO KK.
XX
XX WPI; 1994-089332/11.
XX
XX New polypeptide - used in physiologically active agents having
PT e.g. hypotensive antioxidative and calcium absorption promoting
PT activity
XX
XX Claim 1-2; Page 9; 10pp; Japanese.
XX
XX Sequences (AAR58319-341) are used in conjunction with
CC physiologically active agents showing a property such as
CC hypotensive activity, calcium absorption promoting activity and
CC antioxidative activity. The peptides are non-toxic and can be
CC used in physiologically active agents.
XX
XX Sequence 8 AA;
XX
XX Query Match 27.3%; Score 6; DB 15; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;

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Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 RDMPIQ 22
Db 1 RDMPIQ 6

RESULT 48
AAU83288
ID AAU83288 standard; Peptide; 9 AA.
XX
XX AAU83288;
XX
XX 23-APR-2002 (first entry)
XX
XX Antiviral composition peptide-A, fragment #6.
XX
XX Virucide; Immunostimulant; interleukin-8; viral infection;
XX monocyte chemotactic protein 1; immune system.
XX
XX Synthetic.
XX
XX US2002004579-A1.
XX
XX 10-JAN-2002.
XX
XX 17-JAN-2001; 2001US-0764017.
XX
XX 22-OCT-1996; 96US-0735236.
XX
XX 25-JUN-1999; 99US-0344095.
XX
XX (ADVI-) ADVANCED VIRAL RES CORP.
XX
XX Friedland B, Hirschman SZ, Taraporewala IB;
XX
XX WPI; 2002-163727/21.
XX
XX New peptides compositions, useful for treating viral infections and
PT stimulating the immune system -
XX
XX Disclosure; Page 7; 37pp; English.
XX
XX The invention relates to a new peptide composition comprising a specified
CC peptide sequence. The composition comprises nucleotide-peptide comprising
CC a peptide linked through a serine residue and diphosphodiester to a
CC nucleotide; or peptides with about 31 amino acid residues capable of
CC stimulating production of interleukin-8 in cultured cells; or peptides
CC with about 31 amino acid residues capable of stimulating production of
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
CC for treating viral infections and stimulating the immune system. the
CC AAU83282-AAU83401 represent peptides used in the composition of the
CC invention.
XX
XX Sequence 9 AA;
XX
XX Query Match 27.3%; Score 6; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKAVP 15
Db 1 PQKAVP 6

RESULT 49
AAU83289
ID AAU83289 standard; Peptide; 9 AA.
XX
XX AAU83289;
XX
XX 23-APR-2002 (first entry)
XX
XX Antiviral composition peptide-A, fragment #7.
DE

```



CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX SQ Sequence 10 AA;  
 DT

Query Match 27.3%; Score 6; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKAVP 15  
 |||||  
 Db 1 PQKAVP 6

## RESULT 52

AAU83296  
 ID AAU83296 standard; Peptide; 11 AA.

XX AC AAU83296;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #14.

XX KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX PN US2002004579-A1.

XX XX 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX PS New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -

XX XX Disclosure; Page 7; 37pp; English.

CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX SQ Sequence 11 AA;

Query Match 27.3%; Score 6; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKAVP 15  
 |||||  
 Db 1 PQKAVP 6

## RESULT 53

AAU80311  
 ID AAR80311 standard; peptide; 14 AA.

XX AC AAR80311;

XX DT 17-APR-1996 (first entry)

XX DE Bovine casein isopeptide substrate consensus sequence.

XX KW Pendant group; repeating unit; enzyme recognition site; sealant; elastin;  
 KW enzymatic cross-linking; biocompatible material; structural integrity;  
 KW medical adhesive; wound closure; tissue repair.

XX OS Synthetic.

XX PN WO9523611-A1.

XX PD 08-SEP-1995.

XX PF 03-MAR-1995; 95WO-US02728.

XX PR 03-MAR-1994; 94US-0205518.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;

XX DR WPI; 1995-320413/41.

XX PT Protein polymers comprising repeating units and sequences - capable  
 PT of enzyme-catalysed covalent bond formation useful as a  
 PT biocompatible material for wound closure and tissue repair

XX PS Disclosure; Page 16; 138pp; English.

XX CC The sequence of the isopeptide substrate motif from bovine casein. The  
 CC sequence corresponds to residues 162-175 of the protein. The motif can  
 CC be used in a novel polymer comprising two spaced enzyme recognition site  
 CC and may contain repetitive units of 3-8 amino acids with at least two  
 CC pendant groups. The polymers contg. the multimeric repeat sequence can  
 CC be used as substrates for enzymatic cross-linking. The polymers can be  
 CC used in biological systems where in situ formation of a biocompatible  
 CC material with structural integrity is required e.g. as medical adhesives  
 CC and sealants or for wound closure or tissue repair.

XX SQ Sequence 14 AA;

Query Match 27.3%; Score 6; DB 16; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
 |||||  
 Db 8 KVLVPV 13

## RESULT 54

AAU80314  
 ID AAR80314 standard; peptide; 14 AA.

XX AC AAR80314;

XX DT 17-APR-1996 (first entry)

XX DE Synthetic peptide contg. Factor VIIa cross-linking sequence.

XX KW Pendant group; repeating unit; enzyme recognition site; sealant; elastin;  
 KW enzymatic cross-linking; biocompatible material; structural integrity;  
 KW medical adhesive; wound closure; tissue repair.

XX OS Synthetic.

```

FN WO9523611-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US02728.
XX
PR 03-MAR-1994; 94US-0205518.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1995-320413/41.
XX
PT Protein polymers comprising repeating units and sequences - capable
PT of enzyme-catalysed covalent bond formation useful as a
PT biocompatible material for wound closure and tissue repair
XX
PS Example 2; Page 33; 138pp; English.
XX
CC The sequence of a synthetic peptide corresponding to the bovine B-casein
CC residues 162-175. The sequence is known to be a factor VIIIa
CC cross-linking substrate. The motif can be used in a novel polymer
CC comprising two spaced enzyme recognition site and may contain repetitive
CC units of 3-8 amino acids with at least two pendent groups. The polymers
CC contg. the multimeric repeat sequence can be used as substrates for
CC enzymatic cross-linking. The polymers can be used in biological systems
CC where in situ formation of a biocompatible material with structural
CC integrity is required e.g. as medical adhesives and sealants or for wound
CC closure or tissue repair.
XX
SQ Sequence 14 AA;

Query Match 27.3%; Score 6; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
DB 8 KVLVPV 13

RESULT 55
AAW49705
ID AAW49705 standard; Peptide; 14 AA.
XX
AC AAW49705;
XX
DT 25-MAR-2003 (updated)
DT 12-OCT-1998 (first entry)
XX
DE Casein consensus for enzyme-catalysed isopeptide formation.
XX
KW Protein polymer; cross-linking; casein; adhesive; sealant;
KW wound healing.
XX
OS Bos taurus.
XX
PN US5773577-A.
XX
PD 30-JUN-1998.
XX
PF 02-MAR-1995; 95US-0397633.
XX
PR 02-MAR-1995; 95US-0397633.
PR 03-MAR-1994; 94US-0205518.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1998-387091/33.
XX

PT New recombinant protein polymers - containing naturally occurring
PT repetitive units for crosslinking by enzymes, useful as medical
PT adhesives and sealants, depots and matrices
XX
XX Disclosure; Column 9; 70pp; English.
XX
XX This peptide comprises a bovine casein consensus sequence (amino
XX acid residues 162-175) for enzyme-catalysed isopeptide formation.
XX A claimed recombinant protein polymer of 15-250 kDa comprises a
XX repetitive amino acid backbone of repetitive units having a
XX collagen, fibroin, elastin or keratin motif and at least 2 enzyme
XX recognition sequences comprising a glutamine capable of
XX enzyme-catalysed isopeptide formation, separated by an intervening
XX sequence of at least 25 amino acids. Such polymers are capable of
XX covalent crosslinking by enzymatic reaction to form products which
XX set quickly and have good adhesive properties and high strength.
XX The compositions can be used as medical adhesives and sealants, in
XX the closure of wounds and repair of damaged tissues, prosthesis
XX coatings, drug depots, and matrices for the transplantation of
XX cells. They can also be used in assays for analytes.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 14 AA;

Query Match 27.3%; Score 6; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
DB 8 KVLVPV 13

RESULT 56
AAR80352
ID AAR80352 standard; peptide; 15 AA.
XX
AC AAR80352;
XX
DT 19-APR-1996 (first entry)
XX
DE Protein polymeric adhesion substrate glutamine donor peptide #2.
XX
KW Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;
KW enzymatic cross-linking; biocompatible material; structural integrity;
KW medical adhesive; wound closure; tissue repair; transglutaminase;
KW protein polymer adhesive substrate.
XX
OS Synthetic.
XX
PN WO9523611-A1.
XX
PD 08-SEP-1995.
XX
PF 03-MAR-1995; 95WO-US02728.
XX
PR 03-MAR-1994; 94US-0205518.
XX
PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
PI Cappello J;
XX
DR WPI; 1995-320413/41.
XX
PT Protein polymers comprising repeating units and sequences - capable
PT of enzyme-catalysed covalent bond formation useful as a
PT biocompatible material for wound closure and tissue repair
XX
XX Example 9; Page 75; 138pp; English.
XX
XX The peptides AAR80351-70 are examples of glutamine donor peptides which
XX can be used to generate protein polymeric adhesion substrate (PPAS)
XX contg. repeats of non-fibrin cross-linking donor peptide sequences (see

```

CC AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.

XX SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
| | | | |  
Db 9 KVLVPV 14

RESULT 57  
AAR80355  
ID AAR80355 standard; peptide; 15 AA.

XX AC AAR80355;

XX DT 19-APR-1996 (first entry)

XX DE Protein polymeric adhesion substrate glutamine donor peptide #5.

XX KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase; protein polymer adhesive substrate.

XX OS Synthetic.

XX PN WO9523611-A1.

XX PD 08-SEP-1995.

XX PF 03-MAR-1995; 95WO-US02728.

XX PR 03-MAR-1994; 94US-0205518.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;

XX DR WPI; 1995-320413/41.

XX PT Protein polymers comprising repeating units and sequences - capable of enzyme-catalysed covalent bond formation useful as a biocompatible material for wound closure and tissue repair

XX PS Example 9; Page 75; 138pp; English.

XX CC The peptides AAR80351-70 are examples of glutamine donor peptides which can be used to generate protein polymeric adhesion substrate (PPAS) contg. repeats of non-fibrin cross-linking donor peptide sequences (see AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used as substrates in enzymatic cross-linking reactions catalysed by a transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.

XX SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 16; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
| | | | |

Db 9 KVLVPV 14

RESULT 58

AAR49740

ID AAR49740 standard; Peptide; 15 AA.

XX AC AAR49740;

XX DT 25-MAR-2003 (updated)

XX DT 12-OCT-1998 (first entry)

XX DE Glutamine donor peptide.

XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.

XX OS Synthetic.

XX PN US5773577-A.

XX PD 30-JUN-1998.

XX PF 02-MAR-1995; 95US-0397633.

XX PR 02-MAR-1995; 95US-0397633.

XX PR 03-MAR-1994; 94US-0205518.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J;

XX DR WPI; 1998-387091/33.

XX PT New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices

XX PS Example 9; Column 48; 70pp; English.

XX CC This is an example of a glutamine donor peptide that can be utilised in novel recombinant protein polymers of the invention. Such polymers (see AAR49710-28) typically comprise a repetitive amino acid backbone of repetitive units having a collagen, fibroin, elastin or keratin motif and at least 2 enzyme recognition sequences comprising a glutamine and/or lysine capable of catalysed isopeptide formation. The polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high strength. They can be used as medical adhesives and sealants, in the closure of wounds and repair of damaged tissues, prosthesis coatings, drug depots, and matrices for the transplantation of cells.

XX CC (Updated on 25-MAR-2003 to correct PF field.)

XX SQ Sequence 15 AA;

Query Match 27.3%; Score 6; DB 19; Length 15;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
| | | | |

Db 9 KVLVPV 14

RESULT 59

AAU83319

ID AAU83319 standard; Peptide; 15 AA.

XX AC AAU83319;

XX DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #37.

XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.  
 XX  
 PI Friedland B, Hirschman SZ, Taraporewala IB;  
 XX WPI; 2002-163727/21.  
 DR  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 27.3%; Score 6; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 17;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 POKAVP 15  
 Db |||||  
 3 POKAVP 8  
 RESULT 60  
 AAU83335  
 ID AAU83335 standard; Peptide; 16 AA.  
 XX  
 AC AAU83335;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #53.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX Synthetic.  
 OS  
 PN US2002004579-A1.  
 PD 10-JAN-2002.  
 XX  
 PF 17-JAN-2001; 2001US-0764017.  
 XX  
 PR 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 PA (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 DR  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 XX Disclosure; Page 8; 37pp; English.  
 XX  
 CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 SQ Sequence 16 AA;  
 Query Match 27.3%; Score 6; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 18;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 17 RDMPIQ 22  
 Db |||||  
 1 RDMPIQ 6  
 RESULT 61  
 AAR58332  
 ID AAR58332 standard; peptide; 18 AA.  
 XX  
 AC AAR58332;  
 XX  
 DT 22-SEP-1994 (first entry)  
 XX  
 DE Hypotensive polypeptide.  
 XX  
 KW Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 XX  
 OS Lactobacillus helveticus.  
 XX  
 PN JP06041191-A.  
 XX  
 PD 15-FEB-1994.  
 XX  
 PF 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 PA (CALV ) CALPIS SHOKUHN KOGYO KK.  
 XX  
 DR WPI; 1994-089332/11.  
 XX  
 PT New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxidative and calcium absorption promoting  
 PT activity  
 XX  
 PS Claim 1-2; Page 8; 10pp; Japanese.  
 XX  
 CC Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX  
 SQ Sequence 18 AA;



```
Query Match      27.3%; Score 6; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPV 10
   |||||
Db 12 KVLVPV 17

RESULT 62
AAU83285
ID AAU83285 standard; Peptide; 8 AA.
XX
AC AAU83285;
XX
DT 23-APR-2002 (first entry)
XX
DE Antiviral composition peptide-A, fragment #3.
XX
KW Virucide; Immunostimulant; interleukin-8; viral infection;
KW monocyte chemotactic protein 1; immune system.
XX
OS Synthetic.
XX
FN US2002004579-A1.
XX
PD 10-JAN-2002.
XX
PF 17-JAN-2001; 2001US-0764017.
XX
PR 22-OCT-1996; 96US-0735236.
PR 25-JUN-1999; 99US-0344095.
XX
PA (ADVI-) ADVANCED VIRAL RES CORP.
XX
PI Friedland B, Hirschman SZ, Taraporewala IB;
XX
DR WPI; 2002-163727/21.
XX
New peptides compositions, useful for treating viral infections and
stimulating the immune system -
PS Disclosure; Page 7; 37pp; English.
XX
The invention relates to a new peptide composition comprising a specified
peptide sequence. The composition comprises nucleotide-peptide comprising
a peptide linked through a serine residue and diphosphodiester to a
nucleotide; or peptides with about 31 amino acid residues capable of
stimulating production of interleukin-8 in cultured cells; or peptides
with about 31 amino acid residues capable of stimulating production of
monocyte chemotactic protein 1 in cultured cells. The peptides are useful
for treating viral infections and stimulating the immune system.
CC AAU83282-AAU83401 represent peptides used in the composition of the
invention.
XX
SQ Sequence 8 AA;

Query Match      22.7%; Score 5; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMPIQ 22
   |||||
Db 1 DMPIQ 5

RESULT 63
ABG67718
ID ABG67718 standard; Peptide; 9 AA.
XX
AC ABG67718;
XX
DT 07-OCT-2002 (first entry)
XX

Human ADPI tryptic digest peptide #427.
Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
Alzheimer's disease-associated feature; neuroprotective;
Alzheimer's disease-associated protein isoform; nontropic;
ADPI tryptic digest peptide.
Homo sapiens.
WO200246767-A2.
13-JUN-2002.
29-NOV-2001; 2001WO-GB05289.
08-DEC-2000; 2000US-254431P.
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
Herath HMAC, Parekh RB, Rohlf C;
WPI; 2002-508575/54.
Screening, diagnosis or prognosis of Alzheimer's disease in subject,
comprises detecting Alzheimer's disease-associated features or
Alzheimer's disease-associated protein isoforms in brain tissue
from the subject -
Claim 7; Page 70; 427pp; English.
The present invention relates to methods and compositions for the
screening, diagnosis or prognosis of Alzheimer's disease (AD) in
a subject. The method comprises analysing a sample of brain tissue
from a subject by 2D electrophoresis to generate a 2D array of
Alzheimer's disease-associated features (ADFs), whose relative
abundance correlates with the presence, absence, stage or severity of
AD and comparing the abundance of each feature with the abundance of
that chosen feature in brain tissue from persons free from AD. The
invention also describes Alzheimer's disease-associated protein
isoforms (ADPIs) detectable in brain tissue. The methods and
compositions of the invention are useful for the screening, diagnosis
or prognosis of AD in a subject, for determining the stage or severity
of AD in a subject, for identifying a subject at risk of developing AD,
or for monitoring the effect of therapy administered to a subject
having AD. Antibodies capable of binding to ADPIs are useful for
treating or preventing AD, and for determining the efficacy of a given
treatment regime. An agent that modulates the activity of ADPI is
useful in the manufacture of a medicament for the treatment or
prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
tryptic digest peptides.
Sequence 9 AA;

Query Match      22.7%; Score 5; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVPOR 17
   |||||
Db 5 AVPOR 9

RESULT 64
AAW25911
ID AAW25911 standard; peptide; 10 AA.
XX
AC AAW25911;
XX
DT 04-NOV-1997 (first entry)
XX
DE Beta-2-microglobulin cryptic epitope 10 as anti-HIV peptide.
XX
```

KW Beta-2-microglobulin; cryptic; epitope; human immunodeficiency virus;  
 KW HIV; multiplication; release; determinant; antigenic; extracellular; CMV;  
 KW infectious agent; intracellular stage; host; reproductive cycle; vaccine;  
 KW intracellular; parasite; enveloped virus; mutation; cytomegalovirus; HPV.  
 XX Synthetic.  
 OS  
 PN WO9702344-A2.  
 XX  
 PD 23-JAN-1997.  
 XX  
 XX 28-JUN-1996; 96WO-FR01006.  
 PF  
 XX 30-JUN-1995; 95FR-0007914.  
 PR  
 XX (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.  
 PA  
 XX Chermann J, Galea P, Le Contel C;  
 PI  
 XX WPI; 1997-108957/10.  
 DR  
 XX Vaccine against diseases where the pathogen has an intracellular  
 PT stage - contains cryptic epitope of component carried with the  
 PT pathogen when it migrates out of the cell, esp. for treatment or  
 PT prevention of HIV infection  
 PT  
 PS Claim 4; Page 35; 60pp; French.  
 XX  
 CC Peptides AAW25902-23 represent peptides derived from the  
 CC beta-2-microglobulin protein which act as cryptic epitopes and are  
 CC revealed esp. when HIV multiplies and is released from an infected cell.  
 CC The cryptic epitope is preferably on a host cell determinant but only  
 CC become antigenic when they are carried extracellularly by the released  
 CC infectious agent. The cryptic epitopes are used in a method for the  
 CC treatment and/or prevention of infectious diseases caused by an  
 CC infectious agent which has at least one intracellular stage in the host  
 CC during its reproductive cycle. The method is used to protect against  
 CC intracellular parasites or enveloped viruses, particularly where these  
 CC are subject to rapid mutation, esp. CMV, HPV or esp. HIV.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 22.7%; Score 5; DB 18; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LSQPK 5  
 Db 2 LSQPK 6  
 RESULT 65  
 ABB56257  
 ID ABB56257 standard; Peptide; 10 AA.  
 XX  
 AC ABB56257;  
 XX  
 DT 15-FEB-2002 (first entry)  
 DE  
 DE Vascular dementia-associated protein isoform (VPI) 457.  
 XX  
 KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;  
 KW diagnosis; prognosis; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200169261-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 14-MAR-2001; 2001WO-GB01106.  
 XX  
 PR 15-MAR-2000; 2000GB-0006285.  
 PR

PR 24-NOV-2000; 2000GB-0028734.  
 PR 28-NOV-2000; 2000US-0724391.  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA  
 XX Herath HMAc, Parekh RB, Rohlf C;  
 PI  
 XX WPI; 2001-557937/62.  
 DR  
 XX Screening, diagnosis or prognosis of vascular dementia (VD), useful for  
 PT determining stage of VD and monitoring the effect of VD therapy,  
 PT comprises analysing body fluid by 2-dimensional electrophoresis for  
 PT features correlated with VD -  
 XX  
 PS Claim 6; Page 39; 151pp; English.  
 XX  
 CC The invention relates to screening, diagnosis or prognosis of Vascular  
 CC Dementia (VD) in a subject comprising analysing body fluid from the  
 CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of  
 CC features containing at least one chosen feature whose relative abundance  
 CC correlates with the presence, absence, stage or severity of VD or  
 CC predicts the onset or course of VD, especially detecting in a sample of  
 CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated  
 CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the  
 CC specification. Detecting VD-associated features and VPI is useful for the  
 CC screening, diagnosis or prognosis of VD, for determining the stage or  
 CC severity of VD, for identifying a subject at risk of VD or for  
 CC monitoring the effect of therapy administered to a subject having VD.  
 CC Nucleic acids encoding a VPI or inhibiting the function of a VPI are  
 CC useful for the treatment of VD and for gene therapy.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 22.7%; Score 5; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LSQPK 5  
 Db 6 LSQPK 10  
 RESULT 66  
 AAU68209  
 ID AAU68209 standard; Peptide; 10 AA.  
 XX  
 AC AAU68209;  
 XX  
 DT 16-JAN-2002 (first entry)  
 DE  
 DE Human Breast cancer-associated protein isoform, BPI-39 peptide.  
 XX  
 KW Human; Breast cancer-associated protein isoform; breast cancer;  
 KW immunogen; cytostatic; BPI; tryptic digest peptide.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200171357-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 20-MAR-2001; 2001WO-GB01219.  
 XX  
 PR 20-MAR-2000; 2000GB-0006695.  
 PR  
 PR 24-MAR-2000; 2000GB-0007265.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA  
 XX Herath HMAc, O'Hare MJ, Page MJ, Parekh RB, Waterfield MD;  
 PI  
 XX WPI; 2001-611532/70.  
 DR  
 XX Identifying proteins for clinical screening, diagnosis and prognosis of  
 PT

PT breast cancer, comprises detecting Breast Cancer-Associated Protein  
 PT Isoforms (BPIs) using two-dimensional electrophoresis -  
 XX Claim 9; Page 47; 197pp; English.  
 XX  
 CC The invention relates to diagnosing, determining the stage or severity,  
 CC or identifying the risk of a subject developing cancer (especially  
 CC breast cancer), or monitoring the effect of therapy on a subject with  
 CC cancer, comprising analysing a test sample using two-dimensional  
 CC electrophoresis and detecting Breast Cancer-Associated Protein  
 CC Isoforms (BPIs). The methods disclosed are used for the diagnosis and  
 CC prognosis of breast cancer, for determining the severity of breast  
 CC cancer, and for identifying a subject at risk of developing breast  
 CC cancer, and monitoring the effect of therapy administered to a subject.  
 CC Antibodies raised against the binding domain of a BPI, the binding domain  
 CC of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits  
 CC the function of a BPI can be incorporated into a pharmaceutical  
 CC composition for treating or preventing breast cancer. The methods use  
 CC sensitive and specific biomarkers provide early diagnosis of breast  
 CC cancer, and the compositions are more potent, specific, and has a more  
 CC rapid effect with fewer side effects than other prior art methods.  
 CC The present sequence is a tryptic digest peptide from a BPI of the  
 CC invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 22.7%; Score 5; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LSQPK 5  
 DB 6 LSQPK 10  
 |||||  
 RESULT 67  
 AAU68513  
 ID AAU68513 standard; Peptide; 10 AA.  
 XX  
 AC AAU68513;  
 XX  
 DT 16-JAN-2002 (first entry)  
 XX  
 DE Human Expression reference protein isoform, ERPI-5 peptide.  
 XX  
 KW Human; Breast cancer-associated protein isoform; breast cancer;  
 KW immunogen; cytostatic; BPI; tryptic digest peptide; ERPI;  
 KW expression reference protein isoform.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200171357-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 20-MAR-2001; 2001WO-GB01219.  
 XX  
 PR 20-MAR-2000; 2000GB-0006695.  
 PR 24-MAR-2000; 2000GB-0007265.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HWAC, O'Hare WJ, Page MJ, Parekh RB, Waterfield MD;  
 XX  
 DR WPI; 2001-611532/70.  
 XX  
 PT Identifying proteins for clinical screening, diagnosis and prognosis of  
 PT breast cancer, comprises detecting Breast Cancer-Associated Protein  
 PT Isoforms (BPIs) using two-dimensional electrophoresis -  
 XX  
 PS Disclosure; Page 59; 197pp; English.  
 XX  
 CC The invention relates to diagnosing, determining the stage or severity,

CC or identifying the risk of a subject developing cancer (especially  
 CC breast cancer), or monitoring the effect of therapy on a subject with  
 CC cancer, comprising analysing a test sample using two-dimensional  
 CC electrophoresis and detecting Breast Cancer-Associated Protein  
 CC Isoforms (BPIs). The methods disclosed are used for the diagnosis and  
 CC prognosis of breast cancer, for determining the severity of breast  
 CC cancer, and for identifying a subject at risk of developing breast  
 CC cancer, and monitoring the effect of therapy administered to a subject.  
 CC Antibodies raised against the binding domain of a BPI, the binding domain  
 CC of a BPI, a nucleic acid encoding a BPI, or a nucleic acid that inhibits  
 CC the function of a BPI can be incorporated into a pharmaceutical  
 CC composition for treating or preventing breast cancer. The methods use  
 CC sensitive and specific biomarkers provide early diagnosis of breast  
 CC cancer, and the compositions are more potent, specific, and has a more  
 CC rapid effect with fewer side effects than other prior art methods.  
 CC The present sequence is a tryptic digest peptide from an ERPI (expression  
 CC reference protein isoform) against which the BPIs of the invention are  
 CC normalised.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 22.7%; Score 5; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LSQPK 5  
 DB 6 LSQPK 10  
 |||||  
 RESULT 68  
 ABG32209  
 ID ABG32209 standard; peptide; 10 AA.  
 XX  
 AC ABG32209;  
 XX  
 DT 05-NOV-2002 (first entry)  
 XX  
 DE Sheep colostrinin derived peptide #3.  
 XX  
 KW Sheep; colostrinin; colostrum; cytokine inducer; antigen; dementia;  
 KW central nervous system disorder; neurological disorder; neurosis;  
 KW mental disorder; psychosis; neurodegenerative disorder;  
 KW Alzheimer's disease; motor neuron disease; immune system disorder;  
 KW acquired immunological deficiency; bacterial infection; viral infection;  
 KW amyloid plaque; dietary supplement; cachexia; weight loss;  
 KW senile dementia; Parkinson's disease; emotional disturbance; depression;  
 KW drug addiction; drug withdrawal.  
 XX  
 OS Ovis aries.  
 XX  
 PN WO200246211-A2.  
 XX  
 PD 13-JUN-2002.  
 XX  
 PF 05-DEC-2001; 2001WO-GB05376.  
 XX  
 PR 06-DEC-2000; 2000GB-0029777.  
 XX  
 PA (REGS-) REGEN THERAPEUTICS PLC.  
 XX  
 PI Georgiades JA;  
 XX  
 DR WPI; 2002-619016/66.  
 XX  
 PT Novel peptides isolated from colostrinin polypeptide, useful for  
 PT treating viral and bacterial infections, disorders of immune system and  
 PT central nervous system e.g., Alzheimer's disease, dementia, and as food  
 PT additive -  
 XX  
 PS Claim 1; Page 8; 16pp; English.  
 XX  
 CC The invention relates to a peptide derived from colostrinin (a colostrum

CC protein known to be a cytokine inducer) substantially entirely consists  
 CC of the peptide sequences appearing as ABG32207-ABG32223. Also included  
 CC are a composition comprising two or more of the peptides in combination  
 CC with a carrier, a dietary supplement comprising an orally ingestible  
 CC combination of the peptide in combination with a carrier and an antibody  
 CC which binds to the peptide, and which is obtainable by using peptide as  
 CC an antigen. The peptide is useful as a medicament for treating chronic  
 CC disorders of central nervous system e.g., neurological disorders and/or  
 CC mental disorders such as psychosis and/or neurosis, dementia,  
 CC neurodegenerative disorders such as Alzheimer's disease, motor  
 CC neuron disease, chronic disorders of immune system, diseases  
 CC with bacterial and viral etiology, acquired immunological deficiencies,  
 CC chronic bacterial, viral infections. The peptide is also useful for  
 CC treating diseases characterised by presence of amyloid plaque. The  
 CC peptide is also useful as a dietary supplement for babies, small  
 CC children, adults who have been subjected to chemotherapy and/or  
 CC adults who have suffered from cachexia or weight loss due to chronic  
 CC disease. The peptide is also useful for treating senile dementia,  
 CC Parkinson's disease, emotional disturbances and depression. The peptides  
 CC may also be used as an auxiliary withdrawal treatment for drug addicts,  
 CC after a period of detoxification, and in persons dependent on stimulants.  
 CC The present sequence is a colostrin derived peptide of the invention.

XX Sequence 10 AA;

Query Match 22.7%; Score 5; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 9  
 |||||  
 Db 6 KVLVP 10

# RESULT 69

ABBB4035  
 ID ABBB4035 standard; peptide; 10 AA.

AC ABBB4035;

DT 21-AUG-2002 (first entry)

XX Transglutaminase inhibitory peptide cr type #5.

XX Transglutaminase inhibitor; Factor XIII inhibitor; XIIIa inhibitor;  
 KW ophthalmological; antiinflammatory; antirheumatic; antiarthritic;  
 KW thrombolytic; neuroprotective; nootropic; antiseborrheic; dermatological;  
 KW cystostatic; anti-HIV; antipsoriatic; cataract; inflammatory disease;  
 KW arthritis; thrombosis; Alzheimer's disease; Huntington's chorea;  
 KW acne; cancer; HIV infection; psoriasis.

XX Unidentified.

OS WO200236798-A2.

PN 10-MAY-2002.

PD 02-NOV-2001; 2001WO-EF12727.

PF 03-NOV-2000; 2000DE-1054687.

PR (NZYM-) N ZYME BIOTEC GMBH.

PA Fuchsbauser H, Pasternack R, Zotzel J;

PI WPI; 2002-444364/47.

XX New amino acid or peptide derivatives or analogs, are selective  
 PT transglutaminase inhibitors useful e.g. for treating cataract,  
 PT inflammatory diseases, rheumatoid arthritis, thrombosis, Alzheimer's  
 PT disease and cancer  
 XX Disclosure; Page 13; 44pp; German.

XX This invention describes novel amino acid or peptide derivatives or  
 CC analogues (I), containing a modified side-chain (e.g. containing a formyl  
 CC group) which are transglutaminase inhibitors and Factor XIII/XIIIa  
 CC inhibitors. The products of the invention have ophthalmological,  
 CC antiinflammatory, antirheumatic, antiarthritic, thrombolytic,  
 CC neuroprotective, nootropic, antiseborrheic, dermatological, cystostatic,  
 CC anti-HIV and antipsoriatic activity. (I) are transglutaminase inhibitors,  
 CC especially inhibitors of crosslinking of proteins or peptides  
 CC (specifically fibrin and/or alpha 2-plasmin inhibitor), incorporation of  
 CC primary amines in proteins and peptides, hydrolysis of the  
 CC gamma-carboxamide group of glutamine residues bound in proteins or  
 CC peptides, blood factor XIII/XIIIa and mammalian, human, tissue, liver,  
 CC brain, eye lens, keratinocyte, epidermal, prostate, plant, parasitic  
 CC and/or bacterial transglutaminases. The products of the invention can be  
 CC used for treating cataract, inflammatory diseases, rheumatoid arthritis,  
 CC chronic arthritis, thrombosis, Alzheimer's disease, Huntington's chorea,  
 CC acne, cancer (by induction of apoptosis), HIV infections and psoriasis.  
 CC (I) Are targeted and specific transglutaminase inhibitors, which can  
 CC inhibit a specific type of transglutaminase in the human or animal body  
 CC without affecting other transglutaminases. ABBB4001-ABBB4049 represent  
 CC transglutaminase inhibitors described in the method of the invention.

XX Sequence 10 AA;

Query Match 22.7%; Score 5; DB 23; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 9  
 |||||  
 Db 2 KVLVP 6

# RESULT 70

AAU83300

ID AAU83300 standard; Peptide; 12 AA.

AC AAU83300;

DT 23-APR-2002 (first entry)

XX Antiviral composition peptide-A, fragment #18.

XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX Synthetic.

XX US2002004579-A1.

XX 10-JAN-2002.

XX 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.

XX 25-JUN-1999; 99US-0344095.

XX (ADVI-) ADVANCED VIRAL RES CORP.

XX Friedland B, Hirschman SZ, Taraporewala IB;

XX WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system

XX Disclosure; Page 7; 37pp; English.

XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of

CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX Sequence 12 AA;  
 SQ Query Match 22.7%; Score 5; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 DMPTQ 22  
 |||||  
 Db 1 DMPTQ 5

RESULT 71  
 AAM98483  
 ID AAM98483 standard; Peptide; 13 AA.

XX AC AAM98483;  
 XX DT 24-JAN-2002 (first entry)

XX Human peptide #1758 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US-0173419.

XX PR 27-DEC-2000; 2000US-0173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -

XX Disclosure; Page 4053; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus

CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.

XX Sequence 13 AA;

XX Query Match 22.7%; Score 5; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 KAVPQ 16  
 |||||  
 Db 6 KAVPQ 10

RESULT 72  
 AAM98484  
 ID AAM98484 standard; Peptide; 13 AA.

XX AC AAM98484;

XX DT 24-JAN-2002 (first entry)

XX Human peptide #1759 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;  
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;  
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;  
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;  
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;  
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;  
 KW multifactorial disease; autoimmune disease; infection;  
 KW nervous system disease.

XX OS Homo sapiens.

XX PN WO200147944-A2.

XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US35498.

XX PR 28-DEC-1999; 99US-0173419.

XX PR 27-DEC-2000; 2000US-0173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g.  
 PT cancer, autoimmune diseases and infections -

XX Disclosure; Page 4053; 4143pp; English.

XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms.

```

XX SQ Sequence 13 AA;
XX Query Match 22.7%; Score 5; DB 22; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 KAVPQ 16
DB 6 KAVPQ 10

RESULT 73
AAU83309
ID AAU83309 standard; Peptide; 13 AA.
XX AC AAU83309;
XX AC AAU83309;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #27.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX FN US2002004579-A1.
XX PD 10-JAN-2002.
XX PF 17-JAN-2001; 2001US-0764017.
XX PR 22-OCT-1996; 96US-0735236.
XX PR 25-JUN-1999; 99US-0344095.
XX PA (ADVI-) ADVANCED VIRAL RES CORP.
XX PI Friedland B, Hirschman SZ, Taraporewala IB;
XX DR WPI; 2002-163727/21.
XX PT New peptides compositions, useful for treating viral infections and
XX PT stimulating the immune system -
XX PS Disclosure; Page 7; 37pp; English.
XX CC The invention relates to a new peptide composition comprising a specified
XX CC peptide sequence. The composition comprises nucleotide-peptide comprising
XX CC a peptide linked through a serine residue and diphosphodiester to a
XX CC nucleotide; or peptides with about 31 amino acid residues capable of
XX CC stimulating production of interleukin-8 in cultured cells; or peptides
XX CC with about 31 amino acid residues capable of stimulating production of
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful
XX CC for treating viral infections and stimulating the immune system.
XX CC AAU83282-AAU83401 represent peptides used in the composition of the
XX CC invention.
XX SQ Sequence 13 AA;
XX Query Match 22.7%; Score 5; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1.5e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 DMPIQ 22
DB 1 DMPIQ 5

RESULT 74
AAW49741
ID AAW49741 standard; Peptide; 14 AA.
XX

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AC AAW49741;
XX 25-MAR-2003 (updated)
XX DT 12-OCT-1998 (first entry)
XX DE Glutamine donor peptide.
XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.
XX OS Synthetic.
XX FN US5773577-A.
XX PD 30-JUN-1998.
XX PF 02-MAR-1995; 95US-0397633.
XX PR 02-MAR-1995; 95US-0397633.
XX PR 03-MAR-1994; 94US-0205518.
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PI Cappello J;
XX DR WPI; 1998-387091/33.
XX PT New recombinant protein polymers - containing naturally occurring
XX PT repetitive units for crosslinking by enzymes, useful as medical
XX PT adhesives and sealants, depots and matrices
XX PS Example 9; Column 49; 70pp; English.
XX CC This is an example of a glutamine donor peptide that can be
XX CC utilised in novel recombinant protein polymers of the invention.
XX CC Such polymers (see AAW49710-28) typically comprise a repetitive
XX CC amino acid backbone of repetitive units having a collagen, fibroin,
XX CC elastin or keratin motif and at least 2 enzyme recognition
XX CC sequences comprising a glutamine and/or lysine capable of enzyme
XX CC catalysed isopeptide formation. The polymers are capable of
XX CC covalent crosslinking by enzymatic reaction to form products which
XX CC set quickly and have good adhesive properties and high strength.
XX CC They can be used as medical adhesives and sealants, in the closure
XX CC of wounds and repair of damaged tissues, prostheses coatings, drug
XX CC depots, and matrices for the transplantation of cells.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 14 AA;
XX Query Match 22.7%; Score 5; DB 19; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVP 10
DB 9 VLPVP 13

RESULT 75
AAU83316
ID AAU83316 standard; Peptide; 14 AA.
XX AC AAU83316;
XX DT 23-APR-2002 (first entry)
XX DE Antiviral composition peptide-A, fragment #34.
XX KW Virucide; Immunostimulant; interleukin-8; viral infection;
XX KW monocyte chemotactic protein 1; immune system.
XX OS Synthetic.
XX FN US2002004579-A1.

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XX 10-JAN-2002.  
XX  
XX PD  
XX PF 17-JAN-2001; 2001US-0764017.  
XX  
XX PR 22-OCT-1996; 96US-0735236.  
XX PR 25-JUN-1999; 99US-0344095.  
XX  
XX PA (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
XX PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX  
XX DR WPI; 2002-163727/21.  
XX  
XX PT New peptides compositions, useful for treating viral infections and  
XX PT stimulating the immune system -  
XX  
XX PS Disclosure; Page 8; 37pp; English.  
XX  
XX CC The invention relates to a new peptide composition comprising a specified  
XX CC peptide sequence..The composition comprises nucleotide-peptide comprising  
XX CC a peptide linked through a serine residue and diphosphodiester to a  
XX CC nucleotide; or peptides with about 31 amino acid residues capable of  
XX CC stimulating production of interleukin-8 in cultured cells; or peptides  
XX CC with about 31 amino acid residues capable of stimulating production of  
XX CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
XX CC for treating viral infections and stimulating the immune system.  
XX CC AAU83282-AAU83401 represent peptides used in the composition of the  
XX CC invention.  
XX  
XX SQ Sequence 14 AA;  
  
Query Match 22.7%; Score 5; DB 23; Length 14;  
Best Local Similarity 100.0%; Pred.No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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    |||||  
Db 1 DMPIQ 5  
  
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Job time : 57.1512 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 35.3023 Seconds  
(without alignments)  
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Title: US-09-641-801-27

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Minimum DB seq length: 3

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16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	5	22.7	10	11	US-09-827-345-10
3	5	22.7	15	8	US-08-927-939-64
4	5	22.7	15	11	US-09-827-345-3
5	5	22.7	16	12	US-10-161-791-195
6	5	22.7	19	12	US-10-280-833-7
7	4	18.2	5	11	US-09-788-006-138
8	4	18.2	5	11	US-09-788-006-140
9	4	18.2	6	10	US-09-865-018-23
10	4	18.2	6	10	US-09-071-838-278
11	4	18.2	6	15	US-10-029-115-15
12	4	18.2	6	15	US-10-213-512-278
13	4	18.2	7	9	US-09-832-723-16
14	4	18.2	7	11	US-09-827-345-5
15	4	18.2	7	11	US-09-827-345-21
Sequence 8, Appli					
Sequence 10, Appli					
Sequence 64, Appli					
Sequence 3, Appli					
Sequence 19, App					
Sequence 7, Appli					
Sequence 138, App					
Sequence 140, App					
Sequence 23, Appli					
Sequence 278, App					
Sequence 15, Appli					
Sequence 278, App					
Sequence 16, Appli					
Sequence 5, Appli					
Sequence 21, Appli					

4	18.2	7	12	US-10-303-331-16	Sequence 16, Appli
4	18.2	7	12	US-10-286-457-252	Sequence 252, Appli
4	18.2	7	15	US-10-024-123-4	Sequence 4, Appli
4	18.2	7	15	US-10-028-075B-142	Sequence 142, App
4	18.2	7	15	US-10-029-206A-142	Sequence 142, App
4	18.2	8	15	US-10-028-075B-144	Sequence 144, App
4	18.2	8	15	US-10-029-206A-144	Sequence 144, App
4	18.2	9	12	US-10-137-867-210	Sequence 210, App
4	18.2	9	14	US-10-042-202-49	Sequence 49, Appli
4	18.2	10	9	US-09-220-920-111	Sequence 111, App
4	18.2	10	11	US-09-572-404B-1169	Sequence 1169, Ap
4	18.2	10	11	US-09-915-914B-39	Sequence 39, Appli
4	18.2	10	12	US-10-200-708-372	Sequence 372, App
4	18.2	10	12	US-09-573-822C-600	Sequence 600, App
4	18.2	12	9	US-09-347-064-16	Sequence 16, Appli
4	18.2	12	9	US-09-789-561-163	Sequence 163, App
4	18.2	12	10	US-09-911-838-203	Sequence 203, App
4	18.2	12	11	US-09-845-612B-3	Sequence 3, Appli
4	18.2	12	11	US-09-954-385-124	Sequence 124, App
4	18.2	12	11	US-09-954-385-332	Sequence 332, App
4	18.2	12	12	US-10-247-946-2	Sequence 2, Appli
4	18.2	12	12	US-10-247-946-3	Sequence 3, Appli
4	18.2	12	12	US-10-251-526-2	Sequence 2, Appli
4	18.2	12	12	US-10-251-526-3	Sequence 3, Appli
4	18.2	12	12	US-10-354-955-5	Sequence 5, Appli
4	18.2	13	12	US-10-224-999A-794	Sequence 794, App
4	18.2	13	15	US-10-062-710-34	Sequence 34, Appli
4	18.2	14	12	US-10-125-187-19	Sequence 19, Appli
4	18.2	14	12	US-10-125-187-20	Sequence 20, Appli
4	18.2	14	12	US-10-125-187-21	Sequence 21, Appli
4	18.2	14	12	US-10-125-187-53	Sequence 53, Appli
4	18.2	14	12	US-10-125-187-54	Sequence 54, Appli
4	18.2	14	12	US-10-125-187-55	Sequence 55, Appli
4	18.2	14	12	US-10-224-999A-804	Sequence 804, App
4	18.2	14	12	US-10-224-999A-805	Sequence 805, App
4	18.2	15	7	US-08-996-140-9	Sequence 9, Appli
4	18.2	15	10	US-09-908-322-59	Sequence 59, Appli
4	18.2	15	10	US-09-764-176-13	Sequence 13, Appli
4	18.2	15	11	US-09-783-931-59	Sequence 59, Appli
4	18.2	15	12	US-10-212-198-15	Sequence 15, Appli
4	18.2	15	12	US-10-349-023-18	Sequence 18, Appli
4	18.2	15	12	US-10-294-891-17	Sequence 17, Appli
4	18.2	15	12	US-10-224-999A-815	Sequence 815, App
4	18.2	15	12	US-10-224-999A-816	Sequence 816, App
4	18.2	15	12	US-10-224-999A-817	Sequence 817, App
4	18.2	15	12	US-10-161-791-306	Sequence 306, App
4	18.2	15	15	US-10-126-474A-3	Sequence 3, Appli
4	18.2	15	15	US-10-174-105A-149	Sequence 149, App
4	18.2	15	15	US-10-174-105A-175	Sequence 175, App
4	18.2	15	15	US-10-281-652-5	Sequence 5, Appli
4	18.2	16	11	US-09-880-748-2228	Sequence 2228, Ap
4	18.2	16	11	US-09-880-748-2334	Sequence 2334, Ap
4	18.2	16	12	US-10-224-999A-827	Sequence 827, App
4	18.2	16	12	US-10-224-999A-828	Sequence 828, App
4	18.2	16	12	US-10-224-999A-829	Sequence 829, App
4	18.2	16	12	US-10-224-999A-830	Sequence 830, App
4	18.2	16	12	US-10-006-760-61	Sequence 61, Appli
4	18.2	16	15	US-10-043-487-442	Sequence 442, App
4	18.2	17	11	US-09-996-069-30	Sequence 30, Appli
4	18.2	17	11	US-09-996-069-31	Sequence 31, Appli
4	18.2	17	12	US-10-195-730-375	Sequence 375, App
4	18.2	17	12	US-10-224-999A-840	Sequence 840, App
4	18.2	17	12	US-10-224-999A-841	Sequence 841, App
4	18.2	17	12	US-10-224-999A-842	Sequence 842, App
4	18.2	17	12	US-10-224-999A-843	Sequence 843, App
4	18.2	17	12	US-10-224-999A-844	Sequence 844, App
4	18.2	17	12	US-10-224-999A-845	Sequence 845, App
4	18.2	17	12	US-10-029-386-29377	Sequence 29377, A
4	18.2	17	12	US-10-029-386-33100	Sequence 33100, A
4	18.2	17	15	US-10-028-075B-139	Sequence 139, App
4	18.2	17	9	US-09-864-761-48166	Sequence 48166, A
4	18.2	18	10	US-09-554-000-56	Sequence 56, Appli



89                   4   18.2   18   11   US-09-994-595-54                   Sequence 54, Appl  
 90                   4   18.2   18   12   US-10-158-825-131                  Sequence 131, App  
 91                   4   18.2   18   12   US-10-239-701-19                  Sequence 19, App  
 92                   4   18.2   18   12   US-10-239-701-20                  Sequence 20, Appl  
 93                   4   18.2   18   12   US-10-262-435-71                  Sequence 71, Appl  
 94                   4   18.2   18   12   US-10-224-999A-854                  Sequence 854, App  
 95                   4   18.2   18   12   US-10-224-999A-855                  Sequence 855, App  
 96                   4   18.2   18   12   US-10-224-999A-856                  Sequence 856, App  
 97                   4   18.2   18   12   US-10-224-999A-857                  Sequence 857, App  
 98                   4   18.2   18   12   US-10-224-999A-858                  Sequence 858, App  
 99                   4   18.2   18   12   US-10-224-999A-859                  Sequence 859, App  
 100                  4   18.2   18   12   US-10-269-806-14                  Sequence 14, Appl

## ALIGNMENTS

RESULT 1  
 US-10-305-346-8  
 ; Sequence 8, Application US/10305346  
 ; Publication No. US20030130195A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: AMIOT, Jean  
 ; TITLE OF INVENTION: ENZYMIC HYDROLYSATE OF MILK PROTEINS  
 ; FILE REFERENCE: 6013-57"US"-1  
 ; CURRENT APPLICATION NUMBER: US/10/305,346  
 ; PRIOR FILING DATE: 2002-11-27  
 ; PRIOR FILING DATE: 2002-11-26  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 8  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins  
 US-10-305-346-8

Query Match                   31.8%; Score 7; DB 16; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy                   6 VLPVPQK 12  
 Db                   1 VLPVPQK 7  
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RESULT 2  
 US-09-827-345-10  
 ; Sequence 10, Application US/09827345  
 ; Publication No. US20030021800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHERMANN, JEAN-CLAUDE  
 ; APPLICANT: LE CONTEL, CAROLE  
 ; APPLICANT: GALEA, PASCALE  
 ; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN  
 ; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
 ; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
 ; TITLE OF INVENTION: DIAGNOSIS  
 ; FILE REFERENCE: 065691-0216  
 ; CURRENT APPLICATION NUMBER: US/09/827,345  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: 09/599,549  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: PCT/FR96/01006  
 ; PRIOR FILING DATE: 1996-06-28  
 ; PRIOR APPLICATION NUMBER: 08/973,551  
 ; PRIOR FILING DATE: 1998-02-19  
 ; PRIOR APPLICATION NUMBER: FR 95/07914  
 ; PRIOR FILING DATE: 1995-06-30  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: peptide  
 US-09-827-345-10

Query Match                   22.7%; Score 5; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy                   1 LSQPK 5  
 Db                   2 LSQPK 6  
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RESULT 3  
 US-08-927-939-64  
 ; Sequence 64, Application US/08927939  
 ; Publication No. US20010006640A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Grainger, David J.  
 ; APPLICANT: Tatalick, Lauren Marie  
 ; TITLE OF INVENTION: Compounds and methods to inhibit or  
 ; TITLE OF INVENTION: augment an inflammatory response.  
 ; FILE REFERENCE: 295.022US1  
 ; CURRENT APPLICATION NUMBER: US/08/927,939  
 ; CURRENT FILING DATE: 1997-09-11  
 ; NUMBER OF SEQ ID NOS: 83  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 64  
 ; LENGTH: 15  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-08-927-939-64

Query Match                   22.7%; Score 5; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy                   10 POKAV 14  
 Db                   11 POKAV 15  
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RESULT 4  
 US-09-827-345-3  
 ; Sequence 3, Application US/09827345  
 ; Publication No. US20030021800A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHERMANN, JEAN-CLAUDE  
 ; APPLICANT: LE CONTEL, CAROLE  
 ; APPLICANT: GALEA, PASCALE  
 ; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN  
 ; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
 ; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
 ; TITLE OF INVENTION: DIAGNOSIS  
 ; FILE REFERENCE: 065691-0216  
 ; CURRENT APPLICATION NUMBER: US/09/827,345  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: 09/599,549  
 ; PRIOR FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: PCT/FR96/01006  
 ; PRIOR FILING DATE: 1996-06-28  
 ; PRIOR APPLICATION NUMBER: 08/973,551  
 ; PRIOR FILING DATE: 1998-02-19  
 ; PRIOR APPLICATION NUMBER: FR 95/07914  
 ; PRIOR FILING DATE: 1995-06-30  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3

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/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-827-345-3
Query Match      22.7%; Score 5; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQPK 5
Db      9 LSQPK 13

RESULT 5
US-10-161-791-195
; Sequence 195, Application US/10161791
; Publication No. US20030186863A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-195
Query Match      22.7%; Score 5; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVPQR 17
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Db      8 AVPQR 12

RESULT 6
US-10-280-833-7
; Sequence 7, Application US/10280833
; Publication No. US20030195150A1
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Charles Eric
; APPLICANT: Dashper, Stuart Geoffrey
; APPLICANT: O'Brien-Simpson, Neil Martin
; APPLICANT: Talbo, Gert Hoy
; APPLICANT: Malkoski, Marina
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES
; FILE REFERENCE: BDWP-001CON
; CURRENT APPLICATION NUMBER: US/10/280,833
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/554,997
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: PP 0514
; PRIOR FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 19
; TYPE: PRT
; ORGANISM: bovine
US-10-280-833-7
Query Match      22.7%; Score 5; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18 DMPIQ 22
      |||||
Db      1 DMPIQ 5

RESULT 7
US-09-788-006-138
; Sequence 138, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, &
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 138
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-138
Query Match      18.2%; Score 4; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
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Db      2 VLPV 5

RESULT 8
US-09-788-006-140
; Sequence 140, Application US/09788006
; Publication No. US20030036093A1
; GENERAL INFORMATION:
; APPLICANT: Floudas, Christopher A.
```

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; APPLICANT: Klepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-140

Query Match      18.2%; Score 4; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLPV 9
      ||||
Db      1 VLPV 4

RESULT 9
US-09-865-018-23
; Sequence 23, Application US/09865018
; Patent No. US2002011086A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-865-018-23

Query Match      18.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Kiepeis, John L.
; TITLE OF INVENTION: Methods of Ab Initio Prediction of Alpha Helices, Beta Sheets, and
; FILE REFERENCE: PU-0007
; CURRENT APPLICATION NUMBER: US/09/788,006
; CURRENT FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 140
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-788-006-140

Query Match      18.2%; Score 4; DB 11; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 VLPV 9
      ||||
Db      1 VLPV 4

RESULT 9
US-09-865-018-23
; Sequence 23, Application US/09865018
; Patent No. US2002011086A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/865,018
; FILING DATE: 24-May-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,039
; FILING DATE: 09-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-865-018-23

Query Match      18.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 LSQP 4
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Db      1 LSQP 4

RESULT 10
US-09-071-838-278
; Sequence 278, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-0861000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-071-838-278

Query Match      18.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
      ||||
Db      3 PKVL 6

RESULT 11
US-10-029-115-15
; Sequence 15, Application US/10029115
; Publication No. US20030077597A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Fu, Alan C
; APPLICANT: Shen, Mary
; TITLE OF INVENTION: No. US20030077597A1 Germlinal Center Kinase Cell Cycle Protei
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: A-70229/RMS/DHR
; CURRENT APPLICATION NUMBER: US/10/029,115
```

```
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-115-15

Query Match      18.2%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 VPQR 17
Db      3 VPQR 6

RESULT 12
US-10-213-512-278
; Sequence 278, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Vadehari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; FILE REFERENCE: 023070-086110US
; CURRENT APPLICATION NUMBER: US/10/213,512
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: US/09/177,206
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 278
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-10-213-512-278

Query Match      18.2%; Score 4; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 PKVL 7
Db      3 PKVL 6

RESULT 13
US-09-832-723-16
; Sequence 16, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 117

; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-09-832-723-16

Query Match      18.2%; Score 4; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQP 4
Db      1 LSQP 4

RESULT 14
US-09-827-345-5
; Sequence 5, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: GALEA, PASCAL
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: 065691-0216
; CURRENT APPLICATION NUMBER: US/09/827,345
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/599,549
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: PCT/FR96/01006
; PRIOR FILING DATE: 1996-06-28
; PRIOR APPLICATION NUMBER: 08/973,551
; PRIOR FILING DATE: 1998-02-19
; PRIOR APPLICATION NUMBER: FR 95/07914
; PRIOR FILING DATE: 1995-06-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-827-345-5

Query Match      18.2%; Score 4; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SQPK 5
Db      1 SQPK 4

RESULT 15
US-09-827-345-21
; Sequence 21, Application US/09827345
; Publication No. US20030021800A1
; GENERAL INFORMATION:
; APPLICANT: CHERMANN, JEAN-CLAUDE
; APPLICANT: LE CONTEL, CAROLE
; APPLICANT: GALEA, PASCAL
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN
; TITLE OF INVENTION: INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
```

; TITLE OF INVENTION: DIAGNOSIS  
; FILE REFERENCE: 065691-0216  
; CURRENT APPLICATION NUMBER: US/09/827,345  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/599,549  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: PCT/FR96/01006  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/973,551  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: FR 95/07914  
; PRIOR FILING DATE: 1995-06-30  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-827-345-21

Query Match 18.2%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQPK 5  
Db 1 SQPK 4

RESULT 16  
US-10-303-331-16  
; Sequence 16, Application US/10303331  
; Publication No. US20030152976A1  
; GENERAL INFORMATION:  
; APPLICANT: Janssen, Giselle G.  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Winetzk, Deborah S.  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: G6617-3  
; CURRENT APPLICATION NUMBER: US/10/303,331  
; CURRENT FILING DATE: 2002-11-25  
; PRIOR APPLICATION NUMBER: US 09/832,723  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-10-303-331-16

Query Match 18.2%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4  
Db 1 LSQP 4

RESULT 17  
US-10-286-457-252  
; Sequence 252, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.

; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-P01-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 252  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, be  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-252

Query Match 18.2%; Score 4; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 PQKA 13  
Db 2 PQKA 5

RESULT 18  
US-10-024-123-4  
; Sequence 4, Application US/10024123  
; Publication No. US2003002263A1  
; GENERAL INFORMATION:  
; APPLICANT: Kastan, Michael  
; APPLICANT: Carman, Christine  
; APPLICANT: Kim, Seong-Tae  
; APPLICANT: Lim, Dae-Sik  
; APPLICANT: St. Jude Children's Research Hospital  
; TITLE OF INVENTION: ATM Kinase Modulation for Screening and  
; FILE REFERENCE: 2427/1F142  
; CURRENT APPLICATION NUMBER: US/10/024,123  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 09/400,653  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: 09/248,061  
; PRIOR FILING DATE: 1999-02-10  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: PHOSPHORYLATION  
; LOCATION: 4  
; OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-10-024-123-4

Query Match 18.2%; Score 4; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4  
Db 3 LSQP 6

RESULT 19  
US-10-028-075B-142  
; Sequence 142, Application US/10028075B  
; Publication No. US2003011373A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Nisar A.

```
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-028-075B-142

Query Match      18.2%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
      ||||
Db      4 PVPQ 7

RESULT 20
US-10-029-206A-142
; Sequence 142, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 142
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-142

Query Match      18.2%; Score 4; DB 15; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
      ||||
Db      4 PVPQ 7

RESULT 21
US-10-028-075B-144
; Sequence 144, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EP 01203748.7
; PRIOR FILING DATE: 2001-10-04

; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-144

Query Match      18.2%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
      ||||
Db      5 PVPQ 8

RESULT 22
US-10-029-206A-144
; Sequence 144, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 144
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-144

Query Match      18.2%; Score 4; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PVPQ 11
      ||||
Db      5 PVPQ 8

RESULT 23
US-10-137-867-210
; Sequence 210, Application US/10137867
; Publication No. US20030207349A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
```

```
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C146
; CURRENT APPLICATION NUMBER: US/10/137,867
; PRIOR FILING DATE: 2002-05-03
; PRIOR Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 210
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-867-210

Query Match      18.2%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL P 8
Db 3 KVL P 6

RESULT 24
US-10-042-202-49
; Sequence 49, Application US/10042202
; Publication No. US20020136733A1
; GENERAL INFORMATION:
; APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,
; Catherine Elizabeth Margaret ALLSOPP, Ajit LALVANI, Magdalena
; PLEBANSKI, Hilton Carter WHITTLE,
; TITLE OF INVENTION: MALARIA PEPTIDES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800,
; CITY: Washington
; STATE: D.C.,
; COUNTRY: U.S.A.
; ZIP: 20006-1021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordpad for Windows 95
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/042,202
; FILING DATE: 11-Jan-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/714,175
; FILING DATE: 28-JAN-1997
; APPLICATION NUMBER: WO PCT/GB95/26982
; FILING DATE: 30-MAR-1995
; APPLICATION NUMBER: GB 9406492.0
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER: 2002_0026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 49:
US-10-042-202-49
```

```
Query Match      18.2%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7
Db 6 PKVL 9

RESULT 25
US-09-220-920-111
; Sequence 111, Application US/09220920
; Patent No. US20020002269A1
; GENERAL INFORMATION:
; APPLICANT: Milbrandt, Jeffrey D.
; APPLICANT: Baloh, Robert H.
; TITLE OF INVENTION: Artemin, A No. US20020002269A1el Neurotrophic Factor
; FILE REFERENCE: 6029-7996
; CURRENT APPLICATION NUMBER: US/09/220,920
; CURRENT FILING DATE: 1998-12-24
; EARLIER APPLICATION NUMBER: 09/163,283
; EARLIER FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: 60/108,148
; EARLIER FILING DATE: 1998-11-12
; EARLIER APPLICATION NUMBER: 09/218,698
; EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 111
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-220-920-111

Query Match      18.2%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9
Db 2 VLPV 5

RESULT 26
US-09-572-404B-1169
; Sequence 1169, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1169
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C3AR1 OR C3R1 OR A23B OR HNFAG09 at 10-19
; OTHER INFORMATION: interact with sequence 1170 in this patent.
US-09-572-404B-1169

Query Match      18.2%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4
Db 5 LSQP 8
```

RESULT 27  
US-09-915-914B-39  
; Sequence 39, Application US/09915914B  
; Publication No. US20030119725A1  
; GENERAL INFORMATION:  
; APPLICANT: Divita, Gilles  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Heitz, Frederic  
; APPLICANT: Morris, May  
; APPLICANT: Mery, Jean  
; APPLICANT: Archdeacon, John  
; APPLICANT: Horndorp, Kyle  
; TITLE OF INVENTION: PEPTIDE-MEDIATED DELIVERY OF MOLECULES INTO CELLS  
; FILE REFERENCE: AM-00105-P.1.1  
; CURRENT APPLICATION NUMBER: US/09/915,914B  
; CURRENT FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: US 60/221,932  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic sequence  
US-09-915-914B-39

Query Match 18.2%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
Db 2 SQPK 5

RESULT 28  
US-10-200-708-372  
; Sequence 372, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 372  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-372

Query Match 18.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
Db 5 SQPK 8

RESULT 29  
US-09-573-822C-600  
; Sequence 600, Application US/09573822C  
; Publication No. US20030199011A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome  
; FILE REFERENCE: Microbe patent  
; CURRENT APPLICATION NUMBER: US/09/573,822C  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 804  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 600  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: mycoplasma genitalium  
; FEATURE:  
; OTHER INFORMATION: Sequence located in MG458 at 12-21 and may interact with Sequ  
US-09-573-822C-600

Query Match 18.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 8.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QXAV 14  
Db 7 QXAV 10

RESULT 30  
US-09-347-064-16  
; Sequence 16, Application US/09347064A  
; Patent No. US20020045208A1  
; GENERAL INFORMATION:  
; APPLICANT: Eck, Jurgen  
; APPLICANT: Schmidt, Arno  
; APPLICANT: Zinke, Holger  
; TITLE OF INVENTION: Recombinant Fusion Proteins Based on  
; TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum  
; FILE REFERENCE: 09282-5  
; CURRENT APPLICATION NUMBER: US/09/347,064A  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: PCT/EP98/00009  
; EARLIER FILING DATE: 1998-01-02  
; EARLIER APPLICATION NUMBER: EP 97 10 0012.0  
; EARLIER FILING DATE: 1997-01-02  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Fig. 20: amino  
; OTHER INFORMATION: acid sequence encoded by portion of SEQ ID NO: 15  
US-09-347-064-16

Query Match 18.2%; Score 4; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 9.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
Db 9 LPVP 12

RESULT 31  
US-09-789-561-163  
; Sequence 163, Application US/09789561  
; Patent No. US20020064818A1  
; GENERAL INFORMATION:



```
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163

Query Match      18.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
Db      3 PKVL 6

RESULT 32
US-09-911-838-203
; Sequence 203, Application US/09911838
; Patent No. US20020151678A1
; GENERAL INFORMATION:
; APPLICANT: ARLINGHAUS, RALPH
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY OF ACQUIRED IMMUNODEFICIENCY
; FILE REFERENCE: UTSC:267USC1
; CURRENT APPLICATION NUMBER: US/09/911,838
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 07/834,923
; PRIOR FILING DATE: 1992-02-13
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-911-838-203

Query Match      18.2%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 PVPQ 11
Db      6 PVPQ 9

RESULT 33
US-09-845-612B-3
; Sequence 3, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANTUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCHONDRIAL
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795

; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 163
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-789-561-163

Query Match      18.2%; Score 4; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 PKVL 7
Db      3 PKVL 6

RESULT 32
US-09-911-838-203
; Sequence 203, Application US/09911838
; Patent No. US20020151678A1
; GENERAL INFORMATION:
; APPLICANT: ARLINGHAUS, RALPH
; TITLE OF INVENTION: PROPHYLAXIS AND THERAPY OF ACQUIRED IMMUNODEFICIENCY
; FILE REFERENCE: UTSC:267USC1
; CURRENT APPLICATION NUMBER: US/09/911,838
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 07/834,923
; PRIOR FILING DATE: 1992-02-13
; NUMBER OF SEQ ID NOS: 226
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 203
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-911-838-203

Query Match      18.2%; Score 4; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 PVPQ 11
Db      6 PVPQ 9

RESULT 33
US-09-845-612B-3
; Sequence 3, Application US/09845612B
; Publication No. US20030083261A1
; GENERAL INFORMATION:
; APPLICANT: YU, HONGTAO
; APPLICANT: TANG, ZHANTUN
; APPLICANT: LUO, XUELIAN
; APPLICANT: RIZO-REY, JOSE
; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF THE MITOCHONDRIAL
; TITLE OF INVENTION: POINT PROTEIN MAD2
; FILE REFERENCE: UTSD:795

; APPLICANT: Ni et al.
; TITLE OF INVENTION: 52 Human secreted proteins
; FILE REFERENCE: P2043P1
; CURRENT APPLICATION NUMBER: US/09/789,561
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/24008
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,317
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/152,315
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-3

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 LPVP 10
Db      7 LPVP 10

RESULT 34
US-09-954-385-124
; Sequence 124, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-124

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11 QKAV 14
Db      7 QKAV 10

RESULT 35
US-09-954-385-332
; Sequence 332, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzk, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; TITLE OF INVENTION: Complexes
```

```
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-332

Query Match      18.2%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
   ||||
Db 9 LPVP 12

RESULT 36
US-10-247-946-2
; Sequence 2, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-2

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
   ||||
Db 9 SQPK 12

RESULT 37
US-10-247-946-3
; Sequence 3, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-3

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
   ||||
Db 9 SQPK 12

RESULT 38
US-10-251-526-2
; Sequence 2, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-2

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
   ||||
Db 9 SQPK 12

RESULT 39
US-10-251-526-3
; Sequence 3, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; PRIOR FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-3

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5
   ||||
Db 2 SQPK 5

RESULT 40
US-10-354-955-5
; Sequence 5, Application US/10354955
; Publication No. US20030171291A1
; GENERAL INFORMATION:
; APPLICANT: Gary Christie
; APPLICANT: Ishrut Hussain
; APPLICANT: David J. Powell
```

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; TITLE OF INVENTION: No. US20030171291A1el Treatment
; FILE REFERENCE: P22448
; CURRENT APPLICATION NUMBER: US/10/354,955
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 09/693,744
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 9925136.5
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Bovine
US-10-354-955-5

Query Match      18.2%; Score 4; DB 12; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8
Db 7 KVLVP 10

RESULT 41
US-10-224-999A-794
; Sequence 794, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-10-224-999A-794

Query Match      18.2%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
Db 10 LSQP 13

RESULT 42
US-10-062-710-34
; Sequence 34, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
```

```
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-34

Query Match      18.2%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PVPQ 11
Db 7 PVPQ 10

RESULT 43
US-10-125-187-19
; Sequence 19, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC A
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125,187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: AU PQ 9162
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: AU PQ 3485
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: inhibit alpha C amino acid sequence corresponding to peptide 1
US-10-125-187-19

Query Match      18.2%; Score 4; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
Db 9 LPVP 12

RESULT 44
US-10-125-187-20
; Sequence 20, Application US/10125187
; Publication No. US20030162229A1
; GENERAL INFORMATION:
; APPLICANT: MILNE-ROBERTSON, David M.
; APPLICANT: STANTON, Peter G.
; APPLICANT: CAHIR, Nicholas F.
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC A
; TITLE OF INVENTION: METHODS OF USING SAME
; FILE REFERENCE: 10338-9
; CURRENT APPLICATION NUMBER: US/10/125,187
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: PCT/AU00/01248
; PRIOR FILING DATE: 2000-10-18
```

; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 20  
; OTHER INFORMATION: f TABLE 1  
US-10-125-187-20

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|||  
Db 5 LPVP 8

RESULT 45  
US-10-125-187-21  
; Sequence 21, Application US/10125187  
; Publication No. US20030162229A1  
; GENERAL INFORMATION:  
; APPLICANT: MILNE-ROBERTSON, David M.  
; APPLICANT: STANTON, Peter G.  
; APPLICANT: CAHIR, Nicholas F.  
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS  
; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 21  
; OTHER INFORMATION: f TABLE 1  
US-10-125-187-21

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|||  
Db 1 LPVP 4

RESULT 46  
US-10-125-187-53  
; Sequence 53, Application US/10125187  
; Publication No. US20030162229A1  
; GENERAL INFORMATION:  
; APPLICANT: MILNE-ROBERTSON, David M.  
; APPLICANT: STANTON, Peter G.  
; APPLICANT: CAHIR, Nicholas F.  
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS  
; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 53  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-53

; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 2  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-53

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|||  
Db 9 LPVP 12

RESULT 47  
US-10-125-187-54  
; Sequence 54, Application US/10125187  
; Publication No. US20030162229A1  
; GENERAL INFORMATION:  
; APPLICANT: MILNE-ROBERTSON, David M.  
; APPLICANT: STANTON, Peter G.  
; APPLICANT: CAHIR, Nicholas F.  
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS  
; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 54  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 2  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-54

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|||  
Db 5 LPVP 8

RESULT 48  
US-10-125-187-55  
; Sequence 55, Application US/10125187  
; Publication No. US20030162229A1  
; GENERAL INFORMATION:  
; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 2  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-55

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
|||  
Db 1 LPVP 4

RESULT 46  
US-10-125-187-53  
; Sequence 53, Application US/10125187  
; Publication No. US20030162229A1  
; GENERAL INFORMATION:  
; APPLICANT: MILNE-ROBERTSON, David M.  
; APPLICANT: STANTON, Peter G.  
; APPLICANT: CAHIR, Nicholas F.  
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS  
; FILE REFERENCE: 10338-9  
; CURRENT APPLICATION NUMBER: US/10/125,187  
; CURRENT FILING DATE: 2002-04-18  
; PRIOR APPLICATION NUMBER: PCT/AU00/01248  
; PRIOR FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: AU PQ 9162  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: AU PQ 3485  
; PRIOR FILING DATE: 1999-10-18  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 53  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: inhibin alpha C amino acid sequence corresponding to peptide 53  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-53

; APPLICANT: MILNE-ROBERTSON, David M.  
; APPLICANT: STANTON, Peter G.  
; APPLICANT: CAHIR, Nicholas F.  
; TITLE OF INVENTION: NOVEL PEPTIDES FOR DEVELOPMENT OF DIAGNOSTIC AND THERAPEUTIC AGENTS  
; FILE REFERENCE: 5004.01  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 55  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Inhibin alpha C amino acid sequence corresponding to peptide 22 of  
; OTHER INFORMATION: f TABLE 7  
US-10-125-187-55

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10  
Db 1 LPVP 4

RESULT 49  
US-10-224-999A-804  
; Sequence 804, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 804  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-804

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4  
Db 11 LSQP 14

RESULT 50  
US-10-224-999A-805  
; Sequence 805, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott

; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 805  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-805

Query Match 18.2%; Score 4; DB 12; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQP 4  
Db 10 LSQP 13

RESULT 51  
US-08-996-140-9  
; Sequence 9, Application US/08996140  
; Publication No. US20030190318A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shimpai  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,140  
; FILING DATE: 22-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 356,426/1996  
; FILING DATE: 26-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TORIGOE-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids

; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; FRAGMENT TYPE: internal fragment  
 US-08-996-140-9

Query Match 18.2%; Score 4; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9  
 Db 11 VLPV 14

## RESULT 52

US-09-908-322-59  
 ; Sequence 59, Application US/09908322  
 ; Patent No. US20020107194A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ish-Horowicz, David  
 ; Henrique, Domingos Manuel Pinto  
 ; Lewis, Julian Hart  
 ; Artavanis-Tsakonas, Spyridon  
 ; Gray, Grace

TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF  
 VERTEBRATE DELTA GENE AND METHODS BASED THEREON

NUMBER OF SEQUENCES: 94  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Pennie & Edmonds LLP  
 STREET: 1155 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10036/2711

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/908,322  
 FILING DATE: 17-Jul-2001  
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/981,392  
 FILING DATE: 22-DEC-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Mirock, S Leslie  
 REGISTRATION NUMBER: 18,872  
 REFERENCE/DOCKET NUMBER: 7326-123  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212-790-9090  
 TELEFAX: 212-869-8864  
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 59:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:

US-09-908-322-59

Query Match 18.2%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10  
 Db 2 LPVP 5

## RESULT 53

US-09-764-176-13  
 ; Sequence 13, Application US/09764176  
 ; Patent No. US20020127553A1

## GENERAL INFORMATION:

; APPLICANT: NOTEBOEN, Mathieu Hubertus Maria  
 ; APPLICANT: DANEN-VAN OORSCHOT, Astrid Adriana Anna Maria  
 ; APPLICANT: ROHN, Jennifer Leigh  
 ; APPLICANT: WEISS, Bertram

; TITLE OF INVENTION: AOPTIN-ASSOCIATING PROTEIN

; FILE REFERENCE: 4725US

; CURRENT APPLICATION NUMBER: US/09/764,176

; CURRENT FILING DATE: 2001-01-17

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 13

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Description of Artificial Sequence: peptide based on sequence

; OTHER INFORMATION: AAP-2 protei

US-09-764-176-13

## Query Match

18.2%; Score 4; DB 10; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7

Db 12 PKVL 15

## RESULT 54

US-09-783-931-59

; Sequence 59, Application US/09783931

; Publication No. US20030073620A1

## GENERAL INFORMATION:

; APPLICANT: Ish-Horowicz, David

; Henrique, Domingos Manuel Pinto

; Lewis, Julian Hart

; Artavanis-Tsakonas, Spyridon

; Gray, Grace

; TITLE OF INVENTION: ANTIBODIES TO VERTEBRATE DELTA PROTEINS

; AND FRAGMENTS

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/783,931

; FILING DATE: 15-Feb-2001

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/981,392

; FILING DATE: 22-DEC-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Antler, Adriane M.

; REGISTRATION NUMBER: 32,605

; REFERENCE/DOCKET NUMBER: 7326-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-783-931-59

Query Match 18.2%; Score 4; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10  
Db 2 LPVP 5

## RESULT 55

US-10-212-198-15  
Sequence 15, Application US/10212198  
Publication No. US20030138804A1  
GENERAL INFORMATION:  
APPLICANT: Boyle, Bryan J  
APPLICANT: Ford, John E.  
APPLICANT: Mize, Nancy K.  
APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Drmanac, Radoje T.  
APPLICANT: Dickson, Mark C.  
APPLICANT: Arterburn, Matthew C.  
APPLICANT: Binnerts, Minke  
TITLE OF INVENTION: Methods and Materials Relating to No. US20030138804A1el C-type Le  
TITLE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: HYS-SCIP  
CURRENT APPLICATION NUMBER: US/10/212,198  
CURRENT FILING DATE: 2002-08-02  
PRIOR APPLICATION NUMBER: 09/545,283  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 09/496,914  
PRIOR FILING DATE: 2000-02-03  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 15  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-212-198-15

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 VPQK 12  
Db 8 VPQK 11

## RESULT 56

US-10-349-023-18  
Sequence 18, Application US/10349023  
Publication No. US20030133919A1  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
OKURA, Takanori  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/349,023  
FILING DATE: 23-Jan-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/556,972  
FILING DATE: 24-Apr-2000  
APPLICATION NUMBER: US/08/996,338  
FILING DATE: 22-DEC-1997  
APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-10-349-023-18

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPV 9  
Db 11 VLPV 14

## RESULT 57

US-10-294-891-17  
Sequence 17, Application US/10294891  
Publication No. US20030166569A1  
GENERAL INFORMATION:  
APPLICANT: AVERBACK, PAUL  
APPLICANT: GEMMEL, JACK  
TITLE OF INVENTION: PEPTIDES EFFECTIVE IN THE TREATMENT OF TUMORS AND OTHER  
TITLE OF INVENTION: CONDITIONS REQUIRING THE REMOVAL OR DESTRUCTION OF CELLS  
FILE REFERENCE: 59003.000010  
CURRENT APPLICATION NUMBER: US/10/294,891  
CURRENT FILING DATE: 2002-11-15  
PRIOR APPLICATION NUMBER: 60/331,447  
PRIOR FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 17  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-294-891-17

Query Match 18.2%; Score 4; DB 12; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 LSQP 4  
    ||||  
DB 4 LSQP 7

## RESULT 58

US-10-224-999A-815  
; Sequence 815, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 815  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-815

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
    ||||  
DB 12 LSQP 15

## RESULT 59

US-10-224-999A-816  
; Sequence 816, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 816  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-816

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
    ||||  
DB 11 LSQP 14

## RESULT 60

US-10-224-999A-817  
; Sequence 817, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 817  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-817

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
    ||||  
DB 10 LSQP 13

## RESULT 61

US-10-161-791-306  
; Sequence 306, Application US/10161791  
; Publication No. US20030186863A1  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/161,791  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE



; INFORMATION FOR SEQ ID NO: 306:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-10-161-791-306

Query Match 18.2%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10

Db 7 LPVP 10

#### RESULT 62

US-10-126-474A-3

; Sequence 3, Application US/10126474A

; Publication No. US20030054994A1

; GENERAL INFORMATION:

; APPLICANT: No. US20030054994A1eborn, Mathieu H.M.

; APPLICANT: Weiss, Betram

; TITLE OF INVENTION: APOPTOSIS INDUCING PROTEINACEOUS SUBSTANCE

; FILE REFERENCE: 5334US (951373US00)

; CURRENT APPLICATION NUMBER: US/10/126,474A

; CURRENT FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: PCT/NL00/00767

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: EP 99203467.8

; PRIOR FILING DATE: 1999-10-21

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 3

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Immunogenic peptide for production of polyclonal antibodies against TAP proteins

US-10-126-474A-3

Query Match 18.2%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10

Db 4 LPVP 7

#### RESULT 63

US-10-174-105A-149

; Sequence 149, Application US/10174105A

; Publication No. US20030068652A1

; GENERAL INFORMATION:

; APPLICANT: Cell Signaling Technology, Inc.

; APPLICANT: ZHANG, Hui

; APPLICANT: COMB, Michael J.

; APPLICANT: TAN, Yi

; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,

; FILE REFERENCE: CST-138 CIP3

; CURRENT APPLICATION NUMBER: US/10/174,105A

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US 09/148,712

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 193

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 149

; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated  
US-10-174-105A-149

Query Match 18.2%; Score 4; DB 15; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10

Db 10 LPVP 13

#### RESULT 64

US-10-174-105A-175

; Sequence 175, Application US/10174105A

; Publication No. US20030068652A1

; GENERAL INFORMATION:

; APPLICANT: Cell Signaling Technology, Inc.

; APPLICANT: ZHANG, Hui

; APPLICANT: COMB, Michael J.

; APPLICANT: TAN, Yi

; TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPECIFIC,

; FILE REFERENCE: CST-138 CIP3

; CURRENT APPLICATION NUMBER: US/10/174,105A

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US 09/148,712

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: US 09/535,364

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 193

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 175

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic peptide

; NAME/KEY: MOD\_RES

; LOCATION: (9)..(9)

; OTHER INFORMATION: PHOSPHORYLATION; serine at position 9 is phosphorylated  
US-10-174-105A-175

Query Match 18.2%; Score 4; DB 15; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10

Db 10 LPVP 13

#### RESULT 65

US-10-281-652-5

; Sequence 5, Application US/10281652

; Publication No. US20030091606A1

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/10/281,652

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/ CURRENT FILING DATE: 2002-10-28
/ PRIOR APPLICATION NUMBER: US/09/641,803
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: 60/149,310
/ PRIOR FILING DATE: 1999-08-17
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-281-652-5

Query Match      18.2%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
      ||||
Db      6 VLPV 9

RESULT 66
US-09-880-748-2228
/ Sequence 2228, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2228
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2228

Query Match      18.2%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
      ||||
Db      10 VLPV 13

RESULT 67
US-09-880-748-2334
/ Sequence 2334, Application US/09880748
/ Publication No. US2003005937A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523
/ CURRENT APPLICATION NUMBER: US/09/880,748
/ CURRENT FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/212,210
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/ PRIOR FILING DATE: 2000-06-15
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ NUMBER OF SEQ ID NOS: 3239
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 2334
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-880-748-2334

Query Match      18.2%; Score 4; DB 11; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
      ||||
Db      10 VLPV 13

RESULT 68
US-10-224-999A-827
/ Sequence 827, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 827
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Human herpesvirus 4
US-10-224-999A-827

Query Match      18.2%; Score 4; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LSQP 4
      ||||
Db      13 LSQP 16

RESULT 69
US-10-224-999A-828
/ Sequence 828, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
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; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 828  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-828

Query Match 18.2%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
|||  
Db 12 LSQP 15

RESULT 70  
US-10-224-999A-829  
; Sequence 829, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 829  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-829

Query Match 18.2%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
|||  
Db 11 LSQP 14

RESULT 71  
US-10-224-999A-830  
; Sequence 830, Application US/10224999A  
; Publication No. US20030171318A1  
; GENERAL INFORMATION:  
; APPLICANT: Myriad Genetics, Inc.  
; APPLICANT: Morham, Scott  
; APPLICANT: Zavitz, Kenton  
; APPLICANT: Hobden, Adrian  
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection  
; FILE REFERENCE: 5004.01  
; CURRENT APPLICATION NUMBER: US/10/224,999A  
; CURRENT FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/313,695  
; PRIOR FILING DATE: 2001-08-20  
; NUMBER OF SEQ ID NOS: 3484  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 830  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human herpesvirus 4  
US-10-224-999A-830

Query Match 18.2%; Score 4; DB 12; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 LSQP 4  
|||  
Db 10 LSQP 13

RESULT 72  
US-10-006-760-61  
; Sequence 61, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohei  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/249,756  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 61  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: FG loop  
; OTHER INFORMATION: sequence for polypeptide monobody in pYT47F16  
; OTHER INFORMATION: library  
US-10-006-760-61

Query Match 18.2%; Score 4; DB 12; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
|||  
Db 6 LSQP 9

RESULT 73  
US-10-043-487-442  
; Sequence 442, Application US/10043487  
; Publication No. US20030055220A1  
; GENERAL INFORMATION:  
; APPLICANT: HYBERGENICS  
; APPLICANT: Pierre, LEGRAIN  
; TITLE OF INVENTION: Protein-protein interactions between Shigella Flexneri polypep  
; TITLE OF INVENTION: mammalian polypeptides  
; FILE REFERENCE: B4778A  
; CURRENT APPLICATION NUMBER: US/10/043,487  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/261,130  
; PRIOR FILING DATE: 2001-01-12  
; NUMBER OF SEQ ID NOS: 561  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 442  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Shigella Flexneri  
US-10-043-487-442

Query Match 18.2%; Score 4; DB 15; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
|||  
Db 9 VLPV 12

```
RESULT 74
US-09-996-069-30
; Sequence 30, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS
; FILE REFERENCE: M01015/70071
; CURRENT FILING DATE: 2001-11-27
; CURRENT APPLICATION NUMBER: US/09/996,069
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-30

Query Match      18.2%; Score 4; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
Db      6 VLPV 9

RESULT 75
US-09-996-069-31
; Sequence 31, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBITORS
; FILE REFERENCE: M01015/70071
; CURRENT FILING DATE: 2001-11-27
; CURRENT APPLICATION NUMBER: US/09/996,069
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-31

Query Match      18.2%; Score 4; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 VLPV 9
Db      6 VLPV 9

Search completed: November 25, 2003, 20:37:04
Job time : 36.3023 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 17.7791 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-27

Perfect score: 22

Sequence: 1 LSQPKVLPVQKAVPQDMPIQ 22

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	31.8	7	4	US-09-492-766-8
2	6	27.3	14	1	US-08-642-255-103
3	6	27.3	14	1	US-08-397-633A-5
4	6	27.3	14	1	US-08-397-633A-10
5	6	27.3	15	1	US-08-397-633A-80
6	6	27.3	15	1	US-08-397-633A-83
7	6	27.3	20	3	US-08-505-250-12
8	6	27.3	20	3	US-08-505-250-12
9	5	22.7	10	3	US-08-973-551-10
10	5	22.7	15	1	US-08-397-633A-81
11	5	22.7	15	3	US-08-973-551-3
12	5	22.7	16	3	US-08-602-999A-195
13	5	22.7	16	6	US-09-500-124-195
14	5	22.7	18	6	5175113-7
15	4	18.2	6	3	US-09-177-249-278
16	4	18.2	6	3	US-08-776-059-56
17	4	18.2	6	4	US-08-854-039B-23
18	4	18.2	6	4	US-09-645-456A-33
19	4	18.2	6	4	US-09-425-324A-33
20	4	18.2	6	4	US-09-645-791-33
21	4	18.2	7	1	US-08-230-047-37
22	4	18.2	7	3	US-08-373-551-5
23	4	18.2	7	3	US-08-973-551-21
24	4	18.2	7	4	US-09-400-653A-4
25	4	18.2	7	4	US-09-248-061B-4
26	4	18.2	8	1	US-08-571-985-21
27	4	18.2	8	2	US-09-116-766-21
28	4	18.2	4	4	US-08-635-886C-138
29	4	18.2	4	2	US-08-350-260A-385
30	4	18.2	4	2	US-08-318-856A-54
31	4	18.2	4	4	US-09-343-011B-7
32	4	18.2	4	4	US-09-104-337A-385
33	4	18.2	4	10	US-07-869-933-19
34	4	18.2	4	10	US-08-361-517-13
35	4	18.2	4	10	US-08-361-517-14
36	4	18.2	4	10	US-08-361-517-15
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38	4	18.2	4	10	US-08-361-517-17
39	4	18.2	4	10	US-08-361-517-19
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42	4	18.2	4	10	US-09-103-663-19
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44	4	18.2	4	10	PCT-US93-07964-13
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46	4	18.2	4	10	PCT-US93-07964-15
47	4	18.2	4	10	PCT-US93-07964-16
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49	4	18.2	4	10	PCT-US93-07964-19
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51	4	18.2	4	11	US-08-361-517-5
52	4	18.2	4	11	US-08-361-517-31
53	4	18.2	4	11	US-08-802-981-136
54	4	18.2	4	11	PCT-US93-07964-5
55	4	18.2	4	12	US-08-230-047-36
56	4	18.2	4	12	US-08-053-079A-2
57	4	18.2	4	12	US-08-053-079A-3
58	4	18.2	4	12	US-08-397-633A-101
59	4	18.2	4	12	US-08-361-517-4
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61	4	18.2	4	12	US-09-147-208-55
62	4	18.2	4	12	US-09-347-926-16
63	4	18.2	4	12	US-09-550-117A-55
64	4	18.2	4	12	PCT-US93-07964-4
65	4	18.2	4	12	US-08-361-517-3
66	4	18.2	4	13	US-08-361-517-27
67	4	18.2	4	13	US-08-361-517-28
68	4	18.2	4	13	US-08-361-517-29
69	4	18.2	4	13	US-09-043-937A-16
70	4	18.2	4	13	PCT-US93-07964-3
71	4	18.2	4	13	PCT-US94-10257A-13
72	4	18.2	4	13	PCT-US94-10257A-57
73	4	18.2	4	13	5223254-6
74	4	18.2	4	14	US-08-361-517-2
75	4	18.2	4	14	US-08-361-517-6
76	4	18.2	4	14	US-08-361-517-25
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81	4	18.2	4	15	US-08-230-047-28
82	4	18.2	4	15	US-08-449-207-4
83	4	18.2	4	15	US-08-480-190-73
84	4	18.2	4	15	US-08-488-379-73
85	4	18.2	4	15	US-08-361-517-1
86	4	18.2	4	15	US-08-361-517-24
87	4	18.2	4	15	US-08-735-253-18
88	4	18.2	4	15	US-08-159-339A-1120
89	4	18.2	4	15	US-08-996-338-18
90	4	18.2	4	15	US-08-602-999A-306
91	4	18.2	4	15	US-08-981-392-59
92	4	18.2	4	15	US-09-500-124-306
93	4	18.2	4	15	US-09-641-803-5
94	4	18.2	4	15	US-08-475-399A-73
95	4	18.2	4	15	US-09-556-972-18
96	4	18.2	4	15	PCT-US93-07545-73
97	4	18.2	4	15	PCT-US93-07964-1
98	4	18.2	4	15	5378464-31
99	4	18.2	4	16	US-08-133-011-141
100	4	18.2	4	16	US-08-649-619B-5

Sequence 138, App  
Sequence 385, App  
Sequence 54, Appl  
Sequence 7, Appl  
Sequence 185, App  
Sequence 19, Appl  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 15, Appl  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 20, Appl  
Sequence 19, Appl  
Sequence 58, Appl  
Sequence 19, Appl  
Sequence 11, App  
Sequence 13, Appl  
Sequence 14, Appl  
Sequence 15, Appl  
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Sequence 17, Appl  
Sequence 19, Appl  
Sequence 20, Appl  
Sequence 5, Appl  
Sequence 31, Appl  
Sequence 136, App  
Sequence 36, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 101, App  
Sequence 4, Appl  
Sequence 30, Appl  
Sequence 55, Appl  
Sequence 16, Appl  
Sequence 55, Appl  
Sequence 4, Appl  
Sequence 3, Appl  
Sequence 27, Appl  
Sequence 28, Appl  
Sequence 29, Appl  
Sequence 16, Appl  
Sequence 3, Appl  
Sequence 13, Appl  
Sequence 57, Appl  
Patent No. 5203254  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 25, Appl  
Sequence 26, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Patent No. 516482  
Sequence 28, Appl  
Sequence 4, Appl  
Sequence 73, Appl  
Sequence 73, Appl  
Sequence 1, Appl  
Sequence 24, Appl  
Sequence 18, Appl  
Sequence 1120, Ap  
Sequence 18, Appl  
Sequence 306, App  
Sequence 59, Appl  
Sequence 306, App  
Sequence 5, Appl  
Sequence 73, Appl  
Sequence 18, Appl  
Sequence 73, Appl  
Patent No. 5378464  
Sequence 141, App  
Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-09-492-766-8  
; Sequence 8, Application US/09492766  
; Patent No. 6506732  
; GENERAL INFORMATION:  
; APPLICANT: AMIOT, Jean  
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS  
; FILE REFERENCE: 6013-57\*US\*  
; CURRENT APPLICATION NUMBER: US/09/492,766  
; CURRENT FILING DATE: 2000-01-27  
; EARLIER APPLICATION NUMBER: 60/117,661  
; EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
; OTHER INFORMATION: proteins  
US-09-492-766-8

Query Match 31.8%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred.No.2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLPVPQK 12  
Db 1 VLPVPQK 7

RESULT 2  
US-08-642-255-103  
; Sequence 103, Application US/08642255  
; Patent No. 5773249  
; GENERAL INFORMATION:  
; APPLICANT: CAPPELLO, Joseph  
; APPLICANT: FERRARI, Franco A.  
; TITLE OF INVENTION: High Molecular Weight Collagen-Like  
; TITLE OF INVENTION: Protein Polymers  
; NUMBER OF SEQUENCES: 135  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/642,255  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROWLAND, Bertram I.  
; REGISTRATION NUMBER: 20,015  
; REFERENCE/DOCKET NUMBER: A55556-3/BIR  
; TELEPHONE: (415) 494-8700  
; TELEFAX: (415) 494-8771  
; TELEX: 910 277299 FHT UR  
; INFORMATION FOR SEQ ID NO: 103:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-642-255-103

Query Match 27.3%; Score 6; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred.No.2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
Db 8 KVLVPV 13

RESULT 3  
US-08-397-633A-5  
; Sequence 5, Application US/08397633A  
; Patent No. 5773577  
; GENERAL INFORMATION:  
; APPLICANT: CAPPELLO, Joseph  
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE  
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,633A  
; FILING DATE:  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROWLAND, Bertram I.  
; REGISTRATION NUMBER: 20,015  
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-633A-5

Query Match 27.3%; Score 6; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred.No.2.2;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVPV 10  
Db 8 KVLVPV 13

RESULT 4  
US-08-397-633A-10  
; Sequence 10, Application US/08397633A  
; Patent No. 5773577  
; GENERAL INFORMATION:  
; APPLICANT: CAPPELLO, Joseph

```

; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-10

Query Match 27.3%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 5 KVLVPP 10
DB 8 KVLVPP 13

RESULT 5
US-08-397-633A-80
; Sequence 80, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015

```

```

; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-80

Query Match 27.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPP 10
DB 9 KVLVPP 14

RESULT 6
US-08-397-633A-83
; Sequence 83, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-633A-83

Query Match 27.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPP 10
DB 9 KVLVPP 14

```

RESULT 7  
US-08-505-250-12  
; Sequence 12, Application US/08505250  
; Patent No. 6183983  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Haruya  
; APPLICANT: Yamamoto, Keiji  
; APPLICANT: Suzuki, Kokichi  
; APPLICANT: Ikeda, Masahiro  
; APPLICANT: Sakagami, Masahiro  
; APPLICANT: Taniguchi, Makoto  
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD  
; FILE REFERENCE: 110-511  
; CURRENT APPLICATION NUMBER: US/08/505,250  
; CURRENT FILING DATE: 1995-11-29  
; EARLIER APPLICATION NUMBER: PCT/JP95/00298  
; EARLIER FILING DATE: 1995-02-27  
; EARLIER APPLICATION NUMBER: JP 198187/94  
; EARLIER FILING DATE: 1994-08-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-08-505-250-12

Query Match 27.3%; Score 6; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPP 10  
|||  
Db 12 KVLVPP 17

RESULT 8  
US-08-505-250-12  
; Sequence 12, Application US/08505250  
; Patent No. 6322996  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Haruya  
; APPLICANT: Yamamoto, Keiji  
; APPLICANT: Suzuki, Kokichi  
; APPLICANT: Ikeda, Masahiro  
; APPLICANT: Sakagami, Masahiro  
; APPLICANT: Taniguchi, Makoto  
; TITLE OF INVENTION: PROTEIN MODIFICATION METHOD  
; FILE REFERENCE: 110-511  
; CURRENT APPLICATION NUMBER: US/08/505,250  
; CURRENT FILING DATE: 1995-11-29  
; PRIOR APPLICATION NUMBER: PCT/JP95/00298  
; PRIOR FILING DATE: 1995-02-27  
; PRIOR APPLICATION NUMBER: JP 198187/94  
; PRIOR FILING DATE: 1994-08-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-08-505-250-12

Query Match 27.3%; Score 6; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 3.1;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVPP 10  
|||  
Db 12 KVLVPP 17

RESULT 9  
US-08-973-551-10  
; Sequence 10, Application US/08973551  
; Patent No. 6113902  
; GENERAL INFORMATION:  
; APPLICANT: Chermann, Jean-Claude  
; APPLICANT: Le Contel, Carole  
; APPLICANT: Galea, Pascale  
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING  
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
; TITLE OF INVENTION: DIAGNOSIS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/973,551  
; FILING DATE: 30-DEC-1997  
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FR96/01006  
; FILING DATE: 28-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 9507914  
; FILING DATE: 30-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Granados, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 65691/130  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-973-551-10

Query Match 22.7%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5  
|||  
Db 2 LSQPK 6

RESULT 10  
US-08-397-633A-81  
; Sequence 81, Application US/08397633A  
; Patent No. 5773577  
; GENERAL INFORMATION:  
; APPLICANT: Cappello, Joseph



;; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE  
;; NUMBER OF SEQUENCES: 105  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
;; STREET: 4 Embarcadero Center, Suite 3400  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-4187  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/397,633A  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Rowland, Bertram I  
;; REGISTRATION NUMBER: 20,015  
;; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 781-1989  
;; TELEFAX: (415) 398-3249  
;; TELEX: 910 277299  
;; INFORMATION FOR SEQ ID NO: 81:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-397-633A-81

Query Match 22.7%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPVP 10  
|||  
DB 10 VLPVP 14

RESULT 11  
US-08-973-551-3  
; Sequence 3, Application US/08973551  
; Patent No. 6113902  
; GENERAL INFORMATION:  
; APPLICANT: Chermann, Jean-Claude  
; APPLICANT: Le Contel, Carole  
; APPLICANT: Galea, Pascale  
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING  
; TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
; TITLE OF INVENTION: DIAGNOSIS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,551  
; FILING DATE: 30-DEC-1997

;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/FR96/01006  
;; FILING DATE: 28-JUN-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: FR 9507914  
;; FILING DATE: 30-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granados, Patricia D.  
;; REGISTRATION NUMBER: 33,683  
;; REFERENCE/DOCKET NUMBER: 65691/130  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-973-551-3

Query Match 22.7%; Score 5; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQPK 5  
|||  
DB 9 LSQPK 13

RESULT 12  
US-08-602-999A-195  
; Sequence 195, Application US/08602999A  
; Patent No. 6184205  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/602,999A  
; FILING DATE: 16-FEB-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 195:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-602-999A-195

Query Match 22.7%; Score 5; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVPQR 17  
Db 8 AVPQR 12

## RESULT 13

US-09-500-124-195  
; Sequence 195, Application US/09500124  
; Patent No. 6432920

## ; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: KAY, Brian K.  
; APPLICANT: THORN, Judith M.  
; APPLICANT: QUILLIAM, Lawrence A.  
; APPLICANT: DER, Channing J.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: RIDER, James E.  
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF  
; TITLE OF INVENTION: ISOLATING AND USING SAME  
; NUMBER OF SEQUENCES: 467

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/500,124  
; FILING DATE:

## ; CLASSIFICATION:

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/602,999  
; FILING DATE: 16-FEB-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Misrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-202  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 195:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown

## ; MOLECULE TYPE: peptide

US-09-500-124-195

Query Match 22.7%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVPQR 17  
Db 8 AVPQR 12

## RESULT 14

5175113-7  
; Patent No. 5175113  
; APPLICANT: NISSEN, MOGENS H.; ZEUTHEN, JESPER; LARSEN,  
; FLEMMING S.; THIM, LARS; CHRISTENSEN, MOGENS  
; TITLE OF INVENTION: MODIFIED B-2 MICROGLOBULIN  
; NUMBER OF SEQUENCES: 8  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/550,919  
; FILING DATE: 29-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 3436  
; FILING DATE: 15-JAN-1987  
; SEQ ID NO: 7:  
; LENGTH: 18  
5175113-7

## Query Match

Best Local Similarity 22.7%; Score 5; DB 6; Length 18;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LSQPK 5  
Db 7 LSQPK 11

## RESULT 15

US-09-177-249-278  
; Sequence 278, Application US/09177249  
; Patent No. 6229064

## ; GENERAL INFORMATION:

; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Ydegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; TITLE OF INVENTION: Development in Plants  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; CURRENT FILING DATE: 1998-10-22  
; EARLIER APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 278  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-278

## Query Match

Best Local Similarity 18.2%; Score 4; DB 3; Length 6;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7  
Db 3 PKVL 6

## RESULT 16

US-08-776-059-56  
; Sequence 56, Application US/08776059B  
; Patent No. 6271368

## ; GENERAL INFORMATION:

; APPLICANT: LENTZEN, Hans  
; APPLICANT: ECK, Jurgen  
; APPLICANT: BAUR, Axel

; APPLICANT: ZINKE, Holger  
 ; TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)  
 ; FILE REFERENCE: 674503-2003  
 ; CURRENT APPLICATION NUMBER: US/08/776,059B  
 ; CURRENT FILING DATE: 1999-06-19  
 ; EARLIER APPLICATION NUMBER: PCT/EP96/02273  
 ; EARLIER FILING DATE: 1996-06-25  
 ; EARLIER APPLICATION NUMBER: 95109949.8  
 ; EARLIER FILING DATE: 1995-06-26  
 ; NUMBER OF SEQ ID NOS: 56  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 56  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Spodoptera frugiperda  
 US-08-776-059-56

Query Match 18.2%; Score 4; DB 3; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
 ||||  
 Db 3 LPVP 6

RESULT 17  
 US-08-854-039B-23  
 ; Sequence 23, Application US/08854039B  
 ; Patent No. 6355774  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Massague, Joan  
 ; APPLICANT: Roberts, James M.  
 ; APPLICANT: Koff, Andrew  
 ; APPLICANT: Polyak, Kornelia  
 ; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS  
 ; TITLE OF INVENTION: PRODUCTION AND USE  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/854,039B  
 ; FILING DATE: 09-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Vincent, Matthew P.  
 ; REGISTRATION NUMBER: 36,709  
 ; REFERENCE/DOCKET NUMBER: MIV-079.04  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 23:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-854-039B-23

Query Match 18.2%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
 ||||  
 Db 1 LSQP 4  
 RESULT 18  
 US-09-645-456A-33  
 ; Sequence 33, Application US/09645456A  
 ; Patent No. 6562580  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fu, C. Alan  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS  
 ; FILE REFERENCE: A-68344/RMS/DHR  
 ; CURRENT APPLICATION NUMBER: US/09/645,456A  
 ; CURRENT FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US/09/425,324  
 ; PRIOR FILING DATE: 1999-10-21  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 33  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic  
 US-09-645-456A-33

Query Match 18.2%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VPQR 17  
 ||||  
 Db 3 VPQR 6

RESULT 19  
 US-09-425-324A-33  
 ; Sequence 33, Application US/09425324A  
 ; Patent No. 6562591  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fu, C. Alan  
 ; TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEINS, COMPOSITIONS  
 ; FILE REFERENCE: A-68344/RMS/DHR  
 ; CURRENT APPLICATION NUMBER: US/09/425,324A  
 ; CURRENT FILING DATE: 1999-10-21  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 33  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic  
 US-09-425-324A-33

Query Match 18.2%; Score 4; DB 4; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VPQR 17  
 ||||  
 Db 3 VPQR 6

RESULT 20  
 US-09-645-791-33  
 ; Sequence 33, Application US/09645791  
 ; Patent No. 6569658  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Luo, Ying

APPLICANT: Fu, Alan C  
APPLICANT: Shen, Mary  
TITLE OF INVENTION: NOVEL GERMINAL CENTER KINASE CELL CYCLE PROTEIN; COMPOSITIONS AND  
METHODS OF USE  
FILE REFERENCE: A-68344-1/RMS/DHR  
CURRENT APPLICATION NUMBER: US/09/645,791  
CURRENT FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 09/425,324  
PRIOR FILING DATE: 1999-10-21  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 33  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic  
US-09-645-791-33

Query Match 18.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 VPQR 17  
Db 3 VPQR 6

RESULT 21  
US-08-230-047-37  
Sequence 37, Application US/08230047  
Patent No. 5541109  
GENERAL INFORMATION:  
APPLICANT: Searefs III, George H.  
APPLICANT: Ivashchenko, Yuri D.  
APPLICANT: Jaye, Michael C.  
TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
PROTEIN  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.  
STREET: 500 Arcola Road, 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.1  
SOFTWARE: Word 5.0 (PatentIn)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/230,047  
FILING DATE: 19-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goodman, Rosanne  
REGISTRATION NUMBER: 32,534  
REFERENCE/DOCKET NUMBER: A1465-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (610) 454-3817  
TELEFAX: (610) 454-3808  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-230-047-37

Query Match 18.2%; Score 4; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10  
Db 3 LPVP 6

RESULT 22  
US-08-973-551-5  
Sequence 5, Application US/08973551  
Patent No. 6113902  
GENERAL INFORMATION:  
APPLICANT: Chermann, Jean-Claude  
APPLICANT: Le Contel, Carole  
APPLICANT: Galea, Pascale  
TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING  
AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
DIAGNOSIS  
TITLE OF INVENTION: DIAGNOSIS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,551  
FILING DATE: 30-DEC-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01006  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 9507914  
FILING DATE: 30-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Granados, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 65691/130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-551-5

Query Match 18.2%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
Db 1 SQPK 4

RESULT 23  
US-08-973-551-21  
Sequence 21, Application US/08973551  
Patent No. 6113902  
GENERAL INFORMATION:  
APPLICANT: Chermann, Jean-Claude

APPLICANT: Le Contel, Carole  
APPLICANT: Galea, Pascale  
TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING  
TITLE OF INVENTION: AN INTRACELLULAR PHASE, COMPOSITION FOR THE TREATMENT AND  
TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
TITLE OF INVENTION: DIAGNOSIS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,551  
FILING DATE: 30-DEC-1997  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR96/01006  
FILING DATE: 28-JUN-1996  
PRIOR APPLICATION DATA: FR 9507914  
FILING DATE: 30-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Granados, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 65691/130  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-973-551-21

Query Match 18.2%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
DB 1 SQPK 4

RESULT 24  
US-09-400-653A-4  
Sequence 4, Application US/09400653A  
Patent No. 6348311  
GENERAL INFORMATION:  
APPLICANT: Kastan, Michael  
APPLICANT: Canman, Christine  
APPLICANT: Kim, Seong-Tae  
APPLICANT: Lim, Dae-Sik  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies  
FILE REFERENCE: 2427/1F142  
CURRENT APPLICATION NUMBER: US/09/400,653A  
CURRENT FILING DATE: 1999-09-21  
PRIOR APPLICATION NUMBER: 09/248,061  
PRIOR FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 49  
SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PHOSPHORYLATION  
LOCATION: 4  
OTHER INFORMATION: Artificial sequence is a synthetic sequence.  
OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-09-400-653A-4

Query Match 18.2%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
DB 3 LSQP 6

RESULT 25  
US-09-248-061B-4  
Sequence 4, Application US/09248061B  
Patent No. 6387640  
GENERAL INFORMATION:  
APPLICANT: Kastan, M.  
APPLICANT: Canman, C.  
APPLICANT: Kim, S-T.  
APPLICANT: Lim, D-S.  
APPLICANT: St. Jude Children's Research Hospital  
TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies  
FILE REFERENCE: 2427/0F142  
CURRENT APPLICATION NUMBER: US/09/248,061B  
CURRENT FILING DATE: 1999-02-10  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: PHOSPHORYLATION  
LOCATION: 4  
OTHER INFORMATION: Artificial sequence is a synthetic sequence.  
OTHER INFORMATION: Xaa at position seven is any amino acid.  
US-09-248-061B-4

Query Match 18.2%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4  
DB 3 LSQP 6

RESULT 26  
US-08-571-985-21  
Sequence 21, Application US/08571985  
Patent No. 5783557  
GENERAL INFORMATION:  
APPLICANT: Burstein, Yigal  
APPLICANT: Trainin, Nathan  
APPLICANT: Rycus, Avigail  
TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
Compositions Comprising Them  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kohn & Associates  
STREET: 30500 No. 5783557thwestern Hwy., Suite 410  
CITY: Farmington Hills  
STATE: Michigan  
COUNTRY: USA

ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/571.985  
FILING DATE:  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 2163.00048  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (810) 539-5050  
TELEFAX: (810) 539-5055  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-571-985-21

Query Match 18.2%; Score 4; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7  
Db 5 PKVL 8

RESULT 27  
US-09-116-766-21  
; Sequence 21, Application US/09116766  
; Patent No. 5968898  
; GENERAL INFORMATION:  
; APPLICANT: Burstein, Vigal  
; APPLICANT: Trainin, Nathan  
; APPLICANT: Rycus, Avigail  
; TITLE OF INVENTION: THF-gamma2 Analogs and Pharmaceutical  
; TITLE OF INVENTION: Compositions Comprising Them  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kohn & Associates  
; STREET: 30500 No. 596898thwestern Hwy., Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: USA  
; ZIP: 48334  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/116,766  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: IL 106214  
FILING DATE: 01-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Montgomery, Ilene N.  
REGISTRATION NUMBER: 38,972  
REFERENCE/DOCKET NUMBER: 2163.00050  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (248) 539-5050

TELEFAX: (248) 539-5055  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-116-766-21

Query Match 18.2%; Score 4; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PKVL 7  
Db 5 PKVL 8

RESULT 28  
US-08-635-886C-138  
; Sequence 138, Application US/08635886C  
; Patent No. 6555114  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; TITLE OF INVENTION: VIRUS  
; FILE REFERENCE: 2752-18  
; CURRENT APPLICATION NUMBER: US/08/635,886C  
; CURRENT FILING DATE: 1996-04-25  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 138  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-08-635-886C-138

Query Match 18.2%; Score 4; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 AVPQ 16  
Db 1 AVPQ 4

RESULT 29  
US-08-350-260A-385  
; Sequence 385, Application US/08350260A  
; Patent No. 5962255  
; GENERAL INFORMATION:  
; APPLICANT: Winter, Gregory Paul  
; APPLICANT: Griffiths, Andrew David  
; APPLICANT: Williams, Samuel Cameron  
; APPLICANT: Waterhouse, Peter  
; APPLICANT: Nissim, Ahuva  
; APPLICANT: Johnson, Kevin Stuart  
; APPLICANT: Smith, Andrew John Hammond  
; TITLE OF INVENTION: Methods for producing members of specific  
; TITLE OF INVENTION: binding pairs  
; NUMBER OF SEQUENCES: 602  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David W. Clough  
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois

```
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-350-260A-385

Query Match 18.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSQP 4
DB 4 LSQP 7

RESULT 30
US-08-318-856A-54
; Sequence 54, Application US/08318856A
; Patent No. 5972351
; GENERAL INFORMATION:
; APPLICANT: Adrian V.S. Hill, et al.
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1+
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,856A
; FILING DATE: October 3, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 08 068.8
; FILING DATE: April 3, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 17 704.7
; FILING DATE: August 20, 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00711
; FILING DATE: April 5, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 263-PPIR1577US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 721-8200
; TELEFAX: (202) 721-8250
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acid residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-856A-54

Query Match 18.2%; Score 4; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7
DB 2 PKVL 5

RESULT 31
US-09-343-011B-7
; Sequence 7, Application US/09343011B
; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephane Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL
; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343,011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-343-011B-7

Query Match 18.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LPVP 10
DB 4 LPVP 7

RESULT 32
US-09-104-337A-385
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; Sequence 385, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; Griffiths, Andrew David
; Williams, Samuel Cameron
; Waterhouse, Peter
; Nissim, Ahuva
; Johnson, Kevin Stuart
; Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; binding pairs
; NUMBER OF SEQUENCES: 600
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Audrey L. Bartnicki
; STREET: Marshall, Gerstein & Borun
; 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/104,337A
; FILING DATE: 25-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/350,260
; FILING DATE: 05-DEC-1994
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bartnicki, Audrey L.
; REGISTRATION NUMBER: 40,499
; REFERENCE/DOCKET NUMBER: 28111/32372A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 385:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 385:
US-09-104-337A-385
Query Match 18.2%; Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LSQP 4
Db 4 LSQP 7
RESULT 33
US-07-869-933-19
; Sequence 19, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:

```

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; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-869-933-19
Query Match 18.2%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 VPQK 12
Db 2 VPQK 5
RESULT 34
US-08-361-517-13
; Sequence 13, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; ADHESION
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

```



APPLICATION NUMBER: 07/941,652  
FILING DATE: September 8, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0209  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated  
US-08-361-517-13

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
DB 1 KVL P 4

RESULT 35  
US-08-361-517-14  
Sequence 14, Application US/08361517  
Patent No. 5916876  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
TITLE OF INVENTION: Adhesion  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,517  
FILING DATE: herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/941,652  
FILING DATE: September 8, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0209  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated  
US-08-361-517-14

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
DB 1 KVL P 4

RESULT 36  
US-08-361-517-15  
Sequence 15, Application US/08361517  
Patent No. 5916876  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
TITLE OF INVENTION: Adhesion  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/361,517  
FILING DATE: herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/941,652  
FILING DATE: September 8, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0209  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acid residues  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated  
US-08-361-517-15

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
DB 1 KVL P 4

RESULT 37  
US-08-361-517-16  
Sequence 16, Application US/08361517  
Patent No. 5916876  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
TITLE OF INVENTION: Adhesion

```
;
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; US-08-361-517-15

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLP 8
Db 1 KVLP 4

RESULT 38
US-08-361-517-17
; Sequence 17, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
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```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; US-08-361-517-17

Query Match 18.2%; Score 4; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLP 8
Db 1 KVLP 4

RESULT 39
US-08-361-517-19
; Sequence 19, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
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US-08-361-517-19

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
|||  
Db 1 KVL P 4

RESULT 40

US-08-361-517-20  
; Sequence 20, Application US/08361517  
; Patent No. 5916876  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; ADHESION  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; ADDRESSES: and No. 5916876ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361,517  
; FILING DATE: herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/941,852  
; FILING DATE: September 8, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated

US-08-361-517-20

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
|||  
Db 1 KVL P 4

RESULT 41

US-08-318-856A-58  
; Sequence 59, Application US/08318856A  
; Patent No. 5972351  
; GENERAL INFORMATION:  
; APPLICANT: Adrian V.S. Hill, et al.  
; TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-

; TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE  
; TITLE OF INVENTION: ANTIGENS (AS AMENDED)  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
; STREET: 2033 K Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20006

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1+  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/318,856A  
; FILING DATE: October 3, 1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 08 068.8  
; FILING DATE: April 3, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 92 17 704.7  
; FILING DATE: August 20, 1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/GB93/00711  
; FILING DATE: April 5, 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee Cheng  
; REGISTRATION NUMBER: 40,949  
; REFERENCE/DOCKET NUMBER: 263-PP1R1577US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 721-8200  
; TELEFAX: (202) 721-8250  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-318-856A-58

Query Match 18.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKVL 7  
|||  
Db 3 PKVL 6

RESULT 42

US-09-103-663-19  
; Sequence 19, Application US/09103663D  
; Patent No. 6171803  
; GENERAL INFORMATION:  
; APPLICANT: Kinnet et al.  
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta  
; TITLE OF INVENTION: subunit of the high affinity receptor for  
; TITLE OF INVENTION: immunoglobulin E.  
; FILE REFERENCE: 50490  
; CURRENT APPLICATION NUMBER: US/09/103,663D  
; CURRENT FILING DATE: 1998-06-23  
; EARLIER APPLICATION NUMBER: 07/869,933  
; EARLIER FILING DATE: 1992-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-103-663-19

Query Match 18.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPQK 12  
|  
|  
|  
|  
Db 2 VPQK 5

RESULT 43  
US-09-220-528-111  
; Sequence 111, Application US/09220528A  
; Patent No. 6284540  
; GENERAL INFORMATION:  
; APPLICANT: Milbrandt, Jeffrey D.  
; TITLE OF INVENTION: Artemin, A No. 6284540el Neurotrophic Factor  
; FILE REFERENCE: 6029-7998  
; CURRENT APPLICATION NUMBER: US/09/220,528A  
; CURRENT FILING DATE: 1998-12-24  
; EARLIER APPLICATION NUMBER: 09/218,698  
; EARLIER FILING DATE: 1998-12-22  
; EARLIER APPLICATION NUMBER: 60/108,148  
; EARLIER FILING DATE: 1998-11-12  
; EARLIER APPLICATION NUMBER: 09/163,283  
; EARLIER FILING DATE: 1998-09-29  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 111  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-220-528-111

Query Match 18.2%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
|  
|  
|  
|  
Db 2 VLPV 5

RESULT 44  
PCT-US93-07964-13  
; Sequence 13, Application 93/07964  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; ADDRESSEE: Norris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: 93/07964  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated.  
PCT-US93-07964-14

Query Match 18.2%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated.  
PCT-US93-07964-13

Query Match 18.2%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLP 8  
|  
|  
|  
|  
Db 1 KVLP 4

RESULT 45  
PCT-US93-07964-14  
; Sequence 14, Application 93/07964  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; ADDRESSEE: Norris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: 93/07964  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated.  
PCT-US93-07964-14

QY 5 KVL P 8  
 Db 1 KVL P 4

## RESULT 46

PCT-US93-07964-15  
 ; Sequence 15, Application 93/07964  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George A. Heavner and Leon A. Epps  
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
 ; TITLE OF INVENTION: Adhesion  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: WORDPERFECT 5.0  
 ; CURRENT APPLICATION DATA:  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dianne B. Elderkin  
 ; REGISTRATION NUMBER: 28,598  
 ; REFERENCE/DOCKET NUMBER: CCOR-0025  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 15:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE:  
 ; DESCRIPTION: Amide terminated.  
 ; PCT-US93-07964-15

Query Match 18.2%; Score 4; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
 Db 1 KVL P 4

## RESULT 47

PCT-US93-07964-16  
 ; Sequence 16, Application 93/07964  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George A. Heavner and Leon A. Epps  
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
 ; TITLE OF INVENTION: Adhesion  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia

STATE: PA  
 COUNTRY: USA  
 ZIP: 19103  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WORDPERFECT 5.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 93/07964  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dianne B. Elderkin  
 REGISTRATION NUMBER: 28,598  
 REFERENCE/DOCKET NUMBER: CCOR-0025  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-3100  
 TELEFAX: (215) 568-3439  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE:  
 DESCRIPTION: Amide terminated.  
 PCT-US93-07964-16

Query Match 18.2%; Score 4; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVL P 8  
 Db 1 KVL P 4

## RESULT 48

PCT-US93-07964-17  
 ; Sequence 17, Application 93/07964  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George A. Heavner and Leon A. Epps  
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
 ; TITLE OF INVENTION: Adhesion  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: USA  
 ; ZIP: 19103  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS  
 SOFTWARE: WORDPERFECT 5.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 93/07964  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Dianne B. Elderkin  
 REGISTRATION NUMBER: 28,598  
 REFERENCE/DOCKET NUMBER: CCOR-0025

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated.  
PCT-US93-07964-17

Query Match 18.2%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL P 8  
Db 1 KVL P 4

RESULT 49  
PCT-US93-07964-19  
Sequence 19, Application 93/07964  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
ADHESION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 93/07964  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin

REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated.  
PCT-US93-07964-19

Query Match 18.2%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL P 8  
Db 1 KVL P 4

Db 1 KVL P 4  
RESULT 50  
PCT-US93-07964-20  
Sequence 20, Application 93/07964  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
ADHESION  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: Norris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 93/07964  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin

REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0025  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated.  
PCT-US93-07964-20

Query Match 18.2%; Score 4; DB 5; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVL P 8  
Db 1 KVL P 4

RESULT 51  
US-08-361-517-5  
Sequence 5, Application US/08361517  
Patent No. 5916876  
GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
ADHESION  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
ADDRESSEE: and No. 5916876ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: U.S.A.

```
;
;
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; US-08-361-517-5

Query Match      18.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLVP 8
Db      1 KVLVP 4

RESULT 52
US-08-361-517-31
; Sequence 31, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:

Query Match      18.2%; Score 4; DB 3; Length 11;

;
;
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: cysteine forms disulfide bond
; OTHER INFORMATION: with cysteine at position 11
; US-08-361-517-31

Query Match      18.2%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVLVP 8
Db      3 KVLVP 6

RESULT 53
US-08-802-981-136
; Sequence 136, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-0003000US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Aib"
; US-08-802-981-136

Query Match      18.2%; Score 4; DB 3; Length 11;
```

Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SQPK 5  
Db 8 SQPK 11

RESULT 54  
PCT-US93-07964-5  
; Sequence 5, Application 93/07964  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; TITLE OF INVENTION: Adhesion  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; ADDRESSEE: Norris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: WORDPERFECT 5.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: 93/07964  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 568-3100  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated.  
PCT-US93-07964-5

Query Match 18.2%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLP 8  
Db 1 KVLP 4

RESULT 55  
US-08-230-047-36  
; Sequence 36, Application US/08230047  
; Patent No. 5541109  
; GENERAL INFORMATION:  
; APPLICANT: Seafoss III, George H.  
; APPLICANT: Ivashchenko, Yuri D.  
; APPLICANT: Jaye, Michael C.  
; TITLE OF INVENTION: EXPRESSION CLONING OF C-SRC SH3 BINDING  
; TITLE OF INVENTION: PROTEIN  
; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rhone-Poulenc Rorer Inc.  
; STREET: 500 Arcola Road, 3C43  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: System 7.1  
; SOFTWARE: Word 5.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/230,047  
; FILING DATE: 19-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goodman, Rosanne  
; REGISTRATION NUMBER: 32,534  
; REFERENCE/DOCKET NUMBER: A1465-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (610) 454-3817  
; TELEFAX: (610) 454-3808  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-230-047-36

Query Match 18.2%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10  
Db 5 LPVP 8

RESULT 56  
US-08-053-079A-2  
; Sequence 2, Application US/08053079A  
; Patent No. 5606026  
; GENERAL INFORMATION:  
; APPLICANT: Rodman  
; TITLE OF INVENTION: Natural Human Igm Antibodies  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Darby & Darby  
; STREET: 805 Third Ave.  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/053,079A  
; FILING DATE: 26-APR-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Robinson, Joseph, R.  
; REGISTRATION NUMBER: 33,448  
; REFERENCE/DOCKET NUMBER: 4436/160600US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 527-7700  
; TELEFAX: (212) 753-6237  
; TELEX: 236687  
; INFORMATION FOR SEQ ID NO: 2:



SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus type 1  
IMMEDIATE SOURCE:  
CLONE: tat #2

US-08-053-079A-2

Query Match 18.2%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
Db 9 SQPK 12

## RESULT 57

US-08-053-079A-3  
Sequence 3, Application US/08053079A  
Patent No. 5606026

GENERAL INFORMATION:  
APPLICANT: Rodman  
TITLE OF INVENTION: Natural Human IgM Antibodies  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby  
STREET: 805 Third Ave.  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10022

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/053,079A  
FILING DATE: 26-APR-1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph, R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 4436/16060US4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)527-7700  
TELEFAX: (212)753-6237  
TELEX: 236687

## INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: Human immunodeficiency virus type 1  
IMMEDIATE SOURCE:  
CLONE: tat #3

US-08-053-079A-3

Query Match 18.2%; Score 4; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SQPK 5  
Db 2 SQPK 5

## RESULT 58

US-08-397-633A-101  
Sequence 101, Application US/08397633A  
Patent No. 5773577

GENERAL INFORMATION:  
APPLICANT: Cappello, Joseph  
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE  
TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING  
NUMBER OF SEQUENCES: 105  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/397,633A  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Rowland, Bertram I  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 781-1989  
TELEFAX: (415) 398-3249  
TELEX: 910 277299

## INFORMATION FOR SEQ ID NO: 101:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-397-633A-101

## Query Match

18.2%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLP 8  
Db 1 KVLP 4

## RESULT 59

US-08-361-517-4

Sequence 4, Application US/08361517  
Patent No. 5916876

GENERAL INFORMATION:  
APPLICANT: George A. Heavner and Leon A. Epps  
TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
TITLE OF INVENTION: Adhesion  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
ADDRESSEE: and No. 5916876ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia

```
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: unknown
; DESCRIPTION: Amide terminated
; US-08-361-517-4

Query Match 18.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVP 8
Db 2 KVLVP 5

RESULT 60
US-08-361-517-30
; Sequence 30, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; MEDIUM TYPE: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876xis
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598

Query Match 18.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVP 8
Db 2 KVLVP 5

STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,517
FILING DATE: herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/941,652
FILING DATE: September 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Dianne B. Elderkin
REGISTRATION NUMBER: 28,598

Query Match 18.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVP 8
Db 3 KVLVP 6

REFERENCE/DOCKET NUMBER: CCOR-0209
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acid residues
TYPE: amino acid
STRANDEDNESS:
MOLECULE TYPE: unknown
DESCRIPTION: Amide terminated
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: cysteine forms disulfide bond
OTHER INFORMATION: with cysteine at position 11
US-08-361-517-30

Query Match 18.2%; Score 4; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLVP 8
Db 3 KVLVP 6

RESULT 61
US-09-147-208-55
; Sequence 55, Application US/09147208
; Patent No. 6333303
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,208
; FILING DATE: 02-MAR-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Rudolph, John R.
; REGISTRATION NUMBER: 38,003
; REFERENCE/DOCKET NUMBER: 7841-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-147-208-55

Query Match 18.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VLVP 9
```

```

Db          |||||
            5 VLPV 8

RESULT 62
US-09-347-926-16
; Sequence 16, Application US/09347926
; Patent No. 6440386
; GENERAL INFORMATION:
; APPLICANT: LEUNG, SHUI-ON
; TITLE OF INVENTION: STABILIZED RADIOPHOSPHATE-LABELED PROTEINS
; FILE REFERENCE: 018733/0936
; CURRENT APPLICATION NUMBER: US/09/347,926
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-347-926-16

Query Match      18.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          7 LPVP 10
            |||||
Db          2 LPVP 5

RESULT 63
US-09-550-117A-55
; Sequence 55, Application US/09550117A
; Patent No. 6531125
; GENERAL INFORMATION:
; APPLICANT: Boigford, Thor
; TITLE OF INVENTION: Antiviral Ricin-Like Proteins
; FILE REFERENCE: 10447-10
; CURRENT APPLICATION NUMBER: US/09/550.117A
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/147,208
; PRIOR FILING DATE: 1999-03-02
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pAP-205/pAP-206 linker
US-09-550-117A-55

Query Match      18.2%; Score 4; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          6 VLPV 9
            |||||
Db          5 VLPV 8

RESULT 64
PCT-US93-07964-4
; Sequence 4, Application 93/07964
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSSEE: Norris

; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 93/07964
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated.
PCT-US93-07964-4

Query Match      18.2%; Score 4; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          5 KVLV 8
            |||||
Db          2 KVLV 5

RESULT 65
US-08-361-517-3
; Sequence 3, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:

```

```
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; US-08-361-517-3

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVL P 8
Db      3 KVL P 6

RESULT 66
US-08-361-517-27
; Sequence 27, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: cysteine forms disulfide bond
; US-08-361-517-3
```

```
; OTHER INFORMATION: with cysteine at position 13
; US-08-361-517-27

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVL P 8
Db      5 KVL P 8

RESULT 67
US-08-361-517-28
; Sequence 28, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: and No. 5916876ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,517
; FILING DATE: herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/941,652
; FILING DATE: September 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Dianne B. Elderkin
; REGISTRATION NUMBER: 28,598
; REFERENCE/DOCKET NUMBER: CCOR-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acid residues
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE:
; DESCRIPTION: Amide terminated
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 2
; OTHER INFORMATION: cysteine forms disulfide bond
; OTHER INFORMATION: with cysteine at position 12
; US-08-361-517-28

Query Match      18.2%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KVL P 8
Db      4 KVL P 7

RESULT 68
```

US-08-361-517-29  
 ; Sequence 29, Application US/08361517  
 ; Patent No. 5916876  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George A. Heavner and Leon A. Epps  
 ; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
 ; TITLE OF INVENTION: Adhesion  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
 ; ADDRESSEE: and No. 5916876r1s  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/361.517  
 ; FILING DATE: herewith  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 07/941.652  
 ; FILING DATE: September 8, 1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Dianne B. Elderkin  
 ; REGISTRATION NUMBER: 28,598  
 ; REFERENCE/DOCKET NUMBER: CCOR-0209  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 215-568-3100  
 ; TELEFAX: 215-568-3439  
 ; INFORMATION FOR SEQ ID NO: 29:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acid residues  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: Amide terminated  
 ; FEATURE:  
 ; NAME/KEY: Modified-site  
 ; LOCATION: 1  
 ; OTHER INFORMATION: cysteine forms disulfide bond  
 ; OTHER INFORMATION: with cysteine at position 11

US-08-361-517-29  
 Query Match 18.2%; Score 4; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KVLP 8  
 Db 3 KVLP 6

RESULT 69

US-09-043-937A-16  
 ; Sequence 16, Application US/09043937A  
 ; Patent No. 6211432  
 ; GENERAL INFORMATION:

APPLICANT: BOUDET, ALAIN-MICHEL  
 PICHON, MAGALIE  
 GRIMA-PETTENATI, JACQUELINE  
 BECKERT, MICHEL  
 GAVAS, PASCAL  
 BRIAT, JEAN-FRANCOIS

TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA  
 REDUCTASE AND APPLICATIONS THEREOF IN THE CONTROL OF  
 LIGNIN CONTENTS IN PLANTS

NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIXON & VANDERHUYE, P.C.  
 STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR  
 CITY: ARLINGTON  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22201  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/043.937A  
 FILING DATE: 24-Jul-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: WO PCT/FR96/01544  
 FILING DATE: 03-OCT-1996  
 APPLICATION NUMBER: FR 95.11623  
 FILING DATE: 03-OCT-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: SADOFF, B.J.  
 REGISTRATION NUMBER: 36.663  
 REFERENCE/DOCKET NUMBER: 1487-20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-816-4000  
 TELEFAX: 703-816-4100  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 13 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 6  
 OTHER INFORMATION: /label= Xaa  
 /note= "any amino acid"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 US-09-043-937A-16

Query Match 18.2%; Score 4; DB 3; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LPVP 10  
 Db 2 LPVP 5

RESULT 70

PCT-US93-07964-3  
 ; Sequence 3, Application 93/07964  
 ; GENERAL INFORMATION:

APPLICANT: George A. Heavner and Leon A. Epps  
 TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
 TITLE OF INVENTION: Adhesion  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 ADDRESSEE: Norris  
 STREET: One Liberty Place - 46th Floor  
 CITY: Philadelphia  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19103

COMPUTER READABLE FORM:  
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 93/07964  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dianne B. Elderkin  
REGISTRATION NUMBER: 28,598  
REFERENCE/DOCKET NUMBER: CCOR-0025  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE:  
DESCRIPTION: Amide terminated.  
PCT-US93-07964-3

Query Match 18.2%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KVLVP 8  
Db 3 KVLVP 6

## RESULT 71

PCT-US94-10257A-13  
Sequence 13, Application PC/TUS9410257A  
GENERAL INFORMATION:  
APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION  
APPLICANT: BRIGITTE DEVAUX  
APPLICANT: JONATHAN B. ROTHARD  
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE  
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10257A  
FILING DATE: 1 SEPTEMBER 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,824  
FILING DATE: 03-SEP-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ANNE I CRAIG  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 071.1 PCT  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US94-10257A-13

Query Match 18.2%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
Db 9 VLPV 12

## RESULT 72

PCT-US94-10257A-57  
Sequence 57, Application PC/TUS9410257A  
GENERAL INFORMATION:  
APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION  
APPLICANT: BRIGITTE DEVAUX  
APPLICANT: JONATHAN B. ROTHARD  
TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE  
TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION  
STREET: 610 LINCOLN STREET  
CITY: WALTHAM  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02145  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/10257A  
FILING DATE: 1 SEPTEMBER 1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/116,824  
FILING DATE: 03-SEP-1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: ANNE I CRAIG  
REGISTRATION NUMBER: 32,976  
REFERENCE/DOCKET NUMBER: 071.1 PCT  
TELEPHONE: (617) 466-6000  
TELEFAX: (617) 466-6040

INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
PCT-US94-10257A-57

Query Match 18.2%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 VLPV 9  
Db 6 VLPV 9

RESULT 73  
5223254-6  
;PATENT NO. 5223254  
; APPLICANT: PARADISO, PETER R.; HILDRETH, STEPHEN W.; HU,  
; BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/247,017  
; FILING DATE: 20-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 102,180  
; FILING DATE: 29-SEP-1987  
; SEQ ID NO: 6:  
; LENGTH: 13  
5223254-6

Query Match 18.2%; Score 4; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.8e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 18 DMPI 21  
|||  
Db 3 DMPI 6

RESULT 74  
US-08-361-517-2  
; Sequence 2, Application US/08361517  
; Patent No. 5916876  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; TITLE OF INVENTION: Adhesion  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; ADDRESSEE: and No. 5916876ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361,517  
; FILING DATE: herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/941,652  
; FILING DATE: September 8, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated  
US-08-361-517-2

Query Match 18.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KVLP 8  
|||  
Db 4 KVLP 7

RESULT 75  
US-08-361-517-6  
; Sequence 6, Application US/08361517  
; Patent No. 5916876  
; GENERAL INFORMATION:  
; APPLICANT: George A. Heavner and Leon A. Epps  
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte  
; TITLE OF INVENTION: Adhesion  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz  
; ADDRESSEE: and No. 5916876ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/361,517  
; FILING DATE: herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/941,652  
; FILING DATE: September 8, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne B. Elderkin  
; REGISTRATION NUMBER: 28,598  
; REFERENCE/DOCKET NUMBER: CCOR-0209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE:  
; DESCRIPTION: Amide terminated  
US-08-361-517-6

Query Match 18.2%; Score 4; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3e+02; Indels 0;  
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 KVLP 8  
|||  
Db 5 KVLP 8

Search completed: November 25, 2003, 20:30:03  
Job time : 18.7791 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 4.80233 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLLYQE 7

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : PIR\_76:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	17	S05917	chorion class A pr
2	4	57.1	17	S05919	chorion class A pr
3	4	57.1	17	S05921	chorion class A pr
4	3	42.9	9	JN0027	[Phe-6]-mosact - s
5	3	42.9	10	PK0030	triacylglycerol li
6	3	42.9	11	C53652	rhlg protein - pae
7	3	42.9	11	B41835	translation elonga
8	3	42.9	12	S01122	photosystem II 3.7
9	3	42.9	12	S01122	photosystem II 3.7
10	3	42.9	12	S01119	cytokinin-binding
11	3	42.9	13	B47415	mannose-1-phosphat
12	3	42.9	13	I70075	glycophorin B (mis
13	3	42.9	14	S22236	lipoygenase (EC 1
14	3	42.9	14	B36222	exonuclease ABC c
15	3	42.9	14	B61597	cytochrome P450 AL
16	3	42.9	15	C37765	hypothetical prote
17	3	42.9	15	S03955	acidic fibroblast
18	3	42.9	16	S65520	phospholipase A2 (
19	3	42.9	16	S24667	protein-tyrosine k
20	3	42.9	16	F54226	light-harvesting p
21	3	42.9	16	T14224	NADH2 dehydrogenas
22	3	42.9	17	S05913	chorion class A pr
23	3	42.9	17	S71327	hypothetical prote
24	3	42.9	17	A61557	major merozoite su
25	3	42.9	18	D56049	kidney stone prote
26	3	42.9	18	I50389	myosin heavy chain
27	3	42.9	18	A42016	mammary-derived gr
28	3	42.9	19	I40063	shikimate 5-dehydr
29	3	42.9	19	A61144	probable flagellar

30	3	42.9	19	2	A38386	Ca2+-transporting
31	3	42.9	20	2	A60822	cytochrome P450 PB
32	3	42.9	20	2	A26380	cytochrome P450 4A
33	3	42.9	20	2	A38586	GTP-binding protei
34	3	42.9	20	2	PL0161	hemagglutinin - In
35	3	42.9	20	2	A56045	urinary tract ston
36	3	42.9	20	2	S61278	nikkomycin synthes
37	3	42.9	20	2	A61150	2-oxoglutarate dec
38	3	42.9	20	2	PC2248	lambda I12 protein
39	3	28.6	3	3	A33802	thyrotropin-releas
40	2	28.6	3	3	S68328	blood cell protein
41	2	28.6	4	2	A35779	neuropeptide Antho
42	2	28.6	5	2	A26830	mitosis inhibiting
43	2	28.6	5	2	I40469	diazX-like protein
44	2	28.6	5	2	PQ0009	angiotensin-conver
45	2	28.6	5	2	B61445	Leu-enkephalin - b
46	2	28.6	5	2	S69237	surface protein te
47	2	28.6	6	2	A60986	N-formyl oligopept
48	2	28.6	6	2	JH0784	neuropeptide TE-6
49	2	28.6	6	2	A61068	lousutakinin - mig
50	2	28.6	6	2	I37283	Y protein - human
51	2	28.6	6	2	H48394	glycoprotein compo
52	2	28.6	6	2	I49424	cytotoxic T-lympho
53	2	28.6	7	1	A61324	dermorphin - Rohde
54	2	28.6	7	2	S36662	dermorphin (Lys-7)
55	2	28.6	7	2	S21230	dermorphin (Trp-4,
56	2	28.6	7	2	S08606	hypothetical prote
57	2	28.6	7	2	A34818	vicilin 72K chain
58	2	28.6	7	2	S78024	ribosomal protein
59	2	28.6	7	2	A34026	acetylcholinestera
60	2	28.6	7	2	S68004	hucolin, 75K chain
61	2	28.6	7	2	A11483	aspartate transami
62	2	28.6	7	2	PK0008	glucuronosyltransf
63	2	28.6	7	2	PN0649	pullulanase (EC 3.
64	2	28.6	8	2	S20162	leghemoglobin III
65	2	28.6	8	2	B24749	neuropeptide B - b
66	2	28.6	8	2	S37141	tpSA protein - Erw
67	2	28.6	8	2	S68802	nitrate reductase
68	2	28.6	8	2	S16324	hypothetical prote
69	2	28.6	8	2	A46306	spasmogenic toxin
70	2	28.6	8	2	J50317	leucokinin VII - M
71	2	28.6	8	2	S66646	cardiacacceleratory
72	2	28.6	8	2	A28719	thymic humoral fac
73	2	28.6	8	2	A42057	fibroblast growth
74	2	28.6	8	2	PN0043	phosphatidylethano
75	2	28.6	8	2	A35180	neutral proteinase
76	2	28.6	8	2	B45796	dihydrolipoamide S
77	2	28.6	9	2	A61102	parathyroid hormon
78	2	28.6	9	2	S07205	litorin 2-Glu - Au
79	2	28.6	9	2	A61357	phyllocaerulein -
80	2	28.6	9	2	D28854	fibriropeptide B -
81	2	28.6	9	2	E28854	fibriropeptide B -
82	2	28.6	9	2	F28854	quinoline 2-oxidor
83	2	28.6	9	2	S66607	dissimilatory sulf
84	2	28.6	9	2	S63491	ribosomal protein
85	2	28.6	9	2	S36898	endosperm protein,
86	2	28.6	9	2	S70334	alpha/beta-gliadin
87	2	28.6	9	2	S13333	transaldolase (EC
88	2	28.6	9	2	A12872	transaldolase (EC
89	2	28.6	9	2	A11497	cardioactive pepti
90	2	28.6	9	2	A26363	cardioactive pepti
91	2	28.6	9	2	S39766	cardioactive pepti
92	2	28.6	9	2	S27233	cardioactive pepti
93	2	28.6	9	2	S10920	venom protein HR-3
94	2	28.6	9	2	PT0315	ig heavy chain CRD
95	2	28.6	9	2	A28924	fructose-bisphosph
96	2	28.6	9	2	I52974	seminal vesicle pr
97	2	28.6	9	2	PH0942	T-cell receptor be
98	2	28.6	9	2	S39767	cardioactive pepti
99	2	28.6	9	2	PD0027	pev-tachykinin - p
100	2	28.6	10	2	C26997	unspecific monoocy



## ALIGNMENTS

## RESULT 1

S05917  
Chorion class A protein L4 precursor - silkworm (fragment)  
C:Species: Bombyx mori (silkworm)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999  
C:Accession: S05917  
R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.  
J. Mol. Biol. 209, 1-19, 1989  
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization  
A:Reference number: S05913; MUID:90040707; PMID:2810362  
A:Accession: S05917  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-17 <SPO>  
A:Cross-references: EMBL:X15560; NID:g5781; PIDN:CAA33571.1; PID:g5782  
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989  
C:Genetics:  
A:Map position: 2  
C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4  
|  
|  
|  
|  
Db 5 AFL 8

## RESULT 2

S05919  
Chorion class A protein L5 precursor - silkworm (fragment)  
C:Species: Bombyx mori (silkworm)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999  
C:Accession: S05919  
R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.  
J. Mol. Biol. 209, 1-19, 1989  
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization  
A:Reference number: S05913; MUID:90040707; PMID:2810362  
A:Accession: S05919  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-17 <SPO>  
A:Cross-references: EMBL:X15561; NID:g5786; PIDN:CAA33573.1; PID:g5787  
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989  
C:Genetics:  
A:Map position: 2  
C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4  
|  
|  
|  
|  
Db 5 AFL 8

## RESULT 3

S05921  
Chorion class A protein L6 precursor - silkworm (fragment)  
C:Species: Bombyx mori (silkworm)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999  
C:Accession: S05921  
R:Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.  
J. Mol. Biol. 209, 1-19, 1989  
A:Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybridization  
A:Reference number: S05913; MUID:90040707; PMID:2810362  
A:Accession: S05921  
A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA  
A:Residues: 1-17 <SPO>  
A:Cross-references: EMBL:X15562; NID:g5791; PIDN:CAA33575.1; PID:g5792  
A:Note: this sequence was submitted to the EMBL Data Library, Jun-1989  
C:Genetics:  
A:Map position: 2  
C:Superfamily: chorion class A protein pc292

Query Match 57.1%; Score 4; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4  
|  
|  
|  
|  
Db 5 AFL 8

## RESULT 4

JN0027  
[Phe-6]-mosact - sea urchin (Clypeaster japonicus)  
C:Species: Clypeaster japonicus  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Dec-1992  
C:Accession: JN0027  
R:Suzuki, N.; Kurita, M.; Yoshino, K.I.; Kajiuira, H.; Nomura, K.; Yamaguchi, M.  
Zool. Sci. 4, 649-656, 1987  
A:Title: Purification and structure of mosact and its derivatives from the egg jelly  
A:Reference number: JN0025  
A:Accession: JN0027  
A:Molecule type: protein  
A:Residues: 1-9 <SU2>  
C:Comment: Mosact, one of several sperm activating peptides located in egg jelly, and

Query Match 42.9%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
|  
|  
|  
Db 5 AFL 7

## RESULT 5

PX0030  
triacylglycerol lipase (EC 3.1.1.3) II - Yeast (Geotrichum candidum) (fragments)  
C:Species: Geotrichum candidum  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 30-Sep-1993  
C:Accession: PX0030  
R:Sugihara, A.; Shinada, Y.; Tominaga, Y.  
J. Biochem. 107, 426-430, 1990  
A:Title: Separation and characterization of two molecular forms of Geotrichum candidum  
A:Reference number: PX0030; MUID:90256718; PMID:2341377  
A:Accession: PX0030  
A:Molecule type: protein  
A:Residues: 1-10 <SUG>  
C:Comment: Lipase catalyzes the hydrolysis of triacylglycerols. This fungus contains  
C:Keywords: carboxylic ester hydrolase

Query Match 42.9%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5  
|  
|  
|  
Db 7 LLY 9

## RESULT 6

C53652  
rhlR protein - Pseudomonas aeruginosa (fragment)  
C:Species: Pseudomonas aeruginosa  
C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Aug-1998  
C:Accession: C53652  
R:Ochsner, U.A.; Flechter, A.; Reiser, J.

J. Biol. Chem. 269, 19787-19795, 1994  
 A:Title: Isolation, characterization, and expression in *Escherichia coli* of the Pseudomonas  
 A:Reference number: A35582; MUID:94327521; PMID:8051059  
 A:Accession: C53652  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-11 <OCH>  
 A:Cross-references: GB128170  
 C:Superfamily: sdhA regulatory protein

Query Match 42.9%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 7 FLL 9

RESULT 7  
 B41835  
 translation elongation factor EF-G homolog - *Bacillus subtilis* (fragment)  
 C:Species: *Bacillus subtilis*  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Dec-1997  
 C:Accession: B41835  
 R:Mitchell, C.; Morris, P.W.; Vary, J.C.  
 J. Bacteriol. 174, 2474-2477, 1992  
 A:Title: Identification of proteins phosphorylated by ATP during sporulation of *Bacillus*  
 A:Reference number: A41835; MUID:92210489; PMID:1556067  
 A:Accession: B41835  
 A:Molecule type: protein  
 A:Residues: 1-11 <MIT>  
 A:Note: this protein is phosphorylated during stationary phase but not during exponential  
 C:Keywords: phosphoprotein

Query Match 42.9%; Score 3; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 1 FLL 3

RESULT 8  
 S01122  
 photosystem II 3.7K protein - spinach (fragment)  
 C:Species: *Spinacia oleracea* (spinach)  
 C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993  
 C:Accession: S01122  
 R:Schoeder, W.P.; Henrysson, T.; Akerlund, H.E.  
 FEBS Lett. 235, 289-292, 1988  
 A:Title: Characterization of low molecular mass proteins of photosystem II by N-terminal

A:Reference number: S01120  
 A:Accession: S01122  
 A:Molecule type: protein  
 A:Residues: 1-12 <SCH>  
 C:Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
 |||  
 Db 7 AFL 9

RESULT 9  
 A35585  
 cytokinin-binding factor 1 - durum wheat  
 C:Species: *Triticum durum* (durum wheat)  
 C:Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993

C:Accession: A35585  
 R:Brinegar, A.C.; Cooper, G.; Stevens, A.; Hauer, C.R.; Shabanowitz, J.; Hunt, D.F.;  
 Proc. Natl. Acad. Sci. U.S.A. 85, 5927-5931, 1988  
 A:Title: Characterization of a benzyladenine binding-site peptide isolated from a whe  
 by mass spectrometry.  
 A:Reference number: A35585; MUID:88320357; PMID:3413067  
 A:Accession: A35585  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <BRI>

Query Match 42.9%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
 |||  
 Db 1 AFL 3

RESULT 10  
 S01119  
 photosystem II protein psbK - spinach chloroplast (fragment)  
 C:Species: chloroplast *Spinacia oleracea* (spinach)  
 C:Date: 30-Jun-1989 #sequence\_revision 31-Dec-1990 #text\_change 19-Jan-1996  
 C:Accession: S01119  
 R:Murata, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugitara, M.  
 FEBS Lett. 235, 283-288, 1988  
 A:Title: Identification of a new gene in the chloroplast genome encoding a low-molecu  
 A:Reference number: S01119  
 A:Accession: S01119  
 A:Molecule type: protein  
 A:Residues: 1-13 <MUR>  
 C:Genetics:

A:Gene: psbK  
 A:Genome: chloroplast  
 C:Superfamily: photosystem II protein psbK  
 C:Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II;

Query Match 42.9%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
 |||  
 Db 7 AFL 9

RESULT 11  
 B47415  
 mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment  
 N:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain  
 C:Species: *Sus scrofa domestica* (domestic pig)  
 C:Date: 25-Feb-1994 #sequence\_revision 12-Aug-1996 #text\_change 12-Aug-1996  
 C:Accession: B47415  
 R:Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.  
 J. Biol. Chem. 268, 17943-17950, 1993  
 A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and  
 A:Reference number: A47415; MUID:93352609; PMID:7688733  
 A:Accession: B47415  
 A:Molecule type: protein  
 A:Residues: 1-13 <SZU>  
 A:Experimental source: liver  
 C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and G  
 A:Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34  
 C:Keywords: blocked amino end; nucleotidyltransferase

Query Match 42.9%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
|||  
Db 11 FLL 13

## RESULT 12

I70075  
glycophorin B (mistranslated) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 21-Feb-1997 #sequence\_revision 14-Aug-1997 #text\_change 20-Apr-2000  
C:Accession: I70075  
R:Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.  
J. Biol. Chem. 265, 9259-9263, 1990  
A>Title: Identification of the crossing-over point of a hybrid gene encoding human glyco  
A:Reference number: I55334; MUID:90264417; PMID:1971625  
A:Accession: I70075  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-13 <REA>  
A:CROSS-references: GB:M33505; GB:J05465; NID:gi83726; PIDN:AAAS3152.1; PID:g442425  
A>Note: this sequence was not determined in this report; the translation is from an inco  
C:Genetics:  
A:Gene: GDB:GYBP  
A:CROSS-references: GDB:118891  
A:Map position: 4q28-q31

Query Match 42.9%; Score 3; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6  
|||  
Db 11 LYQ 13

## RESULT 13

S22236  
lipoxygenase (EC 1.13.11.12) 1 - barley (fragment)  
C:Species: Hordeum vulgare (barley)  
C>Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C:Accession: S22236  
R:Doderer, A.; Kockelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.  
Biochim. Biophys. Acta 1120, 97-104, 1992  
A>Title: Purification and characterization of two lipoxygenase isoenzymes from germinati  
A:Reference number: S21772; MUID:92207997; PMID:1554746  
A:Accession: S22236  
A:Molecule type: protein  
A:Residues: 1-14 <DOB>  
A:Experimental source: var. Triumph, seed  
C:Function:  
A:Description: catalyzes the peroxidation of polyunsaturates fatty acids to their corres  
C:Superfamily: lipoxygenase  
C:Keywords: monomer; oxidoreductase; seed

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5  
|||  
Db 5 LLY 7

## RESULT 14

B38222  
exonuclease ABC chain C (uvrC) [imported] - Pseudomonas fluorescens (fragment)  
C:Species: Pseudomonas fluorescens  
C>Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000  
C:Accession: B38222  
R:Laville, J.; Voisard, C.; Keel, C.; Maurhofer, M.; Defago, G.; Haas, D.  
Proc. Natl. Acad. Sci. U.S.A. 89, 1562-1566, 1992  
A>Title: Global control in Pseudomonas fluorescens mediating antibiotic synthesis and su  
A:Reference number: A38222; MUID:92179223; PMID:1311842

A:Contents: CHAO  
A:Accession: B38222  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-14 <LAV>  
A>Note: sequence extracted from NCBI backbone (NCBIN:85369, NCBI:94242)

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
|||  
Db 9 AFL 11

## RESULT 15

B61597  
Cytochrome P450 AL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
C:Accession: B61597  
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.  
Drug Metab. Dispos. 19, 291-297, 1991  
A>Title: Purification and aminopyrine monooxygenase activity of liver microsomal cyto  
A:Reference number: A61597; MUID:91292910; PMID:1676625  
A:Accession: B61597  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SHI>

Query Match 42.9%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
|||  
Db 9 FLL 11

## RESULT 16

C37765  
hypothetical protein (cema 3' region) - Chloroflexus aurantiacus (fragment)  
C:Species: Chloroflexus aurantiacus  
C>Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
C:Accession: C37765  
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
J. Bacteriol. 172, 4497-4504, 1990  
A>Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus auranti  
A:Reference number: A37765; MUID:90330558; PMID:2376566  
A:Accession: C37765  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <THE>  
A:CROSS-references: GB:M33964

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5  
|||  
Db 4 LLY 6

## RESULT 17

S03955  
acidic fibroblast growth factor - dog (fragment)  
N:Alternate names: alpha-endothelial cell growth factor  
C:Species: Canis lupus familiaris (dog)  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 18-Jun-1993  
C:Accession: S03955  
R:Quinkler, W.; Maasberg, M.; Bernotat-Danielowski, S.; Luethe, N.; Sharma, H.S.; Sci

Eur. J. Biochem. 181, 67-73, 1989  
A;Title: Isolation of heparin-binding growth factors from bovine, porcine and canine heparin  
A;Reference number: S03953; MUID:89231704; PMID:2714282  
A;Accession: S03955  
A;Molecule type: protein  
A;Residues: 1-15 <QUI>  
C;Keywords: growth factor

Query Match 42.9%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5  
|||  
Db 7 LLY 9

RESULT 18  
S65520  
Phospholipase A2 (EC 3.1.1.4) - Malayan spitting cobra (fragment)  
N;Contains: muscarinic acetylcholine receptor inhibitor  
C;Species: Naja naja sputatrix (Malayan spitting cobra)  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 17-Mar-2000  
C;Accession: S65520  
R;Miyoshi, S.; Tu, A.T.  
Arch. Biochem. Biophys. 328, 17-25, 1996  
A;Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine receptor inhibitor  
A;Reference number: S65520; MUID:96195757; PMID:8638927  
A;Accession: S65520  
A;Molecule type: protein  
A;Residues: 1-16 <MY>  
C;Superfamily: Phospholipase A2  
C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; phospholipase

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 2 LYQ 4

RESULT 19  
S24667  
protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Mar-1994 #sequence\_revision 13-Mar-1997 #text\_change 04-Feb-2000  
C;Accession: S24667  
R;Sorrentino, V.  
submitted to the EMBL Data Library, May 1992  
A;Reference number: S24666  
A;Accession: S24667  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-16 <SOR>  
A;Cross-references: EMBL:X65998; NID:g50433; PIDN:CAA46799.1; PID:g50434  
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
|||  
Db 10 AFL 12

RESULT 20  
F54226  
light-harvesting protein B-830 beta-2 chain - Chromatium purpuratum (fragment)  
C;Species: Chromatium purpuratum  
C;Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996

C;Accession: F54226  
R;Kerfeld, C.A.; Yeates, T.O.; Thornber, J.P.  
Biochemistry 33, 2178-2184, 1994  
A;Title: Purification and characterization of the peripheral antenna of the purple-sulfur bacterium Rhodospirillum rubrum  
A;Reference number: A54226; MUID:94162224; PMID:8117674  
A;Accession: F54226  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-16 <KER>  
C;Keywords: antenna complex; light-harvesting polypeptide

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
|||  
Db 1 AFL 3

RESULT 21  
T14224  
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - Euhadra herklotsi mitochondri  
C;Species: mitochondrion Euhadra herklotsi  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 03-Jun-2002  
C;Accession: T14224  
R;Yamazaki, N.; Ueshima, R.; Terrett, J.A.; Yokobori, S.; Kaifu, M.; Segawa, R.; Koba  
submitted to the EMBL Data Library, May 1996  
A;Description: Evolution of pulmonate gastropod mitochondrial genomes: Comparisons of  
A;Reference number: Z17932  
A;Accession: T14224  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-16 <YAM>  
A;Cross-references: EMBL:Z71694; NID:e912660; PID:e244560; PIDN:CAA96364.1  
A;Experimental source: adult; hepatopancreas  
C;Genetic: 8  
A;Genome: mitochondrion  
C;Keywords: mitochondrion; NAD; oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 10 FLL 12

RESULT 22  
S05913  
chorion class A protein L2 precursor - silkworm (fragment)  
C;Species: Bombyx mori (silkworm)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Aug-1999  
C;Accession: S05913  
R;Spoerel, N.A.; Nguyen, H.T.; Eickbush, T.H.; Kafatos, F.C.  
J. Mol. Biol. 209, 1-19, 1989  
A;Title: Gene evolution and regulation in the chorion complex of Bombyx mori. Hybrid  
A;Reference number: S05913; MUID:90040707; PMID:2810362  
A;Accession: S05913  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-17 <SPO>  
A;Cross-references: EMBL:X15558; NID:g5771; PIDN:CAA33567.1; PID:g5772  
A;Note: this sequence was submitted to the EMBL Data Library, Jun-1989  
C;Genetics: 8  
A;Map position: 2  
C;Superfamily: chorion class A protein pc292

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 7 FLL 9

## RESULT 23

S71327  
hypothetical protein - yeast (Saccharomyces cerevisiae)  
C/Species: Saccharomyces cerevisiae  
C/Date: 23-Jul-1997 #sequence\_revision 01-Aug-1997 #text\_change 29-Oct-1999  
C/Accession: S71327  
R/Sasaki, K.; Abid, M.R.; Miyazaki, M.  
FEBS Lett. 384, 151-154, 1996  
A/Title: Deoxyhypusine synthase Gene is essential for cell viability in the yeast Saccharomyces cerevisiae  
A/Reference number: S71326; MUID:96201956; PMID:8612813  
A/Accession: S71327  
A/Status: preliminary; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-17 <SAS>  
A/Cross-references: EMBL:D78185; NID:gl375086; PIDN:BAA11252.1; PID:d1011914; PID:gi375086

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 12 LYQ 14

## RESULT 24

A61557  
major merozoite surface antigen - malaria parasite (Plasmodium falciparum) (strain FCB-1)  
C/Species: Plasmodium falciparum  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C/Accession: A61557  
R/Heidrich, H.G.  
Biol. Cell 64, 205-214, 1988  
A/Title: Isolation and functional characterization of Plasmodium falciparum merozoite antigen  
A/Reference number: A61557; MUID:89150734; PMID:3067799  
A/Accession: A61557  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-17 <HEI>  
C/Keywords: surface antigen

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7  
|||  
Db 6 YQE 8

## RESULT 25

D56049  
kidney stone protein, 34.5K - unidentified organism (fragment)  
C/Species: unidentified organism  
C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 20-Apr-2000  
C/Accession: D56049  
R/Binette, J.P.; Binette, M.B.  
Scanning Microsc. 8, 233-239, 1994  
A/Title: Sequencing of proteins extracted from stones.  
A/Reference number: A56049; MUID:95215817; PMID:7701298  
A/Accession: D56049  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <BIN>  
A/Experimental source: urate-calcium oxalate kidney stone  
A/Note: the source is designated as Homo sapiens, however the true source probably originates from a different source  
C/Superfamily: sulfate-binding protein

Query Match 42.9%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 16 LYQ 18

## RESULT 26

I50389  
myosin heavy chain - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C/Accession: I50389  
R/Freyer, G.A.; Robbins, J.  
J. Biol. Chem. 258, 7149-7154, 1983  
A/Title: The analysis of a chicken myosin heavy chain cdna clone.  
A/Reference number: I50388; MUID:83213464; PMID:6304080  
A/Accession: I50389  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: mRNA  
A/Residues: 1-18 <FRE>  
A/Cross-references: GB:K00815; NID:G212369; PIDN:AAA48969.1; PID:G212370

Query Match 42.9%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 7 FLL 9

## RESULT 27

A42016  
mammary-derived growth factor 1 - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 10-Jul-1992 #sequence\_revision 10-Jul-1992 #text\_change 30-Sep-1993  
C/Accession: A42016  
R/Bano, M.; Lupu, R.; Kidwell, W.R.; Lippman, M.E.; Dickson, R.B.  
Biochemistry 31, 610-616, 1992  
A/Title: Production and characterization of mammary-derived growth factor 1 in mammary epithelial cells  
A/Reference number: A42016; MUID:92118863; PMID:1731916  
A/Accession: A42016  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <BAN>

Query Match 42.9%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 11 FLL 13

## RESULT 28

I40063  
shikimate 5-dehydrogenase (EC 1.1.1.25) - Buchnera aphidicola (fragment)  
C/Species: Buchnera aphidicola  
C/Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 08-Oct-1999  
C/Accession: I40063  
R/Rouhbkahsh, D.; Baumann, P.  
Gene 155, 107-112, 1995  
A/Title: Characterization of a putative 23S-5S rRNA operon of Buchnera aphidicola (strain 93-1)  
A/Reference number: I40061; MUID:95212914; PMID:7535281  
A/Accession: I40063  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-19 <RES>

A;Cross-references: EMBL:U10497; NID:9854713; PIDN:AAA79126.1; PID:9854714  
 C;Genetics:  
 A;Gene: aroE  
 C;Keywords: oxidoreductase

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 2 FLL 4

## RESULT 29

A61144  
 C;Species: Trypanosoma cruzi  
 C;Date: 10-Mar-1994 #sequence\_revision 07-Apr-1994 #text\_change 24-Feb-1995  
 C;Accession: A61144  
 R;Bua, J.; Bontempi, E.J.; Levin, M.; Orn, A.; Velasco, D.; Moreno, M.; Levi-Yeyati, P.;  
 Exp. Parasitol. 72, 54-62, 1991  
 A;Title: Trypanosoma cruzi: cellular and antibody response against the parasite in mice  
 A;Reference number: A61144; MUID:91130571; PMID:1993465  
 A;Accession: A61144  
 A;Molecule type: mRNA  
 A;Residues: 1-19 <BUA>

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
 |||  
 Db 2 AFL 4

## RESULT 30

A38386  
 C22+-transporting ATPase (EC 3.6.3.8) - rat (fragments)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 19-Apr-2002  
 C;Accession: A38386  
 R;Kessler, F.; Benardini, F.; Bachs, O.; Serratos, J.; James, P.; Caride, A.J.; Gazzoni  
 J. Biol. Chem. 265, 16012-16019, 1990  
 A;Title: Partial purification and characterization of the Ca(2+)-pumping ATPase of the 1  
 A;Reference number: A38386; MUID:90368826; PMID:2144292  
 A;Accession: A38386

A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-19 <KES>  
 C;Keywords: hydrolase

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
 |||  
 Db 3 LYQ 5

## RESULT 31

A60822  
 cytochrome P450 PB-3a - rat (fragment)  
 N;Contains: oxidoreductase (EC 1.1.1.1)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 11-Jun-1999  
 A;Accession: A60822; I55191  
 R;Ameliazad, Z.; Narbonne, J.F.; Wolf, C.R.; Robertson, L.W.; Oesch, F.  
 Biochem. Pharmacol. 37, 3245-3249, 1988  
 A;Title: Effect of nutritional imbalances on cytochrome P-450 isozymes in rat liver.  
 A;Reference number: A60822; MUID:88293349; PMID:3041969

A;Accession: A60822  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-20 <AME>  
 R;Hashimoto, T.; Matsumoto, T.; Nishizawa, M.; Kawabata, S.  
 J. Biochem. 103, 487-492, 1988  
 A;Title: A mutant rat strain deficient in induction of a phenobarbital-inducible form  
 A;Reference number: I55191; MUID:88273074; PMID:2839467  
 A;Accession: I55191  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-20 <RES>  
 A;Cross-references: GB:D00250; NID:9220727; PIDN:BAA00181.1; PID:9220728  
 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
 C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane prot

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 15 FLL 17

## RESULT 32

A26380  
 cytochrome P450 4A2 - rat (fragment)  
 N;Alternate names: cytochrome P450K-5  
 N;Contains: oxidoreductase (EC 1.1.1.1)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 19-Nov-1988 #sequence\_revision 19-Nov-1988 #text\_change 05-Mar-1999  
 C;Accession: A26380  
 R;Imaoka, S.; Funae, Y.  
 Biochem. Biophys. Res. Commun. 141, 711-717, 1986  
 A;Title: Purification and NH2-terminal sequence of cytochrome P-450 from kidney micro  
 A;Reference number: A26380; MUID:87100198; PMID:3801020  
 A;Accession: A26380  
 A;Molecule type: protein  
 A;Residues: 1-20 <IMA>

R;Kimura, S.; Hardwick, J.P.; Kozak, C.A.; Gonzalez, F.J.  
 DNA 8, 517-525, 1989  
 A;Title: The rat clofibrate-inducible CYP4A subfamily II. cDNA sequence of IVA3, mappi  
 A;Reference number: A32966; MUID:89356272; PMID:2766933  
 A;Contents: annotation; identification of constitutive kidney form as CYP4A2  
 C;Genetics:  
 A;Gene: CYP4A2  
 C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology  
 C;Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane prot

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
 |||  
 Db 18 AFL 20

## RESULT 33

A38566  
 GTP-binding protein G25K - bovine (fragments)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 31-Jan-1992 #sequence\_revision 31-Jan-1992 #text\_change 16-Jul-1999  
 A;Accession: A38566  
 R;Yaman, H.K.; Farnsworth, C.C.; Xie, H.; Evans, T.; Howald, W.N.; Gelb, M.H.; Glomse  
 Proc. Natl. Acad. Sci. U.S.A. 88, 286-290, 1991  
 A;Title: Membrane-binding domain of the small G protein G25K contains an S-(all-trans-  
 A;Reference number: A38566; MUID:91095446; PMID:1898776  
 A;Accession: A38566  
 A;Status: preliminary  
 A;Molecule type: protein

A;Residues: 1-20 <YAM>  
 C;Superfamily: ras transforming protein; translation elongation factor Tu homology  
 C;Keywords: GTP binding  
 F;8-11/Region: GTP-binding NKXD motif

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 3 FLL 5

## RESULT 34

PL0161

hemagglutinin - Influenza H2N2 (fragment)

C;Species: Influenza H2N2

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-May-1997

C;Accession: PL0161

R;Sweetser, M.T.; Braciale, V.L.; Braciale, T.J.

J. Exp. Med. 170, 1357-1368, 1989

A;Title: Class I major histocompatibility complex-restricted T lymphocyte recognition of  
 A;Reference number: PL0161; MUID:90010790; PMID:2477491

A;Accession: PL0161

A;Molecule type: mRNA

A;Residues: 1-20 <SWE>

A;Experimental source: strain A/JAP/305/57

C;Comment: This protein plays a major role in initiation of infection and in the pathoge  
 C;Superfamily: Influenza virus hemagglutinin

C;Keywords: hemagglutinin

F;1-20/Region: immunodominant site recognized by T-lymphocytes

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
 |||  
 Db 3 LYQ 5

## RESULT 35

A56045

urinary tract stone matrix protein 12, 43K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 12-Apr-1995

C;Accession: A56045

R;Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A;Description: Isolation, characterization and sequence of stone proteins.

A;Reference number: A56046

A;Accession: A56045

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <BIN>

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 9 FLL 11

## RESULT 36

S61278

nikkomycin synthesis protein P4 - Streptomyces tendae (fragment)

C;Species: Streptomyces tendae

C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999

C;Accession: S61278

R;Moehrle, V.; Roos, U.; Bormann, C.

Mol. Microbiol. 15, 561-571, 1995

A;Title: Identification of cellular proteins involved in nikkomycin production in Str.  
 A;Reference number: S61278; MUID:95302967; PMID:7783626

A;Accession: S61278

A;Molecule type: protein

A;Residues: 1-20 <MOE>

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 8 FLL 10

## RESULT 37

A61150

2-oxoglutarate decarboxylase (EC 4.1.1.71) - Euglena gracilis (fragment)

C;Species: Euglena gracilis

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-Apr-1994

C;Accession: A61150

R;Shigeoka, S.; Nakano, Y.

Arch. Biochem. Biophys. 288, 22-28, 1991

A;Title: Characterization and molecular properties of 2-oxoglutarate decarboxylase fr  
 A;Reference number: A61150; MUID:91378443; PMID:1910306

A;Accession: A61150

A;Molecule type: protein

A;Residues: 1-20 <SHI>

C;Keywords: carbon-carbon lyase; carboxy-lyase; homotetramer; mitochondrion

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 |||  
 Db 12 FLL 14

## RESULT 38

PC2248

lambda 112 protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 17-Sep-1997

C;Accession: PC2248

R;Sakai, N.; Inui, K.; Fujii, N.; Fukushima, H.; Nishimoto, J.; Yanagihara, I.; Isega

Biochem. Biophys. Res. Commun. 198, 485-491, 1994

A;Title: Krabbe disease: isolation and characterization of a full-length cDNA for hum  
 A;Reference number: JC2397; MUID:94128088; PMID:8297359

A;Accession: PC2248

A;Molecule type: mRNA

A;Residues: 1-20 <SAK>

A;Cross-references: DDBJ:D25284

Query Match 42.9%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5  
 |||  
 Db 12 LLY 14

## RESULT 39

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: A33802

R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A;Title: A novel peptide, pyroglutamylglutamylproline amide, in the rabbit prostate c

A:Reference number: A33802; MUID:89255196; PMID:2498305

A:Accession: A33802

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-3 <COC>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end; pyrrolutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 28.6%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7  
||  
Db 1 QE 2

RESULT 40

S68328 Blood cell protein A - Molgula manhattensis (fragment)

C:Species: Molgula manhattensis

C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: S68328

R:Taylor, S.W.; Ross, M.M.; Waite, J.H.

Arch. Biochem. Biophys. 324, 228-240, 1995

A:Title: Novel 3,4-di- and 3,4,5-trihydroxyphenylalanine-containing polypeptides from th

A:Reference number: S68325; MUID:96132650; PMID:8554314

A:Accession: S68328

A:Molecule type: protein

A:Residues: 1-3 <TAY>

Query Match 28.6%; Score 2; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
Db 1 AF 2

RESULT 41

A35779 neuropeptide Antho-RNamide - sea anemone (Anthopleura elegantissima)

C:Species: Anthopleura elegantissima

C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 08-Dec-1995

A:Accession: A35779

R:Grimmelikhuijzen, C.J.P.; Rinehart, K.L.; Jacob, E.; Graff, D.; Reinscheid, R.K.; Noth

Proc. Natl. Acad. Sci. U.S.A. 87, 5410-5414, 1990

A:Title: Isolation of L-3-phenylacetyl-L-leu-Arg-Asn-NH2 (Antho-RNamide), a sea anemone ne

A:Reference number: A35779; MUID:90319122; PMID:1973541

A:Accession: A35779

A:Molecule type: protein

A:Residues: 1-4 <GRI>

C:Comment: The L-3-phenylacetyl blocking group probably arises from an amino-terminal ph

C:Keywords: amidated carboxyl end; neuropeptide; phenylacetylation

F:1/Modified site: L-3-phenylacetic acid (Phe) #status experimental

F:4/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
||  
Db 1 FL 2

RESULT 42

A26830

C:Species: Mus musculus (house mouse)

C:Keywords: mitosis inhibiting peptide - mouse

C:Keywords: Mus musculus (house mouse)

C>Date: 19-Nov-1988 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000

C:Accession: A26830

R:Reichelt, K.; Elgjo, K.; Edminson, P.D.

Biochem. Biophys. Res. Commun. 146, 1493-1501, 1987

A:Title: Isolation and structure of an epidermal mitosis inhibiting pentapeptide.

A:Reference number: A26830; MUID:87298602; PMID:3619940

A:Accession: A26830

A:Molecule type: protein

A:Residues: 1-5 <REI>

C:Superfamily: unassigned animal peptides

C:Keywords: blocked amino end; pyrrolutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7  
||  
Db 1 QE 2

RESULT 43

I40469

dnazK-like protein - Bacillus subtilis (fragment)

C:Species: Bacillus subtilis

C>Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 21-Jul-2000

A:Accession: I40469

R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.

Mol. Gen. Genet. 215, 478-482, 1989

A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.

A:Reference number: I40469; MUID:89218958; PMID:2468993

A:Accession: I40469

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-5 <RES>

C:Cross-references: EMBL:X14796; NID:g40130; PIDN:CAA32902.1; PID:g4376204

C:Genetics:

A:Start Codon: GTG

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQ 6  
||  
Db 3 YQ 4

RESULT 44

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N:Alternate names: ficus latex peptide 2

C:Species: Ficus carica (common fig)

C>Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995

A:Accession: PQ0009

R:Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A:Reference number: PQ0008

A:Accession: PQ0009

A:Molecule type: protein

A:Residues: 1-5 <MAR>

A:Experimental source: latex

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 28.6%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5  
||  
Db 1 LY 2



## RESULT 45

B61445  
 Leu-enkephalin - blue mussel  
 C;Species: Mytilus edulis (blue mussel)  
 C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 21-Jan-2000  
 C;Accession: B61445  
 R;Leung, M.K.; Stefano, G.B.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984  
 A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis  
 A;Reference number: A61445; MUID:84144823; PMID:6583690  
 A;Accession: B61445  
 A;Molecule type: protein  
 A;Residues: 1-5 <LEU>  
 A;Experimental source: pedal ganglia  
 C;Keywords: neuropeptide; opioid peptide

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3  
 Db 4 FL 5

## RESULT 46

S69237  
 surface protein tetrabrachion heavy chain - Staphylothermus marinus (fragment)  
 C;Species: Staphylothermus marinus  
 C;Date: 04-Dec-1997 #sequence\_revision 04-Dec-1997 #text\_change 17-Mar-1999  
 C;Accession: S69237  
 R;Peters, J.; Nitech, M.; Kuehlmoegen, B.; Golbik, R.; Lupas, A.; Kellermann, J.; Engelh  
 J. Mol. Biol. 245, 395-401, 1995  
 A;Title: Tetrabrachion: a filamentous archaeobacterial surface protein assembly of unusua  
 A;Reference number: S69237; MUID:95139068; PMID:7837271  
 A;Accession: S69237  
 A;Molecule type: protein  
 A;Residues: 1-5 <PET>  
 A;Experimental source: strain Fl, DSM 3639  
 C;Keywords: cell wall; glycoprotein; heat-stable protein

Query Match 28.6%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
 Db 3 LL 4

## RESULT 47

A60986  
 N-formyl oligopeptide - Escherichia coli (fragment)  
 C;Species: Escherichia coli  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
 C;Accession: A60986  
 R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.  
 Experientia 45, 1097-1099, 1989  
 A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methion  
 A;Reference number: A60986; MUID:90092408; PMID:2689204  
 A;Accession: A60986  
 A;Molecule type: protein  
 A;Residues: 1-6 <BRO>  
 C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.  
 F;1/Modified site: N-formylmethionine #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4

Db 5 LL 6

## RESULT 48

JH0784  
 neuropeptide TE-6 - pig roundworm (fragment)  
 C;Species: Ascaris suum (pig roundworm)  
 C;Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 28-Apr-1995  
 C;Accession: JH0784  
 R;Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan,  
 Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992  
 A;Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascar  
 A;Reference number: JH0784; MUID:93038603; PMID:1417808  
 A;Accession: JH0784  
 A;Molecule type: protein  
 A;Residues: 1-6 <SMA>  
 A;Experimental source: gonoduct  
 C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 OE 7  
 Db 3 OE 4

## RESULT 49

A61068  
 locustakinin - migratory locust  
 C;Species: Locusta migratoria (migratory locust)  
 C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 08-Dec-1995  
 C;Accession: A61068  
 R;Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.  
 Regul. Pept. 37, 49-57, 1992  
 A;Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation,  
 A;Reference number: A61068; MUID:92262851; PMID:1585017  
 A;Accession: A61068  
 A;Molecule type: protein  
 A;Residues: 1-6 <SCH>  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide; neuropeptide  
 F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
 Db 1 AF 2

## RESULT 50

I37263  
 Y protein - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
 C;Accession: I37263  
 R;Maeder, G.; Habener, J.F.  
 Endocrinology 131, 2010-2015, 1992  
 A;Title: Novel testis germ cell-specific transcript of the CREB gene contains an alte  
 A;Reference number: I37263; MUID:93010691; PMID:1396344  
 A;Accession: I37263  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-6 <RES>  
 A;Cross-references: EMBL:X68994; NID:G396171; PIDN:C448780.1; PID:G579816  
 C;Genetics:  
 A;Gene: CREB

Query Match 28.6%; Score 2; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
||  
5 LL 6

Db

RESULT 51

H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C;Accession: H48394  
R;Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequence numbers.  
A;Reference number: A48394; MUID:93250576; PMID:8485470  
A;Accession: H48394  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <MAT>  
A;Experimental source: milk  
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C;Keywords: glycoprotein

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
||  
3 LL 4

Db

RESULT 52

I49424  
cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment)  
C;Species: Mus spretus (western wild mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: I49424  
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A;Reference number: I48934; MUID:94319082; PMID:8043949  
C;Accession: I49424  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: EMBL:U05745; NID:g497084; PIDN:AAB60481.1; PID:g642831  
C;Keywords: hydrolase; serine proteinase

Query Match 28.6%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
||  
5 LL 6

Db

RESULT 53

A61324  
dermorphin - Rohde's leaf frog  
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C;Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C;Accession: A61324  
R;Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A;Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A;Reference number: A61324; MUID:82029915; PMID:7287302  
A;Accession: A61324

A;Molecule type: protein  
A;Residues: 1-7 <MON>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
F;2/Modified site: D-alanine (Ala) #status experimental  
F;6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F;7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
||  
2 AF 3

Db

RESULT 54

S36662  
dermorphin (Lys-7) [validated] - two-colored leaf frog  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C;Accession: S36662  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil,  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S36662  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
||  
2 AF 3

Db

RESULT 55

S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil,  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
||  
2 AF 3

Db

RESULT 56

S08606  
hypothetical protein 2 estrogen receptor 5'-region - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 18-Aug-2000  
C;Accession: S08606

R;Krust, A.; Green, S.; Argos, P.; Kumar, V.; Walter, P.; Bornert, J.M.; Chambon, P.  
EMBO J. 5, 891-897, 1986  
A;Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes  
A;Reference number: S07192; MUID:86247578; PMID:3755102  
A;Accession: S08606  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <KRU>  
A;Cross-references: EMBL:X03805; NID:G63378; PIDN:CAA27432.1; PID:G584490  
C;Superfamily: unassigned leader peptides

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
DB 2 FL 3

RESULT 57  
A34818  
vicilin 72K chain - pigeon pea (fragment)  
C;Species: Cajanus cajan (pigeon pea)  
C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C;Accession: A34818  
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.  
A;Reference number: A34818; MUID:90165956; PMID:2306256  
A;Accession: A34818  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MAW>

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OE 7  
DB 6 OE 7

RESULT 58  
S78024  
ribosomal protein Yml21, mitochondrial - yeast (Saccharomyces cerevisiae) (fragment)  
C;Species: Saccharomyces cerevisiae  
C;Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 14-Nov-1997  
C;Accession: S78024  
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wittma  
Eur. J. Biochem. 245, 449-456, 1997  
A;Title: Identification and characterization of the genes for mitochondrial ribosomal pr  
A;Reference number: S78018; MUID:97296414; PMID:9151978  
A;Accession: S78024  
A;Molecule type: protein  
A;Residues: 1-7 <KIT>  
C;Genetics:  
A;Genome: nuclear  
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4  
DB 5 LL 6

RESULT 59  
A34026  
acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)

C;Species: Torpedo californica (Pacific electric ray)  
C;Date: 16-Mar-1990 #sequence\_revision 16-Mar-1990 #text\_change 08-Nov-1996  
C;Accession: A34026  
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedwick, T.; Low, M.G.; Taylor, S.S.  
J. Biol. Chem. 263, 1140-1145, 1988  
A;Title: Divergence in primary structure between the molecular forms of acetylcholine:  
A;Reference number: A34026; MUID:88087239; PMID:3335534  
A;Accession: A34026  
A;Molecule type: protein  
A;Residues: 1-7 <GIB>  
C;Keywords: alternative splicing; carboxylic ester hydrolase

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4  
DB 1 LL 2

RESULT 60  
S68004  
hucolin, 75K chain - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C;Accession: S68004  
R;Edgar, P.F.  
FEBS Lett. 375, 159-161, 1995  
A;Title: Hucolin, a new corticosteroid-binding protein from human plasma with structu  
A;Reference number: S68004; MUID:96087107; PMID:7498469  
A;Accession: S68004  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <EDG>

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
DB 2 AF 3

RESULT 61  
A11483  
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)  
N;Alternate names: aspartate aminotransferase, mitochondrial  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 20-Aug-1999  
C;Accession: A11483  
R;Campos-Cavieles, M.; Milstein, C.P.  
Biochem. J. 147, 275-281, 1975  
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mit  
A;Reference number: A11483; MUID:76039441; PMID:1180894  
A;Accession: A11483  
A;Molecule type: protein  
A;Residues: 1-7 <CAM>  
A;Experimental source: liver  
A;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate  
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5  
DB 6 LY 7

RESULT 62

PX0008  
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)  
N;Alternate names: UDP-glucuronyltransferase  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997  
C;Accession: PX0008  
R;Yokota, H.; Yuasa, A.; Sato, R.  
J. Biochem. 104, 531-536, 1988  
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver  
A;Reference number: PX0008; MUID:89197852; PMID:3149280  
A;Accession: PX0008  
A;Molecule type: protein  
A;Residues: 1-7 <YOK>  
C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
Db 3 LL 4

RESULT 63  
PN0649  
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)  
C;Species: Bacillus sp.  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 03-Jun-2002  
C;Accession: PN0649  
R;Kim, C.H.; Choi, H.I.; Lee, D.S.  
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993  
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalophilic  
A;Reference number: PN0649; MUID:94080025; PMID:7764261  
A;Accession: PN0649  
A;Molecule type: protein  
A;Residues: 1-7 <KIM>  
C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of starch  
nment in high maltose syrups.  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 2; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3  
Db 1 FL 2

RESULT 64  
S20162  
leghemoglobin III - Sesbania rostrata (fragment)  
C;Species: Sesbania rostrata  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 04-Mar-2000  
C;Accession: S20162  
R;Metz, B.A.; Welters, P.; Hoffmann, H.J.; Jensen, E.O.; Schell, J.; de Bruijn, F.J.  
Mol. Gen. Genet. 214, 181-191, 1988  
A;Title: Primary structure and promoter analysis of leghemoglobin genes of the stem-nodul  
A;Reference number: S08322; MUID:89181515; PMID:3237206  
A;Accession: S20162  
A;Molecule type: DNA  
A;Residues: 1-8 <MET>  
A;Cross-references: EMBL:X13504; NID:921383; PIDN:CAA31858.1; PID:G579482  
C;Genetics:  
A;Gene: glb3  
C;Superfamily: globin; globin homology  
C;Keywords: heme; oxygen carrier

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QE 7  
Db 7 QE 8

RESULT 65  
B24749  
neuropeptide B - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 28-Jul-1987 #sequence\_revision 28-Jul-1987 #text\_change 18-Aug-2000  
C;Accession: B24749  
R;Yang, H.Y.T.; Pratta, W.; Majane, E.A.; Costa, E.  
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985  
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two  
A;Reference number: A94074; MUID:86067985; PMID:3865193  
A;Accession: B24749  
A;Molecule type: protein  
A;Residues: 1-8 <YAN>  
C;Superfamily: unassigned animal peptides  
C;Keywords: neuropeptide

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3  
Db 1 FL 2

RESULT 66  
S37141  
rpsA protein - Erwinia chrysanthemi  
C;Species: Erwinia chrysanthemi  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 08-Oct-1999  
C;Accession: S37141  
R;Dovillie, A.; Tousaint, A.; Faelen, M.  
Submitted to the EMBL Data Library, August 1993  
A;Description: Identification of the integration host factor genes of E. chrysanthemi.  
A;Reference number: S37139  
A;Accession: S37141  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-8 <DOV>  
A;Cross-references: EMBL:X74750; NID:9399669; PIDN:CAA52769.1; PID:G581108

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
Db 1 AF 2

RESULT 67  
S68802  
nitrate reductase (NADH) inhibitor - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
C;Accession: S68802  
R;Bachmann, M.; Huber, J.L.; Liao, P.C.; Gage, D.A.; Huber, S.C.  
FEBS Lett. 387, 127-131, 1996  
A;Title: The inhibitor protein of phosphorylated nitrate reductase from spinach (Spina  
A;Reference number: S68802; MUID:96244508; PMID:8674533  
A;Accession: S68802  
A;Molecule type: protein  
A;Residues: 1-8 <BAC>  
A;Experimental source: leaves; strain cv. Bloomsdale

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4  
||  
Db 2 LL 3

## RESULT 68

SI6324  
hypothetical protein 2 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 21-Nov-1993 #sequence\_revision 12-May-1995 #text\_change 21-Jul-2000  
C:Accession: SI6324  
R:Kubertli, I.; Sessa, G.; Lucchetti, S.; Morelli, G.  
EMBO J. 10, 1787-1791, 1991  
A:Title: A novel class of plant proteins containing a homeodomain with a closely linked  
A:Reference number: SI6323; MUID:91266907; PMID:1675603  
A:Accession: SI6324  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-8 <RUB>  
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4  
||  
Db 5 LL 6

## RESULT 69

A46306  
spasmogenic toxin PNVI - spider (Phoneutria nigriventer) (fragment)  
C:Species: Phoneutria nigriventer  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 17-Mar-1999  
C:Accession: A46306  
R:Marangoni, S.; Borges, N.C.C.; Marangoni, R.A.; Antunes, E.; Vieira, C.A.; Novello, J.  
Toxicon 31, 377-384, 1993  
A:Title: Biochemical characterization of a vascular smooth muscle contracting polypeptide  
A:Reference number: A46306; MUID:93276438; PMID:8503129  
A:Accession: A46306  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <MAR>

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
Db 2 AF 3

## RESULT 70

JS0317  
leucokinin VII - Madeira cockroach  
C:Species: Leucophaea maderae (Madeira cockroach)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C:Accession: JS0317  
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 31-34, 1987  
A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the first  
A:Reference number: JS0317  
A:Accession: JS0317  
A:Molecule type: protein  
A:Residues: 1-8 <HOL>  
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
C:Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
Db 3 AF 4

## RESULT 71

S66646  
cardioacceleratory protein 2b - tobacco hornworm  
C:Species: Manduca sexta (tobacco hornworm)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S66646  
R:Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.  
FBES Lett. 371, 311-314, 1995  
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the  
A:Reference number: S66646; MUID:96013159; PMID:7556618  
A:Accession: S66646  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <HUE>

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5  
||  
Db 2 LY 3

## RESULT 72

A28719  
thymic humoral factor gamma-2 - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 18-Jun-1993  
C:Accession: A28719  
R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainin, N.  
Biochemistry 27, 4066-4071, 1988  
A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an im  
A:Reference number: A28719; MUID:88326920; PMID:3261994  
A:Accession: A28719  
A:Molecule type: protein  
A:Residues: 1-8 <BUR>

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
||  
Db 7 FL 8

## RESULT 73

A42057  
fibroblast growth factor receptor 1, secreted - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 07-May-1999  
C:Accession: A42057  
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.  
Mol. Cell. Biol. 12, 82-89, 1992  
A:Title: Differential splicing in the extracellular region of fibroblast growth factor  
A:Reference number: A42057; MUID:92107200; PMID:1309595  
A:Accession: A42057  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-8 <WER>  
A:Cross-references: GB:M80363  
C:Keywords: growth factor receptor

Query Match 28.6%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
||  
Db 2 LL 3

RESULT 74  
PN0043  
phosphatidylethanol amine-binding protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
C;Accession: PN0043  
R;Kato, H.  
Kawasaki Igakkaishi 22, 245-259, 1996  
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro  
A;Reference number: PN0041  
A;Accession: PN0043  
A;Molecule type: protein  
A;Residues: 1-8 <KAT>  
A;Experimental source: neuroblastoma cell  
C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked  
C;Keywords: brain

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LY 5  
||  
Db 1 LY 2

RESULT 75  
A35180  
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 21-Mar-1996  
C;Accession: A35180  
R;Yoshihara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.  
J. Biol. Chem. 265, 5809-5815, 1990  
A;Title: Purification of a novel type of calcium-activated neutral protease from rat bra  
A;Reference number: A35180; MUID:90202830; PMID:2318836  
A;Accession: A35180  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <YOS>  
C;Keywords: hydrolase

Query Match 28.6%; Score 2; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
||  
Db 2 LL 3

Search completed: November 25, 2003, 19:36:12  
Job time : 5.80233 secs

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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.48256 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AELLYQE 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	42.9	9	1 MOSF_CLYJA	P19853 clypeaster
2	3	42.9	15	1 AFP3_MALPA	P83137 malva parvi
3	3	42.9	15	1 FGF1_CANFA	P18551 canis famil
4	3	42.9	16	1 PA2_NAUSP	Q10756 naja sputat
5	3	42.9	17	1 EFG_THEAQ	Q01697 thermus aqu
6	3	42.9	17	1 PH3_PERAM	P82696 periplaneta
7	3	42.9	20	1 AF21_MALPA	P83143 malva parvi
8	2	28.6	4	1 FLRF_HIRME	P42561 hirudo medi
9	2	28.6	4	1 FLRN_ATEL	P58707 anthopleura
10	2	28.6	6	1 LOK1_LOCMI	P41491 locusta mig
11	2	28.6	7	1 ALL2_CARMA	P81805 carcinus ma
12	2	28.6	7	1 ALL3_CARMA	P81806 carcinus ma
13	2	28.6	7	1 ALL4_CARMA	P81807 carcinus ma
14	2	28.6	7	1 ALL5_CARMA	P81808 carcinus ma
15	2	28.6	7	1 FARI_HELTI	P41871 helisoma tr
16	2	28.6	7	1 FARI_WACRS	P83274 macrobrachi
17	2	28.6	7	1 FARI_PROCL	P38499 procambarus
18	2	28.6	7	1 FARI_PROCL	P38499 procambarus
19	2	28.6	7	1 GFRP_MOUSE	P99025 mus musculu
20	2	28.6	7	1 PPH2_LYCES	P83379 lycopersico
21	2	28.6	7	1 UN06_PINPS	P81675 pinus pinas
22	2	28.6	8	1 ALL2_CARMA	P81815 carcinus ma
23	2	28.6	8	1 ALL6_CYPDO	P82157 cydia pomon
24	2	28.6	8	1 ALL7_CARMA	P81809 carcinus ma
25	2	28.6	8	1 ALL8_CARMA	P81811 carcinus ma
26	2	28.6	8	1 ALL9_CARMA	P81812 carcinus ma
27	2	28.6	8	1 B4K_PORGI	P81886 porphyromon
28	2	28.6	8	1 CLP_THICU	P80488 thioabacilli
29	2	28.6	8	1 COW2_CONPU	P58785 conus purpu
30	2	28.6	8	1 CPD1_ENTFA	P13269 enterococcu
31	2	28.6	8	1 FARI_PANRE	P41872 panagrellus
32	2	28.6	8	1 FARI_PENMO	P83316 penaeus mon
33	2	28.6	8	1 FAR2_WACRS	P83275 macrobrachi

RESULT 1

## ALIGNMENTS

34	2	28.6	8	1	FAR3_HOMAM	P41486 homarus ame
35	2	28.6	8	1	FAR4_HOMAM	P41487 homarus ame
36	2	28.6	8	1	LCK1_LEUMA	P21140 leucophaea
37	2	28.6	8	1	LCK7_BOVIN	P19989 leucophaea
38	2	28.6	8	1	NPB_BOVIN	P15507 bos taurus
39	2	28.6	8	1	NS3_MYCTU	P81152 mycobacteri
40	2	28.6	8	1	ORMY_ORCLI	P82455 orconetes
41	2	28.6	8	1	RS1_ERWCH	P37985 erwinnia chr
42	2	28.6	8	1	UH09_RAT	P56575 rattus norv
43	2	28.6	8	1	UPA1_HUMAN	P30087 homo sapien
44	2	28.6	9	1	AL10_CARMA	P81814 carcinus ma
45	2	28.6	9	1	AL11_CARMA	P81814 carcinus ma
46	2	28.6	9	1	BUK_GLOPA	P81237 clostridium
47	2	28.6	9	1	CCAF_CARMA	P38556 carcinus ma
48	2	28.6	9	1	FAR2_PANRE	P41873 panagrellus
49	2	28.6	9	1	FAR3_MACRS	P83276 macrobrachi
50	2	28.6	9	1	FAR6_MACRS	P83279 macrobrachi
51	2	28.6	9	1	FAR8_MACRS	P83281 macrobrachi
52	2	28.6	9	1	FARP_CALST	P38495 callinectes
53	2	28.6	9	1	FIBB_PAPAN	P19344 papio anubi
54	2	28.6	9	1	FIBB_PAPHA	P19343 papio hamad
55	2	28.6	9	1	FIBB_THEGE	P19342 theropithec
56	2	28.6	9	1	NEUT_CAVPO	P34966 cavia porce
57	2	28.6	9	1	NEUX_HUMAN	P04277 homo sapien
58	2	28.6	9	1	RS42_LITRU	P82075 litoria rub
59	2	28.6	9	1	TAL1_PICJA	P17440 pichia jadi
60	2	28.6	9	1	TAL3_PICJA	P14517 calliphora
61	2	28.6	9	1	TKC1_CALVO	P31931 homo sapien
62	2	28.6	9	1	ULAE_HUMAN	P31931 homo sapien
63	2	28.6	9	1	UPA7_HUMAN	P30093 homo sapien
64	2	28.6	10	1	CU30_LOCMI	P1735 locusta mig
65	2	28.6	10	1	FAR7_MACRS	P83280 macrobrachi
66	2	28.6	10	1	FARP_LOCMI	P38553 locusta mig
67	2	28.6	10	1	FARP_MANSE	P18523 manduca sex
68	2	28.6	10	1	LQMS_LEUMA	P21144 leucophaea
69	2	28.6	10	1	PORB_METTM	P80901 methanobact
70	2	28.6	10	1	Q20B_COMTE	P8465 comamonas t
71	2	28.6	10	1	TEMK_FANTE	P5923 rana tempor
72	2	28.6	11	1	CS15_BACSU	P81095 bacillus su
73	2	28.6	11	1	MHBI_KLEPN	P80580 klebsiella
74	2	28.6	11	1	RE41_LITRU	P82074 litoria rub
75	2	28.6	11	1	TKC2_CALVO	P41518 calliphora
76	2	28.6	11	1	TKN1_UPEIN	P82026 uperoleia i
77	2	28.6	11	1	TKN1_UPERU	P08612 uperoleia r
78	2	28.6	11	1	TKN_ELEMO	P31293 eledone mos
79	2	28.6	11	1	ULAG_HUMAN	P31933 homo sapien
80	2	28.6	12	1	CD11_LITXA	P56245 litoria xan
81	2	28.6	12	1	CD14_LITXA	P56246 litoria xan
82	2	28.6	12	1	FRE1_LITIN	P82021 litoria inf
83	2	28.6	12	1	GRAR_RANRU	P40754 rana rugosa
84	2	28.6	12	1	PA21_MICPM	P25072 micrurus fu
85	2	28.6	12	1	PA2B_VIPBO	P31859 vipera beru
86	2	28.6	13	1	CD71_LITBW	P82051 litoria ewi
87	2	28.6	13	1	CHEP_PARID	P42718 parapolybia
88	2	28.6	13	1	CRBL_ICASP	P17237 icaria sp
89	2	28.6	13	1	CRBL_VESAN	P17233 vespa anali
90	2	28.6	13	1	CRBL_VESCR	P01518 vespa crabr
91	2	28.6	13	1	CRBL_VESLE	P17235 vespa manda
92	2	28.6	13	1	CRBL_VESMA	P17232 vespa tropi
93	2	28.6	13	1	CRBL_VESYR	P17231 vespa tropi
94	2	28.6	13	1	CRBL_VESXA	P17234 vespa xanth
95	2	28.6	13	1	CRBC_BOVIN	P28489 bos taurus
96	2	28.6	13	1	FARB_ASCSU	P43173 ascaris suu
97	2	28.6	13	1	HPA1_RANES	P32415 rana esculi
98	2	28.6	13	1	HPB9_RANES	P32416 rana esculi
99	2	28.6	13	1	NEUT_CAVPO	P32560 cavia porce
100	2	28.6	13	1	NO40_PEA	P55959 pisum sativ

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MOSF_CLYJA          STANDARD;          PRT;          9 AA.
ID  MOSF_CLYJA
AC  P19853;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  01-FEB-1991 (Rel. 17, Last annotation update)
DE  [Phe-6]-mosact.
OS  Clypeaster japonicus (Sand dollar).
OC  Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC  Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroidea;
OC  Clypeasteridae; Clypeaster.
OX  NCBI_TaxID=7644;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Egg jelly;
RA  Suzuki N., Kurita M., Yoshino K.I., Kajiuura H., Nomura K.,
RA  Yamauchi M.;
RT  "Purification and structure of mosact and its derivatives from the
RT  egg jelly of the sea urchin Clypeaster japonicus.";
RL  Zool. Sci. 4:649-656(1987).
CC  -!- FUNCTION: Stimulates sperm respiration and motility.
DR  PIR; JN0027; JN0027.
SQ  SEQUENCE 9 AA; 924 MW; 93245729CDC5BAB5 CRC64;

Query Match          42.9%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 AFL 3
    |||
Db  5 AFL 7

RESULT 2
APP3_MALPA
ID  APP3_MALPA          STANDARD;          PRT;          15 AA.
AC  P83137;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Antifungal protein 3 (CW-3) (Fragment).
OS  Malva parviflora (Little mallow) (Cheeseweed).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX  NCBI_TaxID=145753;
RN  [1]
RP  SEQUENCE AND FUNCTION.
RC  TISSUE=Seed.
RX  MEDLINE=21199399; PubMed=11302747;
RA  Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT  "Purification and characterization of three antifungal proteins from
RT  cheeseweed (Malva parviflora).";
RL  Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
CC  -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC  not F.graminearum.
CC  -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC  concentration.
DR  GO; GO:0003799; F:antifungal peptide activity; IDA.
DR  GO; GO:0007275; P:development; NAS.
KW  Fungicide; Antibiotic.
FT  NON_TER 15
SQ  SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match          42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 YQE 7
    |||
Db  8 YQE 10

RESULT 3
FGF1_CANFA
ID  FGF1_CANFA          STANDARD;          PRT;          15 AA.
AC  P18651;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Heparin-binding growth factor 1 (HBGF-1) (Acidic fibroblast growth
DE  factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
GN  FGF1 OR FGF-1.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=89231704; PubMed=2714282;
RA  Quinkler W., Maaberg M., Bernotat-Danielowski S., Luethe N.,
RA  Sharma H.S., Schaper W.;
RT  "Isolation of heparin-binding growth factors from bovine, porcine and
RT  canine hearts.";
RL  Eur. J. Biochem. 181:67-73(1989).
CC  -!- FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS
CC  IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN
CC  VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND
CC  CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC  -!- SUBUNIT: Monomer.
CC  -!- MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY
CC  THAN DOES BPGF.
CC  -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR  InterPro; IPR002348; IL1_HBGF.
DR  PROSITE; PS00247; HBGF_FGF; PARTIAL.
KW  Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT  NON_TER 15
SQ  SEQUENCE 15 AA; 1732 MW; 53CC9A3CADDDDAA1 CRC64;

Query Match          42.9%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  3 LLY 5
    |||
Db  7 LLY 9

RESULT 4
PA2_NAJSP
ID  PA2_NAJSP          STANDARD;          PRT;          16 AA.
AC  Q10756;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
DE  (Muscarinic inhibitor) (Fragment).
OS  Naja sputatrix (Malayan spitting cobra).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC  Elapidae; Elapinae; Naja.
OX  NCBI_TaxID=33626;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Venom;
RX  MEDLINE=96195757; PubMed=8638927;
RA  Miyoshi S.-I., Tu A.T.;
RT  "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
RT  acetylcholine receptor inhibitor.";
RL  Arch. Biochem. Biophys. 328:17-25(1996).
CC  -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC  acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
CC  transmission at the postsynaptic site. Binds to the muscarinic
CC  acetylcholine receptor.
CC  -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-

```



CC acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion (By similarity).  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I  
 SUBFAMILY.  
 CC PIR: S65520; S65520.  
 DR HSP; P00598, IPOA.  
 DR InterPro: IPR001211; PhospholipaseA2.  
 DR Pfam: PF00068; Phoslip; 1.  
 DR PROSITE; PS00119; PA2 ASP; PARTIAL.  
 DR PROSITE; PS00118; PA2 HIS; PARTIAL.  
 KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;  
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor.  
 FT NON\_TER 16  
 SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834B585F0 CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 LYQ 6  
 Db 2 LYQ 4  
 RESULT 5  
 EFG THEAQ STANDARD; PRT; 17 AA.  
 AC Q01697;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Elongation factor G (EF-G) (Fragment).  
 GN FUSA OR FUS.  
 OS Thermus aquaticus.  
 CC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
 CC Thermus.  
 CC NCBI\_TaxID=271;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EP 00276;  
 RX MEDLINE=92362620; PubMed=1499561;  
 RA Voss R.H., Hartmann R.K., Lippmann C., Alexander C., Jahn O.,  
 RA Erdmann V.;  
 RT "Sequence of the tufA gene encoding elongation factor EF-Tu from  
 RT Thermus aquaticus and overproduction of the protein in Escherichia  
 RT coli.";  
 RL Eur. J. Biochem. 207:839-846(1992).  
 CC -!- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION  
 OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE  
 RIBOSOME.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 EF-G/EF-2 SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X66322; CAA46997.1; -.  
 DR HANAP; MF\_00054; -; 1.  
 DR InterPro; IPR000795; EF\_GTPbind.  
 DR PROSITE; PS00301; EFACOR\_GTP; PARTIAL.  
 KW Elongation factor; Protein biosynthesis; GTP-binding.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2094 MW; EA46E1EF05F86E1D CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 YQE 7  
 Db 2 YQE 4  
 RESULT 6  
 PH3 PERAM STANDARD; PRT; 17 AA.  
 AC P82696;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Peptide hormone 3 (Pea-VEAacid 1).  
 OS Periplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 CC NCBI\_TaxID=6978;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Abdominal perisymphathetic organs;  
 RX MEDLINE=20140865; PubMed=10676456;  
 RA Predel R., Eckert M., Holman G.M.;  
 RT "The unique neuropeptide pattern in abdominal perisymphathetic organs  
 RT of insects.";  
 RL Ann. N.Y. Acad. Sci. 897:282-290(1999).  
 CC -!- FUNCTION: UNKNOWN.  
 CC -!- MASS SPECTROMETRY: MW=1651.35; METHOD=MALDI.  
 KW Neuropeptide.  
 SQ SEQUENCE 17 AA; 1807 MW; 2374AC8B1F868EB CRC64;  
 Query Match 42.9%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AFL 3  
 Db 1 AFL 3  
 RESULT 7  
 AF2L MALPA STANDARD; PRT; 20 AA.  
 AC P83143;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 large subunit (CW-2) (Fragment).  
 OS Malva parviflora (little mallow) (Cheeseweed).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 CC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 CC NCBI\_TaxID=145753;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 RT parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but  
 CC not F.graminearum.  
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 CC concentration.  
 CC GO; GO:0003799; F:antifungal peptide activity; IDA.  
 DR Fungicide; Antibiotic.  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

```
Query Match      42.9%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 YOE 7
      |||
Db      8 YOE 10

RESULT 8
FLRP_HIRME      STANDARD;      PRT;      4 AA.
AC P42561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FLRFamide
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421, 27815;
RN [1]
RP SEQUENCE.
RC SPECIES=H.medicinalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rhamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [2]
RP SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
trivolvis.";
RL Peptides 15:31-36(1994).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 582 MW; 69D40729A00000000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FL 3
      ||
Db      1 FL 2

RESULT 9
FLRN_ANTEL      STANDARD;      PRT;      4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
anemone neuropeptide containing an unusual amino-terminal blocking
group.";
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Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Neuron-specific.
-!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR PIR; A35779; A35779.
KW Neuropeptide; Amidation.
FT MOD_RES 1 1
FT MOD_RES 4 4
SQ SEQUENCE 4 AA; 549 MW; 64540729A00000000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FL 3
      ||
Db      1 FL 2

RESULT 10
LOK1_LOCM1      STANDARD;      PRT;      6 AA.
AC P41491;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Locustakinin I.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=92262851; PubMed=1585017;
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA de Loof A.;
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,
isolated, primary structure and synthesis.";
RL Regul. Pept. 37:49-57(1992).
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation
of ion transport and inhibition of diuretic activity in Malpighian
tubules.
CC -!- SUBCELLULAR LOCATION: Secreted.
DR PIR; A61068; A61068.
KW Neuropeptide; Amidation.
FT MOD_RES 6 6
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AF 2
      ||
Db      1 AF 2

RESULT 11
ALL2_CARMA      STANDARD;      PRT;      7 AA.
AC P81805;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 2.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
```

RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 770 MW; 672879CDCB5DB70 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
Db ||  
4 AF 5

RESULT 12  
ALL3 CARMA  
ID ALL3 CARMA STANDARD; PRT; 7 AA.  
AC P81806;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 3.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
Db ||  
4 AF 5

RESULT 13  
ALL4 CARMA  
ID ALL4 CARMA STANDARD; PRT; 7 AA.  
AC P81807;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 4.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.

RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 782 MW; 672879CDCB476AC0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
Db ||  
4 AF 5

RESULT 14  
ALL5 CARMA  
ID ALL5 CARMA STANDARD; PRT; 7 AA.  
AC P81808;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 5.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
RT allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 7  
SQ SEQUENCE 7 AA; 781 MW; 672879CDCB476420 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
Db ||  
4 AF 5

RESULT 15  
FAR1 HELTI  
ID FAR1 HELTI STANDARD; PRT; 7 AA.  
AC P41871;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide GDFPLRF-amide.  
OS Helisoma trivolvis (Snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;  
OC Lymnaeidae; Planorbidae; Helisoma.  
OX NCBI\_TaxID=27815;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Kidney;  
RX MEDLINE=94286417; PubMed=7912428;  
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
RT "FMRamide-related peptides from the kidney of the snail, *Helisoma*  
RT *trivolvis*";  
RL Peptides 15:31-36(1994).  
CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING  
CC -!- THE KIDNEY, MANTLE AND SKIN.  
CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FL 3  
Db ||  
4 FL 5  
RESULT 16  
FAR1\_MACRS STANDARD; PRT; 7 AA.  
AC P83274;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE FMRamide-like neuropeptide FLPI (DRNFLRF-amide).  
OS Macrobrachium rosenbergii (Giant fresh water prawn).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.  
OX NCBI\_TaxID=79674;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RA Sithigongul P., Saraithongkum W., Jaideechoey S., Longyant S.,  
RA Sithigongul W.;  
RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant  
RT freshwater prawn *Macrobrachium rosenbergii*.";  
RL Comp. Biochem. Physiol. 120B:587-595 (1998).  
CC -!- MASS SPECTROMETRY: MW=965.7; METHOD=MALDI.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FL 3  
Db ||  
4 FL 5  
RESULT 17  
FAR1\_PROCL STANDARD; PRT; 7 AA.  
AC P38439;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardioexcitatory FMRamide homolog NF1.  
OS *Procambarus clarkii* (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

OC Astacoidea; Cambaridae; Procambarus.  
RX NCBI\_TaxID=6728;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRamide-related peptides from crayfish  
RT pericardial organs";  
RL Peptides 14:137-143(1993).  
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FL 3  
Db ||  
4 FL 5  
RESULT 18  
FAR2\_PROCL STANDARD; PRT; 7 AA.  
ID FAR2\_PROCL  
AC P38498;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardioexcitatory FMRamide homolog DF2.  
OS *Procambarus clarkii* (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Procambarus.  
OX NCBI\_TaxID=6728;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRamide-related peptides from crayfish  
RT pericardial organs";  
RL Peptides 14:137-143(1993).  
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
CC CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
CC EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7 7 AMIDATION.  
SQ SEQUENCE 7 AA; 967 MW; 69D40729C4540AC0 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FL 3  
Db ||  
4 FL 5  
RESULT 19  
GFRP\_MOUSE STANDARD; PRT; 7 AA.  
ID GFRP\_MOUSE  
AC P99025;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).  
 GN GCHFR OR GFRP.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
 RA Couthorne M.;  
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP  
 CC CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE  
 CC (BY SIMILARITY).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 DR SWISS-2DPAGE; P95025; MOUSE.  
 FT INIT MET 0 7  
 FT NON\_TER 0 7  
 SQ SEQUENCE 7 AA; 806 MW; 7185B057273B4700 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 LL 4  
 Db 3 LL 4  
  
 RESULT 20  
 PP2 LYCES  
 ID PP2 LYCES STANDARD; PRT; 7 AA.  
 AC P83379;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Purple acid phosphatase isozyme LeSP2 (EC 3.1.3.2) (Fragment).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.  
 OX NCBI\_TaxID=4081;  
 RN [1]  
 RP SEQUENCE, CATALYTIC ACTIVITY, SUBUNIT, SUBCELLULAR LOCATION, AND  
 RP GLYCOSYLATION.  
 RC STAIN=cv. Moneymaker; TISSUE=Seed;  
 RX MEDLINE=22361242; PubMed=12473124;  
 RA Bozzo G.G., Raghoebar K.G., Plaxton W.C.;  
 RT "Purification and characterization of two secreted purple acid  
 RT phosphatase isozymes from phosphate-starved tomato (Lycopersicon  
 RT esculentum) cell cultures";  
 RL Eur. J. Biochem. 269:6278-6286 (2002).  
 CC -!- CATALYTIC ACTIVITY: An orthophosphoric monoester + H(2)O = an  
 CC alcohol + phosphate.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Glycosylated.  
 CC -!- MISCELLANEOUS: In L. esculentum there are at least two isozymes of  
 CC purple acid phosphatase.  
 KW Hydrolase; Glycoprotein.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 810 MW; 672AA862C9C729A0 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 2 FL 3  
 Db 1

Db 1 FL 2  
  
 RESULT 21  
 UN06 PINPS  
 ID UN06 PINPS STANDARD; PRT; 7 AA.  
 AC P81675;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Unknown protein from 2D-page of needles (N141) (Fragment).  
 OS Pinus pinaster (Maritime Pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins";  
 RL Electrophoresis 20:1098-1108 (1999).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 823 MW; 69D7672448B5740 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 4 LY 5  
 Db 1 LY 2  
  
 RESULT 22  
 AL12 CARMA  
 ID AL12 CARMA STANDARD; PRT; 8 AA.  
 AC P81815;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 12.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas.";  
 RL Eur. J. Biochem. 250:727-734 (1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 KW Neuropeptide; Multigene family.  
 SQ SEQUENCE 8 AA; 913 MW; 672879CDB569AB7 CRC64;  
  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 AF 2  
 Db 5 AF 6

```

RESULT 23
ID ALL6_CYPDO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LY 5
DB 3 LY 4

RESULT 24
ID ALL7_CARMA STANDARD; PRT; 8 AA.
AC P81809; P81804; P81810;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carcinustatin 7 [Contains: Carcinustatin 6; Carcinustatin 1].
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 825 MW; 922879CDBC4775BD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1-AF 2
DB 1-AF 2

RESULT 25
ID ALL8_CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 795 MW; 922879CDBC47687D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
DB 5 AF 6

RESULT 26
ID ALL9_CARMA STANDARD; PRT; 8 AA.
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 9.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8 8
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDBC476878 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2
DB 5 AF 6

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QY 1-AF 2

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Qy      1 AF 2
Db      ||
        5 AF 6

RESULT 27
B44K_PORGI
ID_B44K_PORGI      STANDARD;      PRT;      8 AA.
AC P81886;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 44 kDa immunogenic protein (Fragment).
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE.
RC STRAIN=VPB 3492;
RX MEDLINE=20198497; PubMed=10731616;
RA Norris J.M., Love D.N.;
RT "Serum antibody responses of cats to soluble whole cell antigens of
RL Vet. Microbiol. 73:37-49(2000).
CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW Antigen.
FT NON TER
SQ SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 YQ 6
Db      ||
        3 YQ 4

RESULT 28
CLP_THICU
ID_CLP_THICU      STANDARD;      PRT;      8 AA.
AC P80488;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Chemolithotroph-specific protein (Fragment).
OS Thiobacillus cuprinus.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Thiomonas.
OX NCBI_TaxID=36860;
RN [1]
RP SEQUENCE.
RC STRAIN=DSM 5494;
RA Marin I., Amaro A.M., Jerez C.A., Anils R., Abad J.P.;
RL Submitted (SEP-1995) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: FOUND SPECIFICALLY IN CELLS CULTURED
CC CHEMOLITHOTROPHICALLY.
FT NON TER
SQ SEQUENCE 8 AA; 785 MW; 91487B06DDC2D76D CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 QE 7
Db      ||
        5 QE 6

RESULT 29
COW2_CONFU
ID_COW2_CONFU      STANDARD;      PRT;      8 AA.

AC P58785;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=9938839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID
FT MOD RES
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 LL 4
Db      ||
        4 LL 5

RESULT 30
CPD1_ENTFA
ID_CPDI_ENTFA      STANDARD;      PRT;      8 AA.
AC P13259;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPD1.
OS Enterococcus faecalis.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cpd1.";
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOCIN PLASMID PPD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 FL 3
Db      ||
        1 FL 2

RESULT 31
FAR1_PANRE
ID_FAR1_PANRE      STANDARD;      PRT;      8 AA.
AC P41872;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide PF1 (SDPNFLRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE.
RX MEDLINE=93027659; PubMed=1408999;
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
RA Garrison R.D., Williams J.F., Friedman A.R.;
RT "Two FMRamide-like peptides from the free-living nematode
RT Panagrellus redivivus.";
RL Peptides 13:209-214(1992).
CC -!- FUNCTION: MYOACTIVE.
CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
CC -!- CAUDALLY TO THE BASE OF THE PHARYNX.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 995 MW; C6D40729C4576AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

RESULT 32
FAR1 PENMO
ID FAR1_PENMO STANDARD; PRT; 8 AA.
AC P83316;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLPI (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21956277; PubMed=11959015;
RA Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,
RA Chaivithangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RT of the giant tiger prawn Penaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1024 MW; 72D40729C4540AAB8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

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RESULT 33
FAR2 MACRS
ID FAR2_MACRS STANDARD; PRT; 8 AA.
AC P83275;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FUF2 (ADKNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RA Sithigorngul P., Saraithongkum W., Jaideechoey S., Longyant S.,
RA Sithigorngul W.;
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant
RT freshwater prawn Macrobrachium rosenbergii.";
RL Comp. Biochem. Physiol. 120B:587-595(1998).
CC -!- MASS SPECTROMETRY: MW=1009.4; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; TAS.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1010 MW; 9CD40729C4433AAD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
Db 5 FL 6

RESULT 34
FAR3 HOMAM
ID FAR3_HOMAM STANDARD; PRT; 8 AA.
AC P41486;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 3 (FLI 3) (F2).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=34297114;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRFamide-like immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26(1987).
CC -!- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 MM
CC -!- POTASSIUM IN THE PRESENCE OF CALCIUM.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1054 MW; C6D40729C4540AB5 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3

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Db 5 FL 6

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
3 AF 4

Db

RESULT 35  
FAR4\_HOMAM  
ID FAR4\_HOMAM STANDARD; PRT; 8 AA.  
AC F41487;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRPamide-like neuropeptide 4 (FLI 4) (F1).  
OS Homarus americanus (American lobster).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Nephropoidea; Nephropidae; Homarus.  
OX NCBI\_TaxID=6706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=88116164; PubMed=3429714;  
RA Trimmer B.A., Kobler E.L.A., Kravitz E.A.;  
RT "Purification and characterization of FMRPamide-like immunoreactive  
RT substances from the lobster nervous system: isolation and sequence  
RT analysis of two closely related peptides.";  
RL J. Comp. Neurol. 266:16-26(1987).  
CC -!- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC  
CC NEUROMUSCULAR JUNCTIONS.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
||  
5 FL 6

Db

RESULT 36  
LCK1\_LEUMA  
ID LCK1\_LEUMA STANDARD; PRT; 8 AA.  
AC P21140;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DE Leucokinin I (L-I).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberoidea; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of two neuropeptides  
RT from Leucophaea maderae: members of a new family of  
RT Cephalomyotropins.";  
RL Comp. Biochem. Physiol. 84C:205-211(1986).  
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 893 MW; DC6365B449CDC76A CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
3 AF 4

Db

RESULT 37  
LCK7\_LEUMA  
ID LCK7\_LEUMA STANDARD; PRT; 8 AA.  
AC P19589;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Leucokinin VII (L-VII).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberoidea; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Head;  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucokinin VII and  
RT VIII: the final members of this new family of cephalomyotropic  
RT peptides isolated from head extracts of Leucophaea maderae.";  
RL Comp. Biochem. Physiol. 88C:31-34(1987).  
CC -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE  
CC ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC -!- SIMILARITY: TO THE OTHER LEUCOKININS.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 866 MW; DC6365A5B9CDC76A CRC64;  
Query Match 28.6%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
||  
3 AF 4

Db

RESULT 38  
NPB\_BOVIN  
ID NPB\_BOVIN STANDARD; PRT; 8 AA.  
AC P15507;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Neuropeptide B.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=86067985; PubMed=3865193;  
RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;  
RT "Isolation, sequencing, synthesis, and pharmacological  
RT characterization of two brain neuropeptides that modulate the action  
RT of morphine.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).  
CC -!- FUNCTION: MODULATES THE ACTION OF MORPHINE.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 8  
SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
 DB 1 FL 2

RESULT 39  
 NS3\_MYCTU  
 ID NS3\_MYCTU STANDARD; PRT; 8 AA.  
 AC P81152;  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE 30 kDa non-secretory protein 3 (Fragment).  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 OX NCBI\_TaxID=1773;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=H37Rv;  
 RA Prasad H.K., Annapurna P.S.;  
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.  
 CC -!- CAUTION: We are unable to find this protein in the translation of  
 CC the genome of strain H37Rv.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 919 MW; 8D3DC40B19CDC2D2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
 DB 3 AF 4

RESULT 40  
 ORMT\_ORCLI  
 ID ORMT\_ORCLI STANDARD; PRT; 8 AA.  
 AC P82455;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Orcomyotropin (OMT).  
 OS Orconectes limosus (Spinycheek crayfish).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Astacoidea; Cambaridae; Orconectes.  
 OX NCBI\_TaxID=28379;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Hindgut;  
 RX MEDLINE=20411310; PubMed=10952880;  
 RA Dirksen H., Burdick S., Sauter A., Keller R.;  
 RT "Two orckinins and the novel octapeptide orcomyotropin in the hindgut  
 RT of the crayfish Orconectes limosus: identified myostimulatory  
 RT neuropeptides originating together in neurones of the terminal  
 RT abdominal ganglion.";  
 RL J. Exp. Biol. 203:2807-2818(2000).  
 CC -!- FUNCTION: MYOTROPIC PEPTIDE, ENHANCES BOTH THE FREQUENCY AND  
 CC AMPLITUDE OF SPONTANEOUS HINDGUT CONTRACTIONS. IT IS SYNTHESIZED  
 CC BY ABDOMINAL GANGLIONIC NEURONS.  
 CC -!- MASS SPECTROMETRY: MW=904.8; METHOD=FAB.  
 KW Amidation; Neuropeptide.  
 FT MOD RES 8 8  
 SQ SEQUENCE 8 AA; 905 MW; 87C861B1A9CDDAA9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
 DB 3 AF 4

RESULT 41  
 RS1\_ERWCH  
 ID RS1\_ERWCH STANDARD; PRT; 8 AA.  
 AC P37985;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE 30S ribosomal protein S1 (Fragment).  
 GN RPSA.  
 OS Erwinia chrysanthemi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Pectobacterium.  
 OX NCBI\_TaxID=556;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3937;  
 RA Douillie A., Toussaint A., Faelen M.;  
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE  
 CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT  
 CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.

CC -----  
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 CC -----

DR EMBL; X74750; CAA52769.1; --  
 DR PIR; S37141; S37141.  
 KW Ribosomal protein; Repeat; RNA-binding.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
 DB 1 AF 2

RESULT 42  
 UH09\_RAT  
 ID UH09\_RAT STANDARD; PRT; 8 AA.  
 AC P56575;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Heart;  
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,  
 RA Jungblut P.R.;  
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.

CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 QE 7  
 Db 1 QE 2

RESULT 43  
 UPAL HUMAN  
 ID UPAL\_HUMAN STANDARD; PRT; 8 AA.  
 AC P30087;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=9302937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing."  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.9, ITS MW IS: 65 kDa.  
 DR SWISS-2DPAGE; P30087; HUMAN.  
 FT NON\_TER 1 1  
 FT UNSURE 8 8  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 QE 7  
 Db 2 QE 3

RESULT 44  
 AL10 CARMA  
 ID AL10\_CARMA STANDARD; PRT; 9 AA.  
 AC P81813;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 10.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=96121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDBC4776C7 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AF 2  
 Db 6 AF 7

RESULT 45  
 AL11 CARMA  
 ID AL11\_CARMA STANDARD; PRT; 9 AA.  
 AC P81814;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Carcinustatin 11.  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=96121193; PubMed=9461295;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,  
 RA Thorpe A.;  
 RT "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab Carcinus maenas."  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 FT MOD\_RES 9  
 SQ SEQUENCE 9 AA; 927 MW; 832D79CDBC46D861 CRC64;  
 Query Match 28.6%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AF 2  
 Db 6 AF 7

RESULT 46  
 BUK CLOPA  
 ID BUK\_CLOPA STANDARD; PRT; 9 AA.  
 AC P81337;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).  
 GN BUK.  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=M5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5."  
 RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl phosphate to butyrate (by similarity).

CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.

CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the acetokinase family.

DR HAMAP; MF\_00542; ; 1.

DR InterPro; IPR000890; Acetate\_kin.

DR PROSITE; PS01075; ACETATE\_KINASE\_1; PARTIAL.

DR PROSITE; PS01076; ACETATE\_KINASE\_2; PARTIAL.

KW Transferase; Kinase.

FT NON\_TER 9

SQ SEQUENCE 9 AA; 1104 MW; 055D4050572732B CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4  
DB 4 LL 5

RESULT 47

CCAP\_CARMA STANDARD; PRT; 9 AA.

ID \_CARMA

AC P38556;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Cardioactive peptide (CCAP).

OS Carcinus maenas (Common shore crab) (Green crab),  
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
Tenebrio molitor (Yellow mealworm), and  
Spodoptera eridania (Southern armyworm).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Fortuonoidea; Portunidae; Carcinus.

OX NCBI\_TaxID=6759, 7130, 7067, 37547;

[1] SEQUENCE.

RP SPECIES=C.maenas; TISSUE=Pericardial organs;  
Stangier J., Hilbich C., Beyreuther K., Keller R.;  
RA "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
RT shore crab Carcinus maenas";  
Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).

RN [2] SEQUENCE.

RP SPECIES=M.sexta;  
RX MEDLINE=93050243; PubMed=1426284;  
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;  
RT "Primary structure of a cardioactive neuropeptide from the tobacco  
hawkmoth, Manduca sexta";  
FEBS Lett. 313:165-168 (1992).

RN [3] SEQUENCE.

RP SPECIES=T.molitor, and S.eridania; TISSUE=Head;  
RX MEDLINE=94176032; PubMed=8129851;  
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
RA Schooley D.A.;  
RT "Isolation and identification of a cardioactive peptide from Tenebrio  
molitor and Spodoptera eridania";  
Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).

CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.  
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED  
INTO THE HEMOLYPH.

DR PIR; A26363; A26363.

DR PIR; S27233; S27233.

KW Neuropeptide; Amidation.

FT DISULFID 3

FT MOD\_RES 9

FT MOD\_RES 9 9

SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AF 2  
DB 5 AF 6

RESULT 48

FAR2\_PANRE STANDARD; PRT; 9 AA.

ID \_PANRE

AC P41873;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).

OS Panagrellus redivivus.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.

OX NCBI\_TaxID=6233;

RN [1] SEQUENCE.

RX MEDLINE=93027659; PubMed=1408999;  
RA Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,  
RA Garrison R.D., Williams J.F., Friedman A.R.;  
RT "Two FMRFamide-like peptides from the free-living nematode  
Panagrellus redivivus";  
Peptides 13:209-214 (1992).

CC -!- FUNCTION: MYOACTIVE.

CC -!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED  
CAUDALLY TO THE BASE OF THE PHARYNX.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.

CC Neuropeptide; Amidation.

FT MOD\_RES 9

SQ SEQUENCE 9 AA; 1066 MW; DA0B0729C4576AAD CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
DB 6 FL 7

RESULT 49

FAR3\_MACRS STANDARD; PRT; 9 AA.

ID \_MACRS

AC P83276;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE FMRFamide-like neuropeptide FLP3 (NYDKNLRP-amide).

OS Macrobrachium rosenbergii (Giant fresh water prawn).

OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
OC Palaemonoidea; Palaemonidae; Macrobrachium.

OX NCBI\_TaxID=79674;

RN [1] SEQUENCE, AND MASS SPECTROMETRY.

RP TISSUE=Eyestalk;

RC Sithigornkul P., Sarathongkum W., Jaidechoey S., Longyant S.,  
RA Sithigornkul W.;  
RT "Novel FMRFamide-like neuropeptides from the eyestalk of the giant  
freshwater prawn Macrobrachium rosenbergii";  
Comp. Biochem. Physiol. 120B:S67-S95 (1998).

CC -!- MASS SPECTROMETRY: MW=1215.4; METHOD=MALDI.

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.

DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.

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FT MOD_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1216 MW; 18220729C443ABB CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
   ||
Db 6 FL 7

RESULT 50
FAR6_MACRS
ID FAR6_MACRS STANDARD; PRT; 9 AA.
AC P83279;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP6 (DGGNFRFP-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
   ||
Db 6 FL 7

RESULT 51
FAR8_MACRS
ID FAR8_MACRS STANDARD; PRT; 9 AA.
AC P83281;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP8 (VSHNFRFP-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1081 MW; 26800729C4540878 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
   ||
Db 6 FL 7

RESULT 53
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
```

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CC -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1133 MW; 845A0729C4441F5 CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
   ||
Db 6 FL 7

RESULT 52
FARP_CALSI
ID FARP_CALSI STANDARD; PRT; 9 AA.
AC P38495;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1996 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krainiak K.G.;
RT "The identification and structure-activity relations of a
RT cardioactive FMRamide-related peptide from the blue crab Callinectes
RT sapidus.";
RL Peptides 12:1295-1302(1991).
CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match
Best Local Similarity 28.6%; Score 2; DB 1; Length 9;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3
   ||
Db 6 FL 7

RESULT 53
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
```

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RT and Theropithecus gelada): their amino acid sequences and
RL evolutionary rates and a molecular phylogeny for the baboons."
CC J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; D28854; D28854.
CC InterPro; IPR002181; Fibrinogen C.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
CC Blood coagulation; Plasma.
CC PEPTIDE 1 9 FIBRINOPEPTIDE B.
CC NON TER 9 9
CC SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 54
FIBB PAFPA
ID FIBB_PAFPA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OC NCBI_TaxID=9557;
RN [1]
RP SEQUENCE
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; D28854; E28854.
CC InterPro; IPR002181; Fibrinogen C.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
CC Blood coagulation; Plasma.
CC PEPTIDE 1 9 FIBRINOPEPTIDE B.
CC NON TER 9 9
CC SEQUENCE 9 AA; 1076 MW; DDFE71E9C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 55
FIBB THEGE
ID FIBB_THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Theropithecus gelada (Gelada baboon).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Theropithecus.
OC NCBI_TaxID=9565;
RN [1]
RP SEQUENCE
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons."
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC PIR; D28854; E28854.
CC InterPro; IPR002181; Fibrinogen C.
CC PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
CC Blood coagulation; Plasma.
CC PEPTIDE 1 9 FIBRINOPEPTIDE B.
CC NON TER 9 9
CC SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QE 7
DB 2 QE 3

RESULT 56
NEUTU CAVPO
ID NEUTU_CAVPO STANDARD; PRT; 9 AA.
AC P34966;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuromedin U-9 (NmuU-9).
GN NmuU.
OS Cavia porcellus (Guinea pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OC NCBI_TaxID=10141;
RN [1]
RP SEQUENCE
RX MEDLINE=90341105; PubMed=2381877;
RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
RT "Isolation and microsequence analysis of a novel form of neuromedin U
RT from guinea pig small intestine."
RL Peptides 11:613-617(1990).

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CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES  
CC SELECTIVE VASOCONSTRICTION.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.

DR InterPro: IPR001942; NMU.

DR Pfam: PF02070; NMU; 1.

DR PROSITE: PS00967; NMU; 1.

KW Amidation; Hormone.

FT MOD RES 9 AMIDATION.

SQ SEQUENCE 9 AA; 1169 MW; 1ECF17749C729DB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3

Db 3 FL 4

RESULT 57

NEUX HUMAN

ID NEUX HUMAN STANDARD; PRT; 9 AA.

AC P04277;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurotensin-related peptide (NRP) (Kinetensin).

OS Homo sapiens (Human), and

OS Bos taurus (Bovine), and

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI\_TaxID=9606, 9913, 9986;

[1]

RP SEQUENCE.

RC SPECIES=Human;

RX MEDLINE=86242180; PubMed=3087352;

RA Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,

RA Shively J.E., Walsh J.H.;

RT "The amino acid sequence of kinetensin, a novel peptide isolated from

RT pepsin-treated human plasma: homology with human serum albumin,

RT neurotensin and angiotensin.";

RL Biochem. Biophys. Res. Commun. 136:983-988 (1986).

[2]

RP SEQUENCE.

RC SPECIES=Human, Bovine, and Rabbit;

RX MEDLINE=87194805; PubMed=2437111;

RA Carraway R.E., Mitra S.P., Cochrane D.E.;

RT "Structure of a biologically active neurotensin-related peptide

RT obtained from pepsin-treated albumin(s).";

RL J. Biol. Chem. 262:5968-5973 (1987).

CC -!- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND

CC BLOOD FLOW (POTENTIAL).

DR PIR; A38885; ABBOS.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0005180; F:peptide hormone; NAS.

DR GO; GO:0007599; P:hemostasis; IDA.

DR GO; GO:0006629; P:lipid metabolism; NAS.

KW Hormone.

SQ SEQUENCE 9 AA; 1172 MW; C804DBA761P4140D CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3

Db 8 FL 9

RESULT 58

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

RE42\_LITRU

ID RE42\_LITRU STANDARD; PRT; 9 AA.

AC P82075; P82093;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Rubellidin 4.2/4.3.

OS Litoria rubella (Desert tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;

OC Pelodyadinae; Litoria.

OX NCBI\_TaxID=104895;

[1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,

RA Tyler M.J., Wallace J.C.;

RT "The structure of new peptides from the Australian red tree frog

RT 'Litoria rubella'. The skin peptide profile as a probe for the study

RT of evolutionary trends of amphibians.";

RL Aust. J. Chem. 49:955-963 (1996).

[2]

RP SEQUENCE.

RC TISSUE=Skin secretion;

RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog

RT Litoria electrica. Comparison with the skin peptides from Litoria

RT rubella.";

RL Aust. J. Chem. 52:639-645 (1999).

CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic

CC activity.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-

CC terminal amidation.

CC -!- MASS SPECTROMETRY: MW=883; METHOD=Fab.

KW Amphibian defense peptide; Amidation.

FT MOD RES 9 9 AMIDATION.

SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4

Db 3 LL 4

RESULT 59

TALI\_PICUA

ID TALI\_PICUA STANDARD; PRT; 9 AA.

AC P17440;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transaldolase I (EC 2.2.1.2) (Fragment).

OS Pichia jadinii (Yeast) (Candida utilis).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI\_TaxID=4903;

[1]

RP SEQUENCE.

RX MEDLINE=77110646; PubMed=556924;

RA Sun S.C., Joris L., Tsolas O.;

RT "Purification of crystallization of transaldolase isozyme I and

RT evidence for different genetic origin of isozymes I and III in

RT Candida utilis.";

RL Arch. Biochem. Biophys. 178:69-78 (1977).

CC -!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF

CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.

CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde

CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.

CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.

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CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A12872; A12872.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
DR Transferrase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1008 MW; 274F31AF0EB1E058 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
Db 8 LL 9

RESULT 60
TAL3_PICJA STANDARD; PRT; 9 AA.
ID TAL3_PICJA
AC P17441;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transaldolase III (EC 2.2.1.2) (Fragment).
OS Candida utilis.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxId=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RT Tsolas O., Sun S.C.;
RA "Isolation of a peptide containing a histidinyl-cysteiny sequence
RT from the active center of transaldolase.";
Arch. Biochem. Biophys. 167:525-533 (1975).
CC -1- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF
CC METABOLITES IN THE PENTOSE-PHOSPHATE PATHWAY.
CC -1- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -1- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -1- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
DR Transferrase; Pentose shunt.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match      28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No.1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LL 4
Db 8 LL 9

RESULT 61
TKC1_CALVO STANDARD; PRT; 9 AA.
ID TKC1_CALVO
AC P41517;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin I.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
DR SWISS-2DPAGE; P30093; HUMAN.
FT NON_TER 1
FT UNSTRE 5
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 YQ 6
Db 8 YQ 9

RESULT 64
CU30_LOCM1
ID CU30_LOCM1 STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cuticle protein 30 (LM-30) (LM-ACP 30) (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=86108304; PubMed=3943519;
RA Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -!- FUNCTION: COMPONENT OF THE CUTICLE OF MIGRATORY LOCUST WHICH
CC CONTAINS MORE THAN 100 DIFFERENT STRUCTURAL PROTEINS.
DR PIR; H24802; H24802.
KW Structural protein; Cuticle.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
Db 2 LL 3

RESULT 65
FAR7_MACRS
ID FAR7_MACRS STANDARD; PRT; 10 AA.
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRamide-like neuropeptide FLP7 (GYGDRNFLRF-amide).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX MEDLINE=21107394; PubMed=11179812;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -!- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540AA8 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3
Db 7 FL 8

RESULT 66
FARP_LOCM1
ID FARP_LOCM1 STANDARD; PRT; 10 AA.
AC P38553;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Schistocerca gregaria (Migratory locust), and
OS Locusta migratoria (Migratory locust), and
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004, 7010;
RN [1]
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=93324430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelinckx M.,
RA de Loof A.;
RT "Isolation, identification, and synthesis of PDVDFLRFamide
RT (SchistocFLRFamide) in Locusta migratoria and its association with the
RT male accessory glands, the salivary glands, the heart, and the
RT oviduct.";
RL Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=89246543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistocFLRF-amide, a
RT FMRP-amide-like neuropeptide from the locust, Schistocerca
RT gregaria.";
RL Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -!- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
CC OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
CC OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -!- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
CC THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A32543; A32543.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1042 MW; 5C14477AEB0772C7 CRC64;

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SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
Db 7 FL 8

RESULT 67  
FARP MANSE STANDARD; PRT; 10 AA.

ID FARP MANSE STANDARD; PRT; 10 AA.  
AC P18523;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide.  
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;  
OC Sphingidae; Sphinginae; Manduca.  
OX NCBI\_TaxID=7130;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91045350; PubMed=2235684;  
RA Kingan T.G., Teplow D.B., Phillips J.M., Riehm J.P., Rao K.R., P.R.,  
RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,  
RA Hunt D.F.;  
RT "A new peptide in the FMRFamide family isolated from the CNS of the  
RT hawkmoth, Manduca sexta.";  
RL Peptides 11:849-856(1990).  
CC -!- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN  
CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL  
CC MUSCLE AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING  
CC FLIGHT BEHAVIOR PATTERNS.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; A43977; A43977.  
KW Amidation; Neuropeptide; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1247 MW; D3C45229D5B1F2D2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
Db 7 FL 8

RESULT 68  
LCMS LEUMA STANDARD; PRT; 10 AA.

ID LCMS LEUMA STANDARD; PRT; 10 AA.  
AC P21144; P41497;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leucomyosuppressin (LMS) (LeM-MS).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberoidea; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Head.  
RA Holman G.M., Cook B.J., Nachman R.J.;  
RT "Isolation, primary structure and synthesis of leucomyosuppressin,  
RT an insect neuropeptide that inhibits spontaneous contractions of the

RT cockroach hindgut.";  
RL Comp. Biochem. Physiol. 85C:329-333(1986).  
CC -!- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH  
CC PROTODEUM (HINDGUT).  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
Db 7 FL 8

RESULT 69  
PORE METTM STANDARD; PRT; 10 AA.

ID PORE METTM STANDARD; PRT; 10 AA.  
AC P80901;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Pyruvate synthase subunit porB (EC 1.2.7.1) (Pyruvate oxidoreductase  
DE beta chain) (POR) (Pyruvic-ferredoxin oxidoreductase beta subunit)  
DE (Fragment).  
GN PORB.  
OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=79929;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=97261844; PubMed=9108258;  
RA Testeegen A., Linder D., Thauer R.K., Hedderich R.;  
RT "Structures and functions of four anaerobic 2-oxoacid oxidoreductases  
RT in Methanobacterium thermoautotrophicum.";  
RL Eur. J. Biochem. 244:862-868(1997).  
CC -!- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-  
CC CoA + CO(2) + reduced ferredoxin.  
CC -!- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE  
CC GAMMA CHAIN.  
CC -!- MISCELLANEOUS: As a pH optimum of 10.0 and an optimal temperature  
CC of 80 degrees Celsius.  
KW Oxidoreductase.  
FT NON\_TER 10 10  
FT SEQUENCE 10 AA; 1232 MW; 167011DAF6DB0760 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04; Indels 0; Gaps 0;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FL 3  
Db 8 FL 9

RESULT 70  
Q2OB COMTE STANDARD; PRT; 10 AA.

ID Q2OB COMTE STANDARD; PRT; 10 AA.  
AC P80465;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Quinoline 2-oxidoreductase, beta chain (EC 1.3.99.17) (Fragment).  
OS Comamonas testasteroni (Pseudomonas testasteroni).  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Comamonadaceae; Comamonas.  
OX NCBI\_TaxID=285;  
RN [1]  
RP SEQUENCE.

RC STRAIN=63;  
 RX MEDLINE=96035889; PubMed-7556204;  
 RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;  
 RT "Quinolone 2-oxidoeductase and 2-oxo-1,2-dihydroquinoline 5,6-  
 RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in  
 RL quinoline and 3-methylquinoline degradation.";  
 RL Eur. J. Biochem. 232:536-544(1995)  
 CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-  
 CC 1,2-DIHYDROQUINOLINE.  
 CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-  
 CC 1(2H)-one + reduced acceptor.  
 CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.  
 CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first  
 CC step.  
 CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND  
 CC TWO GAMMA CHAINS (PROBABLE).  
 KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1241 MW; C2B2C25DD9CDC769 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2  
 ||  
 Db 5 AF 6

RESULT 71  
 TEMK RANTE  
 ID TEMK RANTE STANDARD; PRT; 10 AA.  
 AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Temporin K.  
 OS Rana temporaria (European common frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed-9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 10 10  
 SQ SEQUENCE 10 AA; 1123 MW; 390549B33727457 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4  
 ||  
 Db 1 LL 2

RESULT 72  
 CS15\_BACSU  
 ID CS15\_BACSU STANDARD; PRT; 11 AA.  
 AC P81095;  
 DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=168 / JH642;  
 RA Graumann P.L., Schmid R., Marahiel M.A.;  
 RL Submitted (OCT-1997) to the SWISS-PROT data bank.  
 RW [2]  
 RP CHARACTERIZATION.  
 RC STRAIN=168 / JH642;  
 RX MEDLINE=96345629; PubMed=8755892;  
 RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;  
 RT "Cold shock stress-induced proteins in Bacillus subtilis.";  
 RL J. Bacteriol. 178:4611-4619(1996).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- INDUCTION: In response to low temperature.  
 CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEB6322C330 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FL 3  
 ||  
 Db 9 FL 10

RESULT 73  
 MBEI\_KLEPN  
 ID MBEI\_KLEPN STANDARD; PRT; 11 AA.  
 AC P80580;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).  
 GN MBEI.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96349117; PubMed=8760924;  
 RA Robson N.D., Parrott S., Cooper R.A.;  
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella  
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-  
 RT hydroxybenzoate.";  
 RL Microbiology 142:2115-2120(1996).  
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.  
 KW Isomerase.  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1387 MW; 1E80E2DD49C9D5AB CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LY 5  
 ||  
 Db 3 LY 4

RESULT 74  
 RE41\_LITRU  
 ID RE41\_LITRU STANDARD; PRT; 11 AA.  
 AC P82074;  
 DT 28-FEB-2003 (Rel. 41, Created)

Search completed: November 25, 2003, 19:28:25  
Job time : 3.55399 secs

```
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Rubellidin 4.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA Tyler M.J., Wallace J.C.;
RT 'The structure of new peptides from the Australian red tree frog
RT 'Litoria rubella'. The skin peptide profile as a probe for the study
RT of evolutionary trends of amphibians.';
RL Aust. J. Chem. 49:955-963(1996).
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1040 MW; 84ED5BC2877205A CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LL 4
Db 8 LL 9

RESULT 75
TKC2 CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins."
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: MYOACTIVE PEPTIDE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9CDD444 CRC64;

Query Match 28.6%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AF 2
Db 6 AF 7
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 13.1453 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLYQE 7

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL 23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mmc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	57.1	11	7	Q9TQB3
2	4	57.1	15	8	P92818
3	4	57.1	17	5	Q17205
4	4	57.1	17	5	Q26832
5	4	57.1	17	5	Q9TVY3
6	4	57.1	17	5	Q9TVX7
7	4	57.1	20	2	Q32710
8	3	42.9	7	8	Q99182
9	3	42.9	8	2	Q938F2
10	3	42.9	8	8	Q94VC1
11	3	42.9	8	8	Q8HR64
12	3	42.9	10	5	Q95NT8
13	3	42.9	10	6	Q9TRU6
14	3	42.9	10	13	Q90ZV8
15	3	42.9	11	7	Q77912
16	3	42.9	11	7	O77883

Q9UMQ9	homo sapien	4	Q9UMQ9	17	42.9	3
Q8SEB7	grateloupia	12	Q8SEB7	18	42.9	3
Q9XNR6	pylajella	12	Q9XNR6	19	42.9	3
Q49230	mycoplasma	13	Q49230	20	42.9	3
Q75905	homo sapien	13	Q75905	21	42.9	3
Q14461	homo sapien	13	Q14461	22	42.9	3
Q99188	leptomonas	13	Q99188	23	42.9	3
Q94RE2	leptomonas	13	Q94RE2	24	42.9	3
Q9UHM5	homo sapien	14	Q9UHM5	25	42.9	3
Q85718	reovirus	14	Q85718	26	42.9	3
Q9FB61	corynebacte	15	Q9FB61	27	42.9	3
Q9SAP4	solanum tub	15	Q9SAP4	28	42.9	3
Q9QUY5	rattus sp.	15	Q9QUY5	29	42.9	3
Q9TWN2	macrobella	16	Q9TWN2	30	42.9	3
Q35214	oenothera b	16	Q35214	31	42.9	3
P92070	euhadra her	16	P92070	32	42.9	3
Q8CIS2	mus musculus	16	Q8CIS2	33	42.9	3
Q9EUF4	thermus the	17	Q9EUF4	34	42.9	3
Q9UJH1	homo sapien	17	Q9UJH1	35	42.9	3
Q17203	bombyx mori	17	Q17203	36	42.9	3
Q8HKG6	boophilus k	17	Q8HKG6	37	42.9	3
Q8HCD7	zea mays (m	17	Q8HCD7	38	42.9	3
Q8HAS3	zea mays (m	17	Q8HAS3	39	42.9	3
Q9QUJ4	mus sp. mep	17	Q9QUJ4	40	42.9	3
Q9QZ24	mus musculus	17	Q9QZ24	41	42.9	3
Q9PRU8	gallus gall	17	Q9PRU8	42	42.9	3
Q9UC81	homo sapien	18	Q9UC81	43	42.9	3
Q9UJ81	homo sapien	18	Q9UJ81	44	42.9	3
Q9UCR5	homo sapien	18	Q9UCR5	45	42.9	3
Q8NED1	homo sapien	18	Q8NED1	46	42.9	3
Q26833	trypanosoma	18	Q26833	47	42.9	3
Q9TRG2	oryctolagus	18	Q9TRG2	48	42.9	3
Q8VHM8	mus musculus	18	Q8VHM8	49	42.9	3
Q90912	gallus gall	18	Q90912	50	42.9	3
Q44608	buchnera ap	19	Q44608	51	42.9	3
Q9AIE8	actinobacil	19	Q9AIE8	52	42.9	3
Q99736	lanius coll	19	Q99736	53	42.9	3
Q41472	solanum tub	19	Q41472	54	42.9	3
Q85671	reovirus (t	19	Q85671	55	42.9	3
Q9S15	gallus gall	19	Q9S15	56	42.9	3
Q9PRN4	petromyzon	19	Q9PRN4	57	42.9	3
Q905H9	human immun	19	Q905H9	58	42.9	3
Q905K7	human immun	19	Q905K7	59	42.9	3
Q905H1	human immun	19	Q905H1	60	42.9	3
Q905F9	human immun	19	Q905F9	61	42.9	3
Q905E7	human immun	19	Q905E7	62	42.9	3
Q90RH0	human immun	19	Q90RH0	63	42.9	3
Q905J9	human immun	19	Q905J9	64	42.9	3
Q90RH3	human immun	19	Q90RH3	65	42.9	3
Q905K3	human immun	19	Q905K3	66	42.9	3
Q90RG6	human immun	19	Q90RG6	67	42.9	3
Q905D9	human immun	19	Q905D9	68	42.9	3
Q905G7	human immun	19	Q905G7	69	42.9	3
Q905G3	human immun	19	Q905G3	70	42.9	3
Q905J5	human immun	19	Q905J5	71	42.9	3
Q905H5	human immun	19	Q905H5	72	42.9	3
Q90R12	human immun	19	Q90R12	73	42.9	3
Q905F1	human immun	19	Q905F1	74	42.9	3
Q90RF3	human immun	19	Q90RF3	75	42.9	3
Q905F5	human immun	19	Q905F5	76	42.9	3
Q905L1	human immun	19	Q905L1	77	42.9	3
Q90RF7	human immun	19	Q90RF7	78	42.9	3
Q90RH7	human immun	19	Q90RH7	79	42.9	3
Q90RG2	human immun	19	Q90RG2	80	42.9	3
Q90SE3	human immun	19	Q90SE3	81	42.9	3
Q905I7	human immun	19	Q905I7	82	42.9	3
Q905F0	human immun	19	Q905F0	83	42.9	3
Q905J1	human immun	19	Q905J1	84	42.9	3
Q905I3	human immun	19	Q905I3	85	42.9	3
Q9R4V8	streptococc	20	Q9R4V8	86	42.9	3
Q9R4I1	borderella	20	Q9R4I1	87	42.9	3
Q9R4F1	desulfovibr	20	Q9R4F1	88	42.9	3
Q52918	rhizobium m	20	Q52918	89	42.9	3

90 Q9417 leuconostoc  
 91 Q94m1 streptomyce  
 92 Q46499 desulfovibr  
 93 Q9bpu4 halocynthia  
 94 Q9tw8 leptinotars  
 95 Q9trv0 bos taurus  
 96 Q95947 saccharomyc  
 97 Q9mmf2 buteo rufin  
 98 Q9t2q9 solanum tub  
 99 Q9st52 vicia faba  
 100 Q91x54 mus musculu

## ALIGNMENTS

RESULT 1  
 Q9TQB3  
 ID Q9TQB3 PRELIMINARY; PRT; 11 AA.  
 AC Q9TQB3;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MHC class I related protein 1 (Fragment).  
 GN MR1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98451457; PubMed=9780177;  
 RA Riegert P., Wanner V., Bahram S.;  
 RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-  
 RT related MR1 gene."  
 RL J. Immunol. 161:4066-4077(1998).  
 DR EMBL: AF039526; AAD02172.1; -.  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;

Query Match 57.1%; Score 4; DB 7; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 6 AFLL 9

RESULT 2  
 P92818  
 ID P92818 PRELIMINARY; PRT; 15 AA.  
 AC P92818;  
 DT 01-MAY-1997 (TReMBLrel. 03, Created)  
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE NADH dehydrogenase subunit-4L (Fragment).  
 OS Paralicthys olivaceus (Flounder).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
 OC Pleuronectoidei; Paralicththyidae; Paralicthys.  
 OC NCBI\_TaxID=8255;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RA Saich K.;  
 RT "Characterization of cloned mitochondrial fragments from the Japanese  
 RT flounder."  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB006674; BAA20924.1; -.  
 KW Mitochondrion.

FT NON\_TER 15  
 SQ SEQUENCE 15 AA; 1613 MW; D1BAA2018C95FE80 CRC64;  
 Query Match 57.1%; Score 4; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 11 AFLL 14

RESULT 3  
 Q17205  
 ID Q17205 PRELIMINARY; PRT; 17 AA.  
 AC Q17205;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)  
 DE A.L6 protein (Fragment).  
 GN A.L6.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OC NCBI\_TaxID=7091;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90040707; PubMed=2810362;  
 RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;  
 RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:  
 RT Hybridization and Sequence Analysis of Multiple Developmentally Middle  
 RT A/B Chorion Gene Pairs."  
 RL J. Mol. Biol. 209:1-19(1989).  
 DR EMBL: X15562; CAA33575.1; -.  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1877 MW; 577145043395539D CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 5 AFLL 8

RESULT 4  
 Q26832  
 ID Q26832 PRELIMINARY; PRT; 17 AA.  
 AC Q26832;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE (Irat 1.2) variant surface glycoprotein ELC gene (Fragment).  
 OS Trypanosoma brucei.  
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
 OC NCBI\_TaxID=5691;  
 RN [1]\_  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86278091; PubMed=2942540;  
 RA Brown K.H., Brentano S.T., Donelson J.E.;  
 RT "Mung bean nuclease cleaves preferentially at the boundaries of  
 RT variant surface glycoprotein gene transpositions in trypanosome DNA."  
 RL J. Biol. Chem. 261:10352-10358(1986).  
 DR EMBL: M14020; AAA30305.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 1973 MW; 9E00FBD261B8FFBF CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 13 AFLL 16

RESULT 5  
 Q9TVY3 PRELIMINARY; PRT; 17 AA.

AC Q9TVY3;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE A.L10 protein (Fragment).  
 GN A.L10 OR A.L5 OR A.L9.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=703;  
 RX MEDLINE=90040707; PubMed=2810362;  
 RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;  
 RT "Gene evolution and regulation in the chorion complex of Bombyx mori.  
 RT Hybridization and sequence analysis of multiple developmentally middle  
 RT A/B chorion gene pairs.";  
 RL J. Mol. Biol. 209:1-19(1989).  
 DR EMBL; X15565; CAA33581.1; -.  
 DR EMBL; X15561; CAA33573.1; -.  
 DR EMBL; X15564; CAA33579.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1907 MW; 577145043395439C CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 5 AFLL 8

RESULT 6  
 Q9TVX7 PRELIMINARY; PRT; 17 AA.

AC Q9TVX7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE A.X3 protein (Fragment).  
 GN A.X3 OR A.L4 OR A.L13 OR A.R2 OR A.R3 OR A.X1 OR A.X2.  
 OS Bombyx mori (Silk moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;  
 OC Bombycidae; Bombyx.  
 OX NCBI\_TaxID=7091;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=703;  
 RX MEDLINE=90040707; PubMed=2810362;  
 RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;  
 RT "Gene evolution and regulation in the chorion complex of Bombyx mori.  
 RT Hybridization and sequence analysis of multiple developmentally middle  
 RT A/B chorion gene pairs.";  
 RL J. Mol. Biol. 209:1-19(1989).  
 DR EMBL; X15572; CAA33595.1; -.  
 DR EMBL; X15560; CAA33571.1; -.  
 DR EMBL; X15566; CAA33583.1; -.  
 DR EMBL; X15568; CAA33587.1; -.  
 DR EMBL; X15569; CAA33589.1; -.  
 DR EMBL; X15570; CAA33591.1; -.

DR EMBL; X15571; CAA33593.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1901 MW; 5FD3450433955C8C CRC64;

Query Match 57.1%; Score 4; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 5 AFLL 8

RESULT 7  
 O32710 PRELIMINARY; PRT; 20 AA.

AC O32710;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE YHHT protein (Fragment).  
 GN YHHT.  
 OS Klebsiella pneumoniae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97352552; PubMed=9208947;  
 RA Hoenke S., Schmid M., Dimroth P.;  
 RT "Sequence of a gene cluster from Klebsiella pneumoniae encoding  
 RT malonate decarboxylase and expression of the enzyme in Escherichia  
 RT coli.";  
 RL Eur. J. Biochem. 246:530-538(1997).  
 DR EMBL; U95087; AAC45462.1; -.  
 FT NON TER 1  
 SQ SEQUENCE 20 AA; 2108 MW; 86A17AAC8BF77BFA CRC64;

Query Match 57.1%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
 Db 11 AFLL 14

RESULT 8  
 O99182 PRELIMINARY; PRT; 7 AA.

AC O99182;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Cytochrome oxidase I (Fragment).  
 GN COI.  
 OS Gnatheobias zonatus.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatheobias.  
 OX NCBI\_TaxID=135316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20072928; PubMed=10603257;  
 RA Murphy W.J., Thomson J.B., Collier G.E.;  
 RT "Phylogeny of the Neotropical killifish family Rivulidae  
 RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA  
 RT sequences.";  
 RL Mol. Phylogenet. Evol. 13:289-301(1999).  
 DR EMBL; AF002591; AAD01074.1; -.  
 KW Mitochondrion.

```
FT NON_TER 1
SQ SEQUENCE 7 AA; 899 MW; 672721F6CBS572030 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 2 LYQ 4

RESULT 9
Q93SP2 PRELIMINARY; PRT; 8 AA.
ID Q93SP2;
AC Q93SP2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Quaternary ammonium compound-resistance protein QacEdelta1
DE (Fragment).
GN QACDELTA1.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YM704; TRANSPOSON=class I integron;
RA Lee K., Chong Y., Yum J.H., Yong D., Livermore D.M.;
RT "VIM-2 metallo-beta-lactamase gene-containing integron in a
RT Pseudomonas aeruginosa clinical isolate.";
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029772; AAK50441.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 920 MW; FE2729C732C87336 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 6 FLL 8

RESULT 10
Q94VC1 PRELIMINARY; PRT; 8 AA.
ID Q94VC1;
AC Q94VC1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus rudicollis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169851;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:0-0(2001).
DR EMBL; AF407521; AAL10116.1; -.
KW Mitochondrion.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1053 MW; FE2729D5A36411A6 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 2 FLL 4
DB 6 FLL 8

RESULT 11
Q8HR64 PRELIMINARY; PRT; 8 AA.
ID Q8HR64;
AC Q8HR64;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Rps16 protein (Fragment).
GN RPS16.
OS Clivia caulescens.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
OC Clivia.
OX NCBI_TaxID=152470;
RN [1]
RP SEQUENCE FROM N.A.
RA Conrad F., Reeves G., Rourke J.P.;
RT "Phylogenetic relationships of the recently discovered species Clivia
RT mirabilis.";
RL Submitted (Nov-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ519544; CAD59437.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 909 MW; 9FA87729C732C9 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 4 FLL 6

RESULT 12
Q95NT8 PRELIMINARY; PRT; 10 AA.
ID Q95NT8;
AC Q95NT8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Cytochrome P450 (Fragment).
GN CYP6D3.
OS Musca domestica (House fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
OC Muscidae; Musca.
OX NCBI_TaxID=7370;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LP9;
RA Kasai S., Scott J.G.;
RT "5' flanking sequence of CYP6D3.";
RL Submitted (Jun-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS;
RA Kasai S., Scott J.G.;
RT "Cytochrome P450 CYP6D3 5' flanking sequence.";
RL Submitted (Jun-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283258; AAK69543.1; -.
DR EMBL; AF283259; AAK69544.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1190 MW; 550408A0572729C7 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 10;
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Best Local Similarity 100.0%; Pred.No.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 1 FLL 6

RESULT 13

Q9TRU6 PRELIMINARY; PRT; 10 AA.  
AC Q9TRU6 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE GAP-3, GTPase-activating protein (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92112868; PubMed=1309786;  
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,  
RA Burgess A.W.  
RT "The purification of a Rap1 GTPase-activating protein from bovine  
RT brain cytosol."  
RL J. Biol. Chem. 267:1546-1553(1992).  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1149 MW; 59370A51A72321A7 CRC64;

Query Match 42.9%; Score 3; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred.No.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 1 FLL 3

RESULT 14

Q90ZV8 PRELIMINARY; PRT; 10 AA.  
AC Q90ZV8 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE Adenylate kinase (Fragment).  
OS Psittacus erithacus (grey parrot).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Psittaciformes; Psittacidae; Psittacus.  
OX NCBI\_TaxID=57247;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Shapiro L.H., Dumbacher J.P.;  
RT "Adenylate kinase intron 5: a new nuclear locus for avian  
RT systematics."  
RL Auk 118:248-255(2001).  
DR EMBL; AF307895; AAK43534.1; -.  
KW Kinase.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 1099 MW; 22847A272731B777 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred.No.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLY 5  
Db 7 LLY 9

RESULT 15

O77912 PRELIMINARY; PRT; 11 AA.  
AC O77912 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 4 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci."  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050023; AAC41362.1; -.  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1288 MW; 87F42A0FB2D5AB45 CRC64;

Query Match 42.9%; Score 3; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred.No.4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
Db 1 AFL 3

RESULT 16

O77983 PRELIMINARY; PRT; 11 AA.  
AC O77983 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 4 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid mhc  
RT class II B loci."  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF049992; AAC41331.1; -.  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1288 MW; 87F42A0FB2D5AB45 CRC64;

Query Match 42.9%; Score 3; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred.No.4.3e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
Db 1 AFL 3

```

RESULT 17
Q2UMQ9
ID Q9UMQ9 PRELIMINARY; PRT; 12 AA.
AC Q9UMQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
GN FBP2.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2037676; PubMed=10773464;
RA Tillmann H., Stein S., Liehr T., Eschrich K.;
RT "Structure and chromosomal localization of the human and mouse muscle
fructose-1,6-bisphosphatase genes.";
RL Gene 247:241-253(2000).
DR EMBL; AJ238490; CAB53366.1; -.
KW Hydrolase.
FT NON_TER 1 1
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1432 MW; 28E901A093072338 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5
DB 9 LLY 11

RESULT 18
Q8SEB7
ID Q8SEB7 PRELIMINARY; PRT; 12 AA.
AC Q8SEB7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN COX3.
OS Grateloupia sp.
OG Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Halymeniales; Halymeniaceae;
OC Grateloupia.
OX NCBI_TaxID=185958;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=1, and 3;
RA Marston M.F., Villalard-Bohnsack M.;
RT "Genetic variability and potential sources of Grateloupia doryphora
(Halymeniaceae, Rhodophyta), an invasive species in Rhode Island
waters (USA).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF414928; AAL85237.1; -.
DR EMBL; AF414929; AAL85239.1; -.
KW Mitochondrion.
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1367 MW; 9CFACBE91CB046C1 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3
DB 2 AFL 4

RESULT 19
Q9XNR6
ID Q9XNR6 PRELIMINARY; PRT; 12 AA.
AC Q9XNR6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH:ubiquinone oxidoreductase subunit 3 (Fragment).
GN NAD3.
OS Pyraliella littoralis.
OG Mitochondrion.
OC Eukaryota; Stramenopiles; Phaeophyceae; Ectocarpales;
OC Acinetosporaceae; Pyraliella.
OX NCBI_TaxID=2885;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=roscoff;
RA MEDLINE=99346148; PubMed=10415341;
RA Oudot M.P., Kloreg B., Loiseaux-de Goer S.;
RT "The mitochondrial Pyraliella littoralis nad1 gene contains only the
N-terminal FeS-binding domain.";
RL Gene 235:131-137(1999).
DR EMBL; AF110139; AAD44051.1; -.
KW Mitochondrion; Ubiquinone.
FT NON_TER 12 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1501 MW; 49750746424B5B13 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 2 FLL 4

RESULT 20
Q49230
ID Q49230 PRELIMINARY; PRT; 13 AA.
AC Q49230;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical 1.6 kDa protein (Fragment).
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=G-37;
RA Peterson S.N.;
RT "Characterization and analysis of the Mycoplasma genitalium genome.";
RL Thesis (1992), University of North Carolina Medical School, USA.
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=G-37;
RA MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.C., Bott K.F., Hutchison C.A. III.;
RT "A survey of the Mycoplasma genitalium genome by using random
sequencing.";
RL J. Bacteriol. 175:7918-7930(1993).
DR EMBL; U01781; AAD10602.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 13 13
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1642 MW; EC726B2670F6D2C1 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 2 FLL 4

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Db          8 FLL 10

RESULT 21
O75905
ID O75905 PRELIMINARY; PRT; 13 AA.
AC O75905; O9HA09;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prosaposin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98426155; PubMed=9751800;
RA Sun Y., Jin P., Witte D.P., Grabowski G.A.;
RT "Isolation and characterization of the human prosaposin promoter.";
RL Gene 218:37-47(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX Sun Y., Jin P., Grabowski G.A.;
RT "Isolation and characterization of the human prosaposin promoter.";
RL Gene 0:0-0(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21205763; PubMed=11309366;
RA Hukova H., Cervenkova M., Ledvinov J., Tochackova M., Hrebicek M.,
RA Poupetova H., Bervenadu A., Berna L., Paton B.C., Harzer K., Boeoe A.,
RA Smid F., Ellender M.;
RT "A novel mutation in the coding region of the prosaposin gene leads to
RT a complete deficiency of prosaposin and saposins, and is associated
RT with a complex sphingolipidosis dominated by lactosylceramide
RT accumulation.";
RL Hum. Mol. Genet. 10:927-940(2001).
DR EMBL; AF057307; AAC64921.2; -.
DR EMBL; AF07850; AAG31635.1; -.
FT NON TER 13
SQ SEQUENCE 13 AA; 1383 MW; 57585B6C1784D727 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 5 FLL 7

RESULT 22
Q14461 PRELIMINARY; PRT; 13 AA.
ID Q14461; O14842;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Glycophorin B (Fragment).
GN GYPB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264417; PubMed=1971625;
RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
RT "Identification of the crossing-over point of a hybrid gene encoding
RT human glycophorin variant Sta. Similarity to the crossing-over point in
RT haptoglobin-related genes.";
RL J. Biol. Chem. 265:9259-9263(1990).
RN [2]

RP SEQUENCE OF 1-9 FROM N.A.
RA Carttron J.P.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-9 FROM N.A.
RX MEDLINE=90005483; PubMed=2792104;
RA Vignal A., Rahuel C., El-Maliki B., London J., Le Vankim C.,
RA Blanchard C.D.;
RT "Molecular analysis of glycophorin A and B gene structure and
RT expression in homozygous Miltnerberger class V (M1. V) human
RT erythrocytes.";
RL Eur. J. Biochem. 184:337-344(1989).
DR EMBL; M33505; AAA53152.1; -.
DR EMBL; X15824; CAA33822.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1565 MW; 466944F750D145B7 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 11 LYQ 13

RESULT 23
O99188 PRELIMINARY; PRT; 13 AA.
ID O99188;
AC O99188;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Ruvulus caudomarginatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
OX NCBI_TaxID=60318;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072928; PubMed=10603257;
RA Murphy W.J., Thomerson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002597; AAD01080.1; -.
GN Mitochondrion.
FT NON TER 1
SQ SEQUENCE 13 AA; 1705 MW; 404DF35AEFF79C7 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 2 LYQ 4

RESULT 24
O949E2 PRELIMINARY; PRT; 13 AA.
ID O949E2;
AC O949E2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATPase (Fragment).
GN A6.

```

OS Leptomonas seymouri.  
 OG Mitochondrion.  
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leptomonas.  
 OX NCBI\_TaxID=5684;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Merzlyak E.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Kolesnikov A.A.;  
 RT "Cyb and A6 gene transcribed and edited in polycistron."  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ313532; CAC67493.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 1 13  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1626 MW; 471B78F48BDCCEB7 CRC64;  
 Query Match 42.9%; Score 3; DB 8; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LLY 5  
 Db |||  
 10 LLY 12  
 RESULT 25  
 Q9UHM5 PRELIMINARY; PRT; 14 AA.  
 AC Q9UHM5  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE Islet cell autoantigen ICA69 (Fragment).  
 GN ICA1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Friday R.P., Trucco M., Pietropaolo M.;  
 RT "Refined genomic organization of the diabetes autoantigen ICA69 gene locus."  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF147807; AAF20021.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 14 AA; 1656 MW; 1AEB6ACD19E2F9CB CRC64;  
 Query Match 42.9%; Score 3; DB 4; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LYQ 6  
 Db |||  
 6 LYQ 8  
 RESULT 26  
 Q85718 PRELIMINARY; PRT; 14 AA.  
 AC Q85718  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Reovirus serotype 1 S2 (Fragment).  
 OS Reovirus (type 1 / strain Lang).  
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.  
 OX NCBI\_TaxID=10884;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE=83017877; PubMed=7123853;  
 RA Gallard R.K., Li J.K., Keene J.D., Joklik W.K.;  
 RT "The sequences at the termini of four genes of the three reovirus RT serotypes."  
 RL Virology 121:320-326(1982).  
 DR EMBL; J02303; AAA47241.1; -.  
 DR InterPro; IPR004317; Sigma\_1\_2.  
 DR Pfam; PF03084; Sigma\_1\_2; 1.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1516 MW; 52F79D201BF900C7 CRC64;  
 Query Match 42.9%; Score 3; DB 12; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFL 3  
 Db |||  
 5 AFL 7  
 RESULT 27  
 Q9FB61 PRELIMINARY; PRT; 15 AA.  
 ID Q9FB61  
 AC Q9FB61  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE 23S rRNA adenine N-6-methyltransferase leader peptide (ErMLP)  
 DE (Putative leader peptide).  
 GN ERMLP.  
 OS Corynebacterium diphtheriae,  
 OS Corynebacterium striatum, and  
 OS Corynebacterium jeikeium.  
 OG Plasmid pNG2, and Plasmid pTP10.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 OX NCBI\_TaxID=1717, 43770, 38289;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.diphtheriae; STRAIN=S601; PLASMID=pNG2;  
 RA Tauch A., Bischoff N., Kalinowski J., Puehler A.;  
 RT "Insights into the genetic organization of the Corynebacterium diphtheriae erythromycin resistance plasmid pNG2 deduced from its complete nucleotide sequence."  
 RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.striatum; STRAIN=M82B; PLASMID=pTP10;  
 RX MEDLINE=20194806; PubMed=10732668;  
 RA Tauch A., Krieff S., Kalinowski J., Puehler A.;  
 RT "The 51,409-bp R-plasmid pTP10 from the multiresistant clinical isolate Corynebacterium striatum M82B is composed of DNA segments initially identified in soil bacteria and in plant, animal, and human pathogens."  
 RL Mol. Gen. Genet. 263:1-11(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=C.jikeium; STRAIN=CJ21;  
 RA Rosato A.E., Lee B.S., Nash K.A.;  
 RT "Inducible macrolide resistance in Corynebacterium jeikeium."  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF492560; AAM12764.1; -.  
 DR EMBL; AF024666; AAG03358.1; -.  
 DR EMBL; AF338705; AAK28909.1; -.  
 KW Methyltransferase, Transferase, Plasmid.  
 SQ SEQUENCE 15 AA; 1749 MW; CA41026982472410 CRC64;  
 Query Match 42.9%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFL 3  
 Db |||

Db 7 AFL 9

## RESULT 28

Q9SAP4  
ID Q9SAP4 PRELIMINARY; PRT; 15 AA.  
AC Q9SAP4;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)  
DE Serine proteinase inhibitor (Fragment).  
OS Solanum tuberosum (Potato).  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.  
OX NCBI\_TaxID=41113;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Irish Cobbler;  
RA Yamagishi K., Kikuta Y.;  
RL Submitted (FEB-1993) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; X70376; CAA49837.1; -.  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1667 MW; 8093D41B4CA0D1EC CRC64;

Query Match 42.9%; Score 3; DB 10; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 9 FLL 11

## RESULT 29

Q9QUY5  
ID Q9QUY5 PRELIMINARY; PRT; 15 AA.  
AC Q9QUY5;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)  
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96085162; PubMed=8521863;  
RA Schulte S., Stoffel W.;  
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate transporter. Copurification, separation and characterization of the two glycoproteins."  
RL Eur. J. Biochem. 233:947-953 (1995).  
SQ SEQUENCE 15 AA; 1657 MW; 844749A06BFFCC CRC64;

Query Match 42.9%; Score 3; DB 11; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
Db 12 AFL 14

## RESULT 30

Q9TWN2  
ID Q9TWN2 PRELIMINARY; PRT; 16 AA.  
AC Q9TWN2;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)

DE Sialidase L (Fragment).  
OS Macrobodella decora (North American leech).  
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Macrobodella.  
OX NCBI\_TaxID=6405;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94308136; PubMed=8034634;  
RT Chou M.Y., Li S.C., Kiso M., Hasegawa A., Li Y.T.;  
RT "Purification and characterization of sialidase L, a NeuAc alpha 2-->3Gal-specific sialidase."  
RL J. Biol. Chem. 269:18821-18826 (1994).  
SQ SEQUENCE 16 AA; 1910 MW; 0822879C798C6BE0 CRC64;

Query Match 42.9%; Score 3; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6  
Db 7 LYQ 9

## RESULT 31

Q35214  
ID Q35214 PRELIMINARY; PRT; 16 AA.  
AC Q35214;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE ATPase alpha subunit (16 aa) (Fragment).  
OS Oenothera bierriana (Bertero's evening primrose).  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Myrtales; Onagraceae; Oenothera.  
OX NCBI\_TaxID=3950;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86312871; PubMed=2875433;  
RA Schuster W., Hiesel R., Isaac P.G., Leaver C.J., Brennicke A.;  
RT "Transcript termini of messenger RNAs in higher plant mitochondria."  
RL Nucleic Acids Res. 14:5943-5954 (1986).  
DR EMBL; X04203; CAA27800.1; -.  
KW Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 16 AA; 1820 MW; 118AC961C9322C91 CRC64;

Query Match 42.9%; Score 3; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3  
Db 4 AFL 6

## RESULT 32

P92070  
ID P92070 PRELIMINARY; PRT; 16 AA.  
AC P92070;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE NADH dehydrogenase subunit 6 (Fragment).  
OS Euhadra herklotsi.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylomatophora;  
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.  
OX NCBI\_TaxID=58912;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hepatopancreas;

RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,  
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,  
RA Watanabe K., Thomas R.H.;  
RT "Evolution of pulmonate gastropod mitochondrial genomes: comparisons  
of complete gene organization of Euhadra, Cepaea and Albinaria and  
RT implications of unusual tRNA secondary structures.";   
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z71694; CAA96364.1; -.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 16 AA; 1836 MW; 258908495BFBFCAE CRC64;

Query Match 42.9%; Score 3; DB 8; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
Db 10 FLL 12

RESULT 33  
QCIS2  
ID Q8CIS2 PRELIMINARY; PRT; 16 AA.  
AC Q8CIS2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Plasminogen (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvJ; TISSUE=Liver;  
RX PubMed=12149246;  
RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L.,  
RA Farmer R.J., Miles L.A.;  
RT "Localization of Regulatory Elements Mediating Constitutive and  
RT Cytokine-stimulated Plasminogen Gene Expression.";   
RL J. Biol. Chem. 277:38579-38588(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvJ; TISSUE=Liver;  
RA Garcia Bannach F., Fowler B.J., Gutierrez A., Bugge T.H., Degen J.L.,  
RA Farmer R.J., Miles L.A.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY134430; AAN15805.1; -.  
FT NON TER 16  
SQ SEQUENCE 16 AA; 1922 MW; 647558FC6EDB15CC CRC64;

Query Match 42.9%; Score 3; DB 11; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
Db 10 FLL 12

RESULT 34  
Q9EUP4  
ID Q9EUP4 PRELIMINARY; PRT; 17 AA.  
AC Q9EUP4;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Cell division associated protein (Fragment).  
GN DTIVA.  
OS Thermus thermophilus.  
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;  
OC Thermus.

OX NCBI\_TaxID=274;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KT8;  
RA Spada S., Gilbert Y., Pembroke J.T., Wall J.G.;  
RT "Cloning and characterisation of the ylmE homologue of Thermus  
RT thermophilus.";   
RL DNA Seq. 11:5007-5014(2001).  
DR EMBL; AJ297409; CAC21427.1; -.  
FT NON TER 17  
SQ SEQUENCE 17 AA; 2084 MW; 0C642E1D509D87E3 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7  
Db 10 YQE 12

RESULT 35  
Q9UJH1  
ID Q9UJH1 PRELIMINARY; PRT; 17 AA.  
AC Q9UJH1;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE DJ436M11.2 (Retinoschisis (X-linked, juvenile) 1 (XLR1))  
DE (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Grafham D.;  
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z94056; CAB40073.1; -.  
FT NON TER 17  
SQ SEQUENCE 17 AA; 2029 MW; 8100B1B78C52C7F9 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
Db 8 FLL 10

RESULT 36  
Q17203  
ID Q17203 PRELIMINARY; PRT; 17 AA.  
AC Q17203;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE A.L2 protein (Fragment).  
GN A.L2.  
OS Bombyx mori (Silk moth).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Bombycoidea;  
OC Bombycidae; Bombyx.  
OX NCBI\_TaxID=7091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=703;  
RX MEDLINE=90040707; PubMed=2810362;  
RA Spoerel N.A., Nguyen H.T., Eickbush T.H., Kafatos F.C.;  
RT "Gene Evolution and Regulation in the Chorion Complex of Bombyx mori:  
RT Hybridization and Sequence Analysis of Multiple Developmentally Middle

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RT A/B Chorion Gene Pairs.";
RL J. Mol. Biol. 209:1-19(1989).
DR EMBL; X15558; CAA33567.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1935 MW; 5FD34DA633955C8C CRC64;

Query Match 42.9%; Score 3; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4
Db 7 FLL 9

RESULT 37
Q8HKG6 PRELIMINARY; PRT; 17 AA.
ID Q8HKG6
AC Q8HKG6;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN NDI.
OS Boophilus kohlsi.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
OX NCBI_TaxID=127004;
RN [1]
RP SEQUENCE FROM N.A.
RA Campbell N.J.H., Murrell A., Barker S.C.;
RT "The value of idiosyncratic markers and conserved tRNA sequences from
RT the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for
RT phylogenetic inference.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059201; AAL79405.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1989 MW; 0F9CD412E9843E0A CRC64;

Query Match 42.9%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 3 AFL 5

RESULT 38
Q8HCD7 PRELIMINARY; PRT; 17 AA.
ID Q8HCD7
AC Q8HCD7;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Zea mays (Maize).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA Betz S.K., Gallagher L.J., Chase C.D.;
RT "Mitochondrial RNA editing truncates a chimeric open reading frame
RT associated with S male sterility in maize.";
RL Curr. Genet. 0:0-0(2002).
DR EMBL; AF536188; AAN40750.1; -.
KW EMBL; AF536189; AAN40752.1; -.

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DR EMBL; AF536190; AAN40754.1; -.
KW Hypothetical protein; Mitochondrion.
SQ SEQUENCE 17 AA; 1991 MW; 1A25865EB2CFA69E CRC64;

Query Match 42.9%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 10 AFL 12

RESULT 39
Q8HAS3 PRELIMINARY; PRT; 17 AA.
ID Q8HAS3
AC Q8HAS3;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE ORF17 (Hypothetical protein).
OS Zea mays (Maize).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Mo17; TISSUE=Microspore;
RX MEDLINE=22378502; PubMed=12491012;
RA Gallagher L.J., Betz S.K., Chase C.D.;
RT "Mitochondrial RNA editing truncates a chimeric open reading frame
RT associated with S male sterility in maize.";
RL Curr. Genet. 42:179-184(2002).
DR EMBL; AF534133; AAN39290.1; -.
KW EMBL; AF536191; AAN40756.1; -.
KW Hypothetical protein; Mitochondrion.
SQ SEQUENCE 17 AA; 2017 MW; 1A25864C22CFA69E CRC64;

Query Match 42.9%; Score 3; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 3
Db 10 AFL 12

RESULT 40
Q9QUJ4 PRELIMINARY; PRT; 17 AA.
ID Q9QUJ4
AC Q9QUJ4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Meprin-B peptide B2 (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=31373354; PubMed=1894622;
RA Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;
RT "Meprin-A and -B. Cell surface endopeptidases of the mouse kidney.";
RL J. Biol. Chem. 266:17350-17357(1991).
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2165 MW; ACA591691044F20B CRC64;

Query Match 42.9%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5  
|||  
Db 4 LLY 6

## RESULT 41

ID Q9QZ24 PRELIMINARY; PRT; 17 AA.  
AC Q9QZ24;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE B7-Ag protein (Fragment).  
OS CD80 OR B7-AG.  
GN Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99453732; PubMed=10524207;  
RA Tone M., Nolan K.F., Walsh L.A., Tone Y., Thompson S.A.J.,  
RA Waldmann H.;  
RT "Structure and chromosomal location of mouse and human CD52 genes.";  
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1446:334-340(1999).  
DR EMBL; AJ132360; CAB51320.1; -.  
DR MGD; MGI:101775; Cd80.  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1992 MW; 8F2B5852B50DB8D7 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 4 FLL 6

## RESULT 42

ID Q9PRU8 PRELIMINARY; PRT; 17 AA.  
AC Q9PRU8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95105151; PubMed=7806494;  
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
RA Yazaki Y., Hirai H.;  
RT "Characterization, partial purification, and peptide sequencing of  
RT p130, the main phosphoprotein associated with v-Crk oncoprotein.";  
RL J. Biol. Chem. 269:32740-32746(1994).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1861 MW; 379058CDE44F8879 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 17;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||

Db 5 LYQ 7

## RESULT 43

ID Q9UC81 PRELIMINARY; PRT; 18 AA.  
AC Q9UC81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE 34.5 kDa stone matrix protein (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95215817; PubMed=7701298;  
RA Binette J.P., Binette M.B.;  
RT "Sequencing of proteins extracted from stones.";  
RL Scanning Microsc. 8:233-239(1994).  
DR HSSP; F02906; 1SBP.  
SQ SEQUENCE 18 AA; 2246 MW; B6CB60E9AC339E35 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 16 LYQ 18

## RESULT 44

ID Q9UJ81 PRELIMINARY; PRT; 18 AA.  
AC Q9UJ81;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
DE CD52 protein (Fragment).  
GN CD52.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99453732; PubMed=10524207;  
RA Tone M., Nolan K.F., Walsh L.A., Tone Y., Thompson S.A.J.,  
RA Waldmann H.;  
RT "Structure and chromosomal location of mouse and human CD52 genes.";  
RL Biochim. Biophys. Acta, Gene Struct. Expr. 1446:334-340(1999).  
DR EMBL; AJ132359; CAB51285.1; -.  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2166 MW; AC6C4590EDA71F29 CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|||  
Db 6 FLL 8

## RESULT 45

ID Q9UCR5 PRELIMINARY; PRT; 18 AA.  
AC Q9UCR5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)



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DE Mammery-derived growth factor 1, MDGF1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92118863; PubMed=1731916;
RA Bano M., Lupu R., Kidwell W.R., Lippman M.E., Dickson R.B.;
RT "Production and characterization of mammary-derived growth factor 1 in
RT mammary epithelial cell lines.";
RL Biochemistry 31:610-616(1992).
FT NON_TER 1
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2060 MW; 720BIA09F9262ACC CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 11 FLL 13

RESULT 46
Q8NED1 Q8NED1 PRELIMINARY; PRT; 18 AA.
AC Q8NED1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032027; AAH32027.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2050 MW; E71A65SE65FD253F CRC64;

Query Match 42.9%; Score 3; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 2 FLL 4

RESULT 47
Q26833 Q26833 PRELIMINARY; PRT; 18 AA.
AC Q26833
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (TaTaT 1.2) variant surface glycoprotein BC gene (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86278091; PubMed=2942540;
RA Brown K.H., Brentano S.T., Donelson J.E.;
RT "Mung bean nuclease cleaves preferentially at the boundaries of
RT variant surface glycoprotein gene transpositions in trypanosome DNA.";

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RL J. Biol. Chem. 261:10352-10358(1986).
DR EMBL; M14021; AAA30306.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2039 MW; 8EA0F51BD630BF8F CRC64;

Query Match 42.9%; Score 3; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3
DB 13 AFL 15

RESULT 48
Q9TRG2 Q9TRG2 PRELIMINARY; PRT; 18 AA.
AC Q9TRG2
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE C1-INHIBITOR-SERINE proteinase inhibitor (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=93264944; PubMed=8495195;
RA Aulak K.S., Davis A.E.III., Donaldson V.H., Harrison R.A.;
RT "Chymotrypsin inhibitory activity of normal C1-inhibitor and a P1 Arg
RT to His mutant: evidence for the presence of overlapping reactive
RT centers.";
RL Protein Sci. 2:727-732(1993).
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; 1.
FT NON_TER 1
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 2134 MW; 6A74AE635AF54C5E CRC64;

Query Match 42.9%; Score 3; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
DB 16 FLL 18

RESULT 49
Q8VHM8 Q8VHM8 PRELIMINARY; PRT; 18 AA.
AC Q8VHM8
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin 10 receptor 2 (Fragment).
GN IL10R2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;
RT "The genomic structure and expression patterns of the gene encoding
RT the second chain of the murine interleukin 10 receptor, IL-10R2.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Hardy M.P., Hertzog P.J., Owczarek C.M.;

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RT "The organization, transcriptional regulation and chromosomal  
 RT localization of the locus encoding the gene for the murine type I  
 RT interferon receptor, Ifnar2.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF440786; AAL40943.1; -.  
 KW Receptor.  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 1888 MW; 8AC62D50E1523831 CRC64;

Query Match 42.9%; Score 3; DB 11; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 Db 14 FLL 16

## RESULT 50

Q90912 ID Q90912 PRELIMINARY; PRT; 18 AA.  
 AC Q90912;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Chicken embryonic myosin heavy chain, 3' end of mRNA, fragment 2 (Fragment).  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83213464; PubMed=6304080;  
 RA Freyer G.A., Robbins J.;  
 RT "the analysis of a chicken myosin heavy chain cdna clone.";  
 RL J. Biol. Chem. 258:7149-7154 (1983).  
 DR EMBL: K00815; AAA48969.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 18 18  
 SQ SEQUENCE 18 AA; 2039 MW; 38DDB38C4184436B CRC64;

Query Match 42.9%; Score 3; DB 13; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 Db 7 FLL 9

## RESULT 51

Q44608 ID Q44608 PRELIMINARY; PRT; 19 AA.  
 AC Q44608;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Shikimate dehydrogenase (Fragment).  
 GN AROE.  
 OS Buchnera aphidicola.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Buchnera.  
 OC NCBI\_TaxID=9;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95212914; PubMed=7535281;  
 RA Rounbakhsh D., Baumann P.;  
 RT "Characterization of a putative 23S-5S rRNA operon of Buchnera  
 RT aphidicola (endosymbiont of aphids) unlinked to the 16S rRNA-encoding  
 RT gene.";  
 RL Gene 156:107-112 (1995).

DR EMBL: U10497; AAA79126.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 19 AA; 2214 MW; 2C1A573F6A4D01D5 CRC64;

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
 Db 2 FLL 4

## RESULT 52

Q9A1E8 ID Q9A1E8 PRELIMINARY; PRT; 19 AA.  
 AC Q9A1E8;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)  
 DE Hypothetical 2.4 kDa protein.  
 OS Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Actinobacillus.  
 OC NCBI\_TaxID=715;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=ATCC27088;  
 RX MEDLINE=21125560; PubMed=11222596;  
 RA Dorae S.M., Mulks M.H.;  
 RT "Identification of an Actinobacillus pleuropneumoniae consensus  
 RT promoter structure.";  
 RL J. Bacteriol. 183:1983-1989 (2001).  
 DR EMBL: AF275729; AAK18080.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 19 AA; 2379 MW; DCA788F5221B03DC CRC64;

Query Match 42.9%; Score 3; DB 2; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
 Db 8 LYQ 10

## RESULT 53

O99736 ID O99736 PRELIMINARY; PRT; 19 AA.  
 AC O99736;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Cytochrome oxidase subunit III (EC 1.9.3.1) (Cytochrome c oxidase polypeptide III) (Fragment).  
 OS Lanius collurio.  
 OS Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Passeriformes; Corvoidea; Laniidae;  
 OC Lanius.  
 OC NCBI\_TaxID=56324;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=24459836; PubMed=12572620;  
 RA Mindell D.P., Sorenson M.D., Dimcheff D.E.;  
 RT "An extra nucleotide is not translated in mitochondrial ND3 of some  
 RT birds and turtles.";  
 RL Mol. Biol. Evol. 15:1568-1571 (1998).  
 CC -!- FUNCTION: SUBUNITS I, II AND III FORM THE FUNCTIONAL CORE OF THE  
 CC ENZYME COMPLEX (BY SIMILARITY).  
 CC -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERRICYTOCHROME  
 CC C + 2 H(2)O.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 3 FAMILY.

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DR EMBL; AF076302; AAC79825.1; -.
DR InterPro; IPR000298; CytC_oxdse_III.
DR Pfam; PF00510; COX3; 1.
DR PROSITE; PS00253; COX3; 1.
KW OXidoreductase; Transmembrane; Mitochondrion.
FT NON TER 1
SQ SEQUENCE 19 AA; 2429 MW; BC991E66D4D98D7C CRC64;

Query Match 42.9%; Score 3; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLY 5
DB 9 LLY 11

RESULT 54
Q41472 ID Q41472 PRELIMINARY; PRT; 19 AA.
AC Q41472
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Potato patatin class II (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OC NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226014; PubMed=3371664;
RA Mignery G.A.; Fikaard C.S.; Park W.D.;
RT "Molecular characterization of the patatin multigene family of
RL Gene 62:27-44(1988).
DR EMBL; M18886; AAA33834.1; -.
FT NON TER 19
SQ SEQUENCE 19 AA; 2107 MW; 07C02E1FCDAB0B78 CRC64;

Query Match 42.9%; Score 3; DB 10; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3
DB 6 AFL 8

RESULT 55
Q85671 ID Q85671 PRELIMINARY; PRT; 19 AA.
AC Q85671
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Reovirus (Serotype 3) S2 gene 5' end (Plus strand) (Fragment).
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OC NCBI_TaxID=10886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81016752; PubMed=7414954;
RA Li J.K.; Scheible P.P.; Keene J.D.; Joklik W.K.;
RT "The plus strand of reovirus gene S2 is identical with its in vitro
RT transcript."
RL Virology 105:282-286(1980).
DR EMBL; M10488; AAA47266.1; -.
DR InterPro; IPR004317; Sigma_1.2.
DR Pfam; PF03084; Sigma_1.2; 1.
FT NON TER 19
SQ SEQUENCE 19 AA; 2027 MW; 44D093E79852F79D CRC64;

Query Match 42.9%; Score 3; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3
DB 5 AFL 7

RESULT 56
Q9PS15 ID Q9PS15 PRELIMINARY; PRT; 19 AA.
AC Q9PS15
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (T-EMBLrel. 14, Last annotation update)
DE Puromycin-sensitive aminopeptidase isozyme II (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE
RX MEDLINE=93250542; PubMed=8485450;
RA Hui K.S.; Saito M.; Hui M.; Saito M.; Lajtha A.; Yamamoto K.;
RA Osawa T.;
RL Neurochem. Int. 22:445-453(1993).
SQ SEQUENCE 19 AA; 2125 MW; 6442523A8A4E7D41 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YQE 7
DB 11 YQE 13

RESULT 57
Q9PRN4 ID Q9PRN4 PRELIMINARY; PRT; 19 AA.
AC Q9PRN4
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
DE Melanotropin MSH-A.
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OC NCBI_TaxID=7757;
RN [1]
RP SEQUENCE
RX MEDLINE=96122167; PubMed=8537171;
RA Takahashi A.; Amemiya Y.; Nozaki M.; Sower S.A.; Joss J.; Gorbman A.;
RA Kawauchi H.;
RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands."
RL Int. J. Pept. Protein Res. 46:197-204(1995).
SQ SEQUENCE 19 AA; 2400 MW; 0F4CD35F7E0BC340 CRC64;

Query Match 42.9%; Score 3; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 4 LYQ 6

RESULT 58
Q905H9

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```
ID Q905H9 PRELIMINARY; PRT; 19 AA.
AC Q905H9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG38;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410444; AAL10243.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2193 MW; 00430F335A711915 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 59
Q905K7 PRELIMINARY; PRT; 19 AA.
AC Q905K7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG14;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410437; AAL10215.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2176 MW; 3516A49DA9711856 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 60
Q905H1 PRELIMINARY; PRT; 19 AA.
ID Q905H1
AC Q905H1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
```

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG275;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410446; AAL10251.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2250 MW; ED16A23424711905 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 61
Q905F9 PRELIMINARY; PRT; 19 AA.
AC Q905F9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG305;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410449; AAL10263.1; -.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2261 MW; 005A7947EB711915 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQ 6
Db 16 LYQ 18

RESULT 62
Q905E7 PRELIMINARY; PRT; 19 AA.
ID Q905E7
AC Q905E7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
```

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 OS Rev protein (Fragment).  
 DE Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=97CG314;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF410452; AAL10275.1; -;  
 DR InterPro; IPR000625; REV\_protein.  
 FT pfam; PF00424; REV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2122 MW; 6B3BB70E0A662B9E CRC64;  
  
 Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LYQ 6  
 Db ||||  
 16 LYQ 18  
  
 RESULT 63  
 Q90RH0 PRELIMINARY; PRT; 19 AA.  
 AC Q90RH0  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Rev protein (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG21;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Hayami M., Ichimura H., Parra J.H.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF127547; AAK84905.1; -;  
 DR InterPro; IPR000625; REV\_protein.  
 DR pfam; PF00424; REV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2276 MW; 740E013424711914 CRC64;  
  
 Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LYQ 6  
 Db ||||  
 16 LYQ 18  
  
 RESULT 64  
 Q90SJ9 PRELIMINARY; PRT; 19 AA.  
 AC Q90SJ9  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Rev protein (Fragment).

OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG22;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
 RA Ichimura H., Parra H.-J.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF410439; AAL10223.1; -;  
 DR InterPro; IPR000625; REV\_protein.  
 DR pfam; PF00424; REV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2120 MW; 7413BAD4EA711B9E CRC64;  
  
 Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LYQ 6  
 Db ||||  
 16 LYQ 18  
  
 RESULT 65  
 Q90RH3 PRELIMINARY; PRT; 19 AA.  
 AC Q90RH3  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Rev protein (Fragment).  
 GN TAT.  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=96CG17;  
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
 RA Hayami M., Ichimura H., Parra J.H.;  
 RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
 RT Republic of Congo-Brazzaville.";  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF127546; AAK84901.1; -;  
 DR InterPro; IPR000625; REV\_protein.  
 DR pfam; PF00424; REV; 1.  
 FT NON\_TER 1  
 FT NON\_TER 19  
 SQ SEQUENCE 19 AA; 2120 MW; 7413BAD4EA711B9E CRC64;  
  
 Query Match 42.9%; Score 3; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 LYQ 6  
 Db ||||  
 16 LYQ 18  
  
 RESULT 66  
 Q90SK3 PRELIMINARY; PRT; 19 AA.  
 AC Q90SK3  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Rev protein (Fragment).

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OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG16;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410438; AAL10219.1; -
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2260 MW; 7415B9997A711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 67
Q90RG6 PRELIMINARY; PRT; 19 AA.
AC Q90RG6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG34;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127548; AAK84908.1; -
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2264 MW; 7413AAD274711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 68
Q905D9 PRELIMINARY; PRT; 19 AA.
AC Q905D9;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.

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OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG316;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410454; AAL10283.1; -
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2160 MW; 740C7E5DA9711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 69
Q905G7 PRELIMINARY; PRT; 19 AA.
AC Q905G7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG281;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410447; AAL10285.1; -
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1
FT NON_TER 19
FT NON_TER 19
SQ SEQUENCE 19 AA; 2332 MW; 740E13BF24662914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 16 LYQ 18

RESULT 70
Q905G3 PRELIMINARY; PRT; 19 AA.
AC Q905G3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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[1]
RN SEQUENCE FROM N.A.
RP STRAIN=97CG284;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410448; AAL10259.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2262 MW; 7405013424711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 16 LYQ 18

RESULT 71
Q905J5
ID Q905J5 PRELIMINARY; PRT; 19 AA.
AC Q905J5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG23;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410440; AAL10227.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2304 MW; 74050B1C24711851 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 16 LYQ 18

RESULT 72
Q905H5
ID Q905H5 PRELIMINARY; PRT; 19 AA.
AC Q905H5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
```

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RP SEQUENCE FROM N.A.
RC STRAIN=97CG152;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,
RA Ichimura H., Parra H.-J.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410445; AAL10247.1; -.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
FT NON_TER 1 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2187 MW; 7416A234246A7000 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 16 LYQ 18

RESULT 73
Q90R12
ID Q90R12 PRELIMINARY; PRT; 19 AA.
AC Q90R12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
GN TAR.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG11;
RA Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengul, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RT Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF127544; AAK84895.2; -.
FT NON_TER 1 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2305 MW; F0B4722C24711905 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
DB 16 LYQ 18

RESULT 74
Q905F1
ID Q905F1 PRELIMINARY; PRT; 19 AA.
AC Q905F1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Rev protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97CG313;
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RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
RA N'Doundou-N'Kodia M.-Y., M'Pandi M., M'Pele P., Harada Y., Hayami M.,  
RA Ichimura H., Parra H.-J.;  
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
RT Republic of Congo-Brazzaville.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF410451; AAL10271.1; --  
DR InterPro; IPR000625; REV\_protein.  
DR Pfam; PF00424; REV; 1.  
FT NON\_TER 1  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2248 MW; 7413BAD374711914 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 16 LYQ 18

## RESULT 75

Q09RF3 PRELIMINARY; PRT; 19 AA.  
AC Q09RF3;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Rev protein (Fragment).  
GN TAT.  
OS Human immunodeficiency virus 1.  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97CG282;  
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,  
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,  
RA Hayami M., Ichimura H., Parra J.H.;  
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in  
RT Republic of Congo-Brazzaville.";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF127551; AAK84918.1; --  
FT NON\_TER 1  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2185 MW; 69D3ABD5FA711911 CRC64;

Query Match 42.9%; Score 3; DB 15; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6  
|||  
Db 16 LYQ 18

Search completed: November 25, 2003, 19:34:09  
Job time : 16.1453 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 17.8663 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLYQE 7

Scoring table: Oligo

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	22	Colostrin derive
2	7	100.0	7	22	Colostrin peptid
3	7	100.0	7	22	Colostrin peptid
4	7	100.0	7	22	Ewe colostrin pe
5	7	100.0	7	23	Colostrin consti
6	7	100.0	7	23	Colostrin consti
7	7	100.0	7	23	Neural cell regula
8	7	100.0	8	23	Antiviral composi
9	7	100.0	9	22	Ewe colostrin pe

10	7	100.0	11	23	Antiviral composi
11	7	100.0	12	23	Antiviral composi
12	7	100.0	12	23	Antiviral composi
13	7	100.0	13	23	Antiviral composi
14	7	100.0	13	23	Antiviral composi
15	7	100.0	13	23	Antiviral composi
16	7	100.0	14	23	Antiviral composi
17	7	100.0	14	23	Antiviral composi
18	7	100.0	15	23	Antiviral composi
19	7	100.0	16	23	Antiviral composi
20	7	100.0	16	23	Antiviral composi
21	7	100.0	16	23	Antiviral composi
22	6	85.7	9	23	Antiviral composi
23	6	85.7	13	22	Colostrin derive
24	6	85.7	13	22	Colostrin peptid
25	6	85.7	13	22	Colostrin peptid
26	6	85.7	13	22	Ewe colostrin pe
27	6	85.7	13	23	Colostrin consti
28	6	85.7	13	23	Colostrin consti
29	6	85.7	13	23	Neural cell regula
30	6	85.7	13	23	Antiviral composi
31	6	85.7	14	23	Antiviral composi
32	6	85.7	15	23	Antiviral composi
33	6	85.7	16	23	Antiviral composi
34	6	85.7	19	20	Casein antimicrobi
35	5	71.4	6	23	Human butyrylcholi
36	5	71.4	7	22	Colostrin peptid
37	5	71.4	8	22	Modified colostrin
38	5	71.4	16	23	Antiviral composi
39	4	57.1	5	17	Linear thrombin re
40	4	57.1	6	22	Human olfactory re
41	4	57.1	6	22	Amino acid sequenc
42	4	57.1	6	22	Amino acid sequenc
43	4	57.1	6	22	Amino acid sequenc
44	4	57.1	6	22	Amino acid sequenc
45	4	57.1	6	22	Amino acid sequenc
46	4	57.1	6	22	Amino acid sequenc
47	4	57.1	6	24	Olfactory receptor
48	4	57.1	6	24	Peptide binding to
49	4	57.1	6	24	Peptide binding to
50	4	57.1	6	24	Peptide binding to
51	4	57.1	6	24	Poliovirus-binding
52	4	57.1	6	24	Poliovirus-binding
53	4	57.1	6	24	Peptide binding to
54	4	57.1	7	17	Hepatitis B virus-
55	4	57.1	9	15	Immunogenic peptid
56	4	57.1	9	20	Immunogenic peptid
57	4	57.1	9	20	Immunogenic peptid
58	4	57.1	9	21	Antiviral antibody
59	4	57.1	9	21	HUA-A*0201 binding
60	4	57.1	9	21	Telomerase peptid
61	4	57.1	9	22	Human MHC class I
62	4	57.1	9	22	Human MHC class I
63	4	57.1	9	22	Human MHC class I
64	4	57.1	9	22	Human MHC class I
65	4	57.1	9	22	Human MHC molecule
66	4	57.1	9	22	Human MHC class I
67	4	57.1	9	22	Human MHC class I
68	4	57.1	9	22	Human MHC class I
69	4	57.1	9	22	Human MHC class I
70	4	57.1	9	22	Human MHC molecule
71	4	57.1	9	22	HIV peptide SEQ ID
72	4	57.1	9	23	Zinc transporter p
73	4	57.1	9	23	Zinc transporter p
74	4	57.1	9	23	Zinc transporter p
75	4	57.1	9	23	Zinc transporter p
76	4	57.1	9	23	Zinc transporter p
77	4	57.1	9	23	Zinc transporter p
78	4	57.1	9	23	Zinc transporter p
79	4	57.1	9	23	Zinc transporter p
80	4	57.1	9	23	Zinc transporter p
81	4	57.1	9	23	Zinc transporter p
82	4	57.1	9	23	Zinc transporter p

83 4 57.1 9 23 ABJ16319 Zinc transporter p  
 84 4 57.1 9 23 ABJ16343 Zinc transporter p  
 85 4 57.1 9 23 ABJ16358 Zinc transporter p  
 86 4 57.1 9 23 ABJ16392 Zinc transporter p  
 87 4 57.1 9 23 ABJ16476 Zinc transporter p  
 88 4 57.1 9 23 ABJ16485 Zinc transporter p  
 89 4 57.1 9 23 ABJ16523 Zinc transporter p  
 90 4 57.1 9 23 ABJ16785 Zinc transporter p  
 91 4 57.1 9 23 ABJ16893 CTL epitope HLA pe  
 92 4 57.1 9 23 ABB94598 CTL epitope HLA pe  
 93 4 57.1 9 23 ABB94616 CTL epitope HLA pe  
 94 4 57.1 9 23 ABB94789 CTL epitope HLA pe  
 95 4 57.1 9 23 ABB94873 CTL epitope HLA pe  
 96 4 57.1 9 23 ABB94904 CTL epitope HLA pe  
 97 4 57.1 9 23 ABB94981 CTL epitope HLA pe  
 98 4 57.1 9 23 ABB95101 Human cancer-relat  
 99 4 57.1 9 24 ABR17385 Human cancer-relat  
 100 4 57.1 9 24 ABR17411 Human cancer-relat

## ALIGNMENTS

RESULT 1  
 AAB72273 standard; peptide; 7 AA.  
 ID AAB72273 standard; peptide; 7 AA.  
 AC AAB72273;  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 28.  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200111937-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 17-AUG-2000; 2000WO-US222818.  
 XX  
 XX 17-AUG-1999; 99US-0149311.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 XX  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrinum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.

XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQE 7  
 Db 1 AFLLYQE 7  
 RESULT 2  
 AAB72526 standard; Peptide; 7 AA.  
 ID AAB72526 standard; Peptide; 7 AA.  
 AC AAB72526;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #27.  
 XX  
 KW Dermatalogical; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200112650-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 17-AUG-2000; 2000WO-US222665.  
 XX  
 XX 17-AUG-1999; 99US-0149310.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 XX Claim 6; Page 26; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 XX SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQE 7  
 Db 1 AFLLYQE 7  
 RESULT 3  
 AAB72558 standard; Peptide; 7 AA.  
 ID AAB72558 standard; Peptide; 7 AA.  
 AC AAB72558;  
 XX  
 XX 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #27.  
XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
KW colostrum.  
XX Unidentified.  
OS  
XX WO2000112651-A2.  
PN  
XX 22-FEB-2001.  
PD  
XX 17-AUG-2000; 2000WO-US22774.  
PF  
XX 17-AUG-1999; 99US-0149633.  
PR  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Boldogh I;  
PI  
XX WPI; 2001-226545/23.  
DR  
XX Use of colostrinin, its constituent peptide or analog as a neural cell  
PT regulator, for promoting neural cell differentiation and treating  
PT damaged neural cells in a patient -  
XX  
XX Claim 6; Page 22; 35pp; English.  
PS  
XX The present invention relates to a method for promoting neural cell  
CC differentiation and treating damaged neural cells, using colostrinin and  
CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
CC  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AFLLYQE 7  
Db 1 AFLLYQE 7  
RESULT 4  
AAB59337  
ID AAB59337 standard; Peptide; 7 AA.  
AC  
XX AAB59337;  
XX  
DT 21-MAR-2001 (first entry)  
DE  
XX Ewe colostrinin peptide fragment C-12.  
DE  
XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
KW  
XX Ovis sp.  
OS  
XX WO200075173-A2.  
PN  
XX 14-DEC-2000.  
PD  
XX 02-JUN-2000; 2000WO-GB02128.  
PF  
XX 02-JUN-1999; 99GB-0012852.  
PR  
XX (REGE-) REGEN THERAPEUTICS PLC.  
PA  
XX Georgiades JA;  
PI  
XX WPI; 2001-071058/08.  
DR  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT

PT colostrinin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX  
PS Claim 7; Page 27; 63pp; English.  
XX  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 7; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AFLLYQE 7  
Db 1 AFLLYQE 7  
RESULT 5  
AAE20255  
ID AAE20255 standard; peptide; 7 AA.  
XX  
AC AAE20255;  
XX  
DT 18-JUN-2002 (first entry)  
DE  
XX Colostrinin constituent peptide #27.  
DE  
XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
KW transplantation; implantation; dermatological; vulnary.  
XX  
XX Unidentified.  
OS  
XX  
XX Key Location/Qualifiers  
FH  
FT Modified-site 7 /note= "Optionally C-terminal amide"  
FT  
XX WO200213850-A1.  
PN  
XX 21-FEB-2002.  
PD  
XX 17-AUG-2000; 2000WO-US22776.  
PF  
XX 17-AUG-2000; 2000WO-US22776.  
PR  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX Stanton GJ, Hughes TK, Boldogh I;  
PI  
XX WPI; 2002-269151/31.  
DR  
XX Composition useful for the modulation of blood cell proliferation in a  
PT patient comprises a blood cell regulator selected from colostrinin, its  
PT constituent peptide and/or analog -  
XX  
XX Claim 6; Page 26; 51pp; English.  
PS  
XX The invention relates to a composition which comprises a blood cell  
CC regulator selected from colostrinin, its constituent peptide and/or  
CC analogue. The invention is used for modulating the oxidative stress  
CC level in a cell e.g. mammalian or human cell present in a cell culture,  
CC tissue, organ, or organism; or for treating oxidative damage to the skin  
CC of a patient e.g. animal or human; to modulate oxidative stress during/  
CC

CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

SQ Sequence 7 AA;  
 Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7  
 |||||  
 Db 1 AFLLYQE 7

RESULT 6  
 AAM51062  
 ID AAM51062 standard; Peptide; 7 AA.

AC AAM51062;  
 XX 30-MAY-2002 (first entry)  
 XX Colostrinin constituent peptide (casein amino acids 202-208).  
 DE Colostrinin; colostrum; immunomodulator; cardiovascular;  
 XX blood cell regulator; cytokine inducer; beta-casein; human.  
 KW Homo sapiens.

XX Key Location/Qualifiers  
 XX Modified-site 7  
 FT /note= "optional C-terminal amidation"

XX WO200213849-A1.  
 XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22775.  
 XX 17-AUG-2000; 2000WO-US22775.

XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (REG-) REGEN THERAPEUTICS PLC.

XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2002-269150/31.

XX Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX Claim 1; Page 34; 54pp; English.

XX The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 202-208. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

SQ Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7  
 |||||  
 Db 1 AFLLYQE 7

RESULT 7  
 AAO14604  
 ID AAO14604 standard; peptide; 7 AA.

XX AAO14604;  
 XX 27-MAY-2002 (first entry)

XX Neutral cell regulatory colostrinin peptide 27.  
 DE Neutral cell differentiation; neural cell regulator; colostrinin peptide;  
 XX neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 KW neural cell treatment.

XX Unidentified.

XX Key Location/Qualifiers  
 XX Modified-site 7  
 FT /note= "Optional C-terminal amide"

XX WO200213851-A1.  
 XX 21-FEB-2002.

XX 17-AUG-2000; 2000WO-US22777.  
 XX 17-AUG-2000; 2000WO-US22777.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Boldogh I, Stanton JG, Hughes TK;  
 XX WPI; 2002-269152/31.

XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX Claim 7; Page 22; 37pp; English.

XX The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 7; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLYQE 7  
Db 1 AFLLYQE 7

RESULT 8

AAU83286  
ID AAU83286 standard; Peptide; 8 AA.

XX AC AAU83286;

DT 23-APR-2002 (first entry)

DE Antiviral composition peptide-A, fragment #4.

KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.

XX Synthetic.

XX US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX New peptides compositions, useful for treating viral infections and  
stimulating the immune system -

XX Disclosure; Page 7; 37pp; English.

CC The invention relates to a new peptide composition comprising a specified  
peptide sequence. The composition comprises nucleotide-peptide comprising  
a peptide linked through a serine residue and diphosphodiester to a  
nucleotide; or peptides with about 31 amino acid residues capable of  
stimulating production of interleukin-8 in cultured cells; or peptides  
with about 31 amino acid residues capable of stimulating production of  
monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
invention.

XX Sequence 8 AA;

Query Match 100.0%; Score 7; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLYQE 7  
Db 1 AFLLYQE 7

RESULT 9

AAU83286

ID AAU83286 standard; Peptide; 9 AA.

XX AAB59356;  
AC 21-MAR-2001 (first entry)  
DT Ewe colostrin peptide fragment derived sequence #16.  
DE Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;  
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
XX Ovis sp.  
XX WO200075173-A2.  
XX PD 14-DEC-2000.  
XX PF 02-JUN-2000; 2000WO-GB021128.  
XX PR 02-JUN-1999; 99GB-0012852.  
XX PA (REGE-) REGEN THERAPEUTICS PLC.  
XX Georgiades JA;  
XX WPI; 2001-071058/08.  
XX Peptides having an N-terminal amino acid sequence isolated from  
PT colostrin for treating e.g. disorders of the central nervous system  
PT and immune system, viral and bacterial infections, and diseases  
PT characterized by amyloid plaques -  
XX Claim 8; Page 27; 63pp; English.  
XX The present invention provides the sequences of a number of peptides  
CC found in ewe's colostrin. Colostrin is the proline-rich polypeptide  
CC fragment of colostrum. These peptides can be used in the treatment of  
CC central nervous system disorders such as senile dementia, Parkinson's  
CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
CC disorders such as bacterial and viral infections, to improve the  
CC development of a child's immune system, as a dietary supplement, and to  
CC promote the dissolution of beta-amyloid plaques.  
XX Sequence 9 AA;  
XX Query Match 100.0%; Score 7; DB 22; Length 9;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AFLLYQE 7  
Db 3 AFLLYQE 9  
RESULT 10  
AAU83297  
ID AAU83297 standard; Peptide; 11 AA.  
XX AC AAU83297;  
XX DT 23-APR-2002 (first entry)  
XX DE Antiviral composition peptide-A, fragment #15.  
XX Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX Synthetic.  
XX US2002004579-A1.  
XX PD 10-JAN-2002.  
XX PF 17-JAN-2001; 2001US-0764017.

XX 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT  
 XX Disclosure; Page 7; 37pp; English.  
 PS  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells; or peptides  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 11 AA;  
 SQ Query Match 100.0%; Score 7; DB 23; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.29; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQE 7  
 Db |||||  
 5 AFLLYQE 11  
 RESULT 11  
 AAU83299  
 ID AAU83299 standard; Peptide; 12 AA.  
 XX  
 AC AAU83299;  
 XX  
 XX 23-APR-2002 (first entry)  
 DT  
 DE Antiviral composition peptide-A, fragment #17.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002004579-A1.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX 17-JAN-2001; 2001US-0764017.  
 PF  
 XX 22-OCT-1996; 96US-0735236.  
 PR  
 XX 25-JUN-1999; 99US-0344095.  
 PR  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT  
 XX Disclosure; Page 7; 37pp; English.  
 PS  
 XX The invention relates to a new peptide composition comprising a specified

CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 12 AA;  
 SQ Query Match 100.0%; Score 7; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.31; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQE 7  
 Db |||||  
 4 AFLLYQE 10  
 RESULT 12  
 AAU83300  
 ID AAU83300 standard; Peptide; 12 AA.  
 XX  
 AC AAU83300;  
 XX  
 XX 23-APR-2002 (first entry)  
 DT  
 DE Antiviral composition peptide-A, fragment #18.  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002004579-A1.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX 17-JAN-2001; 2001US-0764017.  
 PF  
 XX 22-OCT-1996; 96US-0735236.  
 PR  
 XX 25-JUN-1999; 99US-0344095.  
 PR  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA  
 XX Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT  
 XX Disclosure; Page 7; 37pp; English.  
 PS  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 12 AA;  
 SQ Query Match 100.0%; Score 7; DB 23; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.31;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;









XX The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX

SQ Sequence 16 AA;  
Query Match 100.0%; Score 7; DB 23; Length 16;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7  
|||||  
Db 9 AFLLYQE 15

RESULT 21  
AAU83341  
ID AAU83341 standard; Peptide; 19 AA.  
AC AAU83341;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE Antiviral composition peptide-A, fragment #59.  
XX  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
OS Synthetic.  
XX  
PN US2002004579-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 17-JAN-2001; 2001US-0764017.  
XX  
PR 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
PA (ADVT-) ADVANCED VIRAL RES CORP.  
XX  
PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX  
DR WPI; 2002-163727/21.  
XX  
PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
PS Disclosure; Page 8; 37pp; English.  
XX  
CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
SQ Sequence 19 AA;  
Query Match 100.0%; Score 7; DB 23; Length 19;  
Best Local Similarity 100.0%; Pred. No. 0.44;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7  
|||||  
Db 13 AFLLYQE 19

RESULT 22  
AAU83290  
ID AAU83290 standard; Peptide; 9 AA.  
XX  
AC AAU83290;  
XX  
DT 23-APR-2002 (first entry)  
XX  
DE Antiviral composition peptide-A, fragment #8.  
XX  
KW Virucide; Immunostimulant; interleukin-8; viral infection;  
KW monocyte chemotactic protein 1; immune system.  
XX  
OS Synthetic.  
XX  
PN US2002004579-A1.  
XX  
PD 10-JAN-2002.  
XX  
PF 17-JAN-2001; 2001US-0764017.  
XX  
PR 22-OCT-1996; 96US-0735236.  
PR 25-JUN-1999; 99US-0344095.  
XX  
PA (ADVI-) ADVANCED VIRAL RES CORP.  
XX  
PI Friedland B, Hirschman SZ, Taraporewala IB;  
XX  
DR WPI; 2002-163727/21.  
XX  
PT New peptides compositions, useful for treating viral infections and  
PT stimulating the immune system -  
XX  
PS Disclosure; Page 7; 37pp; English.  
XX  
CC The invention relates to a new peptide composition comprising a specified  
CC peptide sequence. The composition comprises nucleotide-peptide comprising  
CC a peptide linked through a serine residue and diphosphodiester to a  
CC nucleotide; or peptides with about 31 amino acid residues capable of  
CC stimulating production of interleukin-8 in cultured cells; or peptides  
CC with about 31 amino acid residues capable of stimulating production of  
CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
CC for treating viral infections and stimulating the immune system.  
CC AAU83282-AAU83401 represent peptides used in the composition of the  
CC invention.  
XX  
SQ Sequence 9 AA;  
Query Match 85.7%; Score 6; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6  
|||||  
Db 4 AFLLYQ 9

RESULT 23  
AAB72277  
ID AAB72277 standard; peptide; 13 AA.  
XX  
AC AAB72277;  
XX  
DT 14-MAY-2001 (first entry)  
XX  
DE Colostrinin derived cytokine inducing peptide SEQ ID 32.

XX Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 XX Synthetic.  
 XX WO200111937-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22818.  
 XX 17-AUG-1999; 99US-0149311.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 XX Inducing a cytokine and modulating an immune response, useful for  
 PT treating central nervous system diseases and bacterial and viral  
 PT infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX Claim 1; Page 34; 50pp; English.  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX SQ Sequence 13 AA;  
 Query Match 85.7%; Score 6; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLYQE 7  
 DB 1 FLLYQE 6  
 RESULT 24  
 AAB72530  
 ID AAB72530 standard; Peptide; 13 AA.  
 XX AC AAB72530;  
 XX 09-MAY-2001 (first entry)  
 XX Colostrinin peptide #31.  
 XX Dermatological; oxidative stress regulator; colostrinin.  
 KW Unidentified.  
 XX WO200112650-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22665.  
 XX

PR 17-AUG-1999; 99US-0149310.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX Claim 6; Page 26; 48pp; English.  
 XX The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidising species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX SQ Sequence 13 AA;  
 Query Match 85.7%; Score 6; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLYQE 7  
 DB 1 FLLYQE 6  
 RESULT 25  
 AAB72562  
 ID AAB72562 standard; Peptide; 13 AA.  
 XX AC AAB72562;  
 XX 09-MAY-2001 (first entry)  
 XX Colostrinin peptide #31.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrum.  
 XX Unidentified.  
 XX WO200112651-A2.  
 XX 22-FEB-2001.  
 XX 17-AUG-2000; 2000WO-US22774.  
 XX 17-AUG-1999; 99US-0149633.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX Boldogh I;  
 XX WPI; 2001-226545/23.  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX Claim 6; Page 22; 35pp; English.  
 XX The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX

```

SQ Sequence 13 AA;
Query Match 85.7%; Score 6; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7
   |||||
Db 1 FLLYQE 6

RESULT 26
AAB59338
ID AAB59338 standard; Peptide; 13 AA.
AC AAB59338;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment C-13.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB02128.
XX
PR 02-JUN-1999; 99GB-0012852.
XX
PA (REG-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system
PT and immune system, viral and bacterial infections, and diseases
PT characterized by amyloid plaques -
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques.
XX
SQ Sequence 13 AA;
Query Match 85.7%; Score 6; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7
   |||||
Db 1 FLLYQE 6

RESULT 27
AAE20259
ID AAE20259 standard; peptide; 13 AA.
XX
AC AAE20259;
XX

DT 18-JUN-2002 (first entry)
XX
DE Colostrinin constituent peptide #31.
XX
KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
KW transplantation; implantation; dermatological; vulnery.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 13
FT /note= "Optionally C-terminal amide"
XX
PN WO200213850-A1.
XX
PD 21-FEB-2002.
XX
PF 17-AUG-2000; 2000WO-US22776.
XX
PR 17-AUG-2000; 2000WO-US22776.
XX
PA (TEXA ) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
PD WPI; 2002-269151/31.
XX
PT Composition useful for the modulation of blood cell proliferation in a
PT patient comprises a blood cell regulator selected from colostrinin, its
PT constituent peptide and/or analog -
XX
PS Claim 6; Page 26; 51pp; English.
XX
CC The invention relates to a composition which comprises a blood cell
CC regulator selected from colostrinin, its constituent peptide and/or
CC analogue. The invention is used for modulating the oxidative stress
CC level in a cell e.g. mammalian or human cell present in a cell culture,
CC tissue, organ, or organism; or for treating oxidative damage to the skin
CC of a patient e.g. animal or human; to modulate oxidative stress during/
CC after a premature birth or normal birth, preventing/delaying aging in a
CC patient, enhancing wound healing, and the reduction of side effects of
CC cosmetic procedures. The method changes the level of an oxidising species
CC in the cell, such as decreases or prevents increase in the level of
CC damage to a biomolecule of the patient selected from DNA, protein and/or
CC lipid, compared to the same conditions when the oxidative stress
CC regulator is not present. The modulation of oxidative stress results in
CC enhanced repair, regeneration, and replacement of cells, tissues and
CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
CC external organs), as well as enhanced preservation of such organs for
CC transplantation, implantation, or scientific research. The present
CC sequence is a colostrinin constituent peptide.
XX
SQ Sequence 13 AA;
Query Match 85.7%; Score 6; DB 23; Length 13;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7
   |||||
Db 1 FLLYQE 6

RESULT 28
AAM51065
ID AAM51065 standard; Peptide; 13 AA.
XX
AC AAM51065;
XX
DT 30-MAY-2002 (first entry)
XX

```

DE Colostrinin constituent peptide (casein amino acids 203-214).  
 XX Colostrinin; colostrum; immunomodulator; cardiovascular;  
 KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 13  
 FT /note= "optional C-terminal amidation"  
 XX  
 PN WO200213849-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22775.  
 XX  
 PR 17-AUG-2000; 2000WO-US22775.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA (REG- ) REGEN THERAPEUTICS PLC.  
 XX  
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX  
 XX WPI; 2002-269150/31.  
 DR  
 XX  
 PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -  
 XX  
 XX Claim 1; Page 34; 54pp; English.  
 XX  
 CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 203-214. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the  
 CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 85.7%; Score 6; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLYQE 7  
 Db |||||  
 1 FLLYQE 6  
 RESULT 29  
 ID AAO14608  
 XX AAO14608 standard; peptide; 13 AA.  
 XX  
 AC AAO14608;  
 XX  
 DT 27-MAY-2002 (first entry)

XX Neural cell regulatory colostrinin peptide 31.  
 DE  
 XX Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX neural cell treatment.  
 XX  
 OS Unidentified.  
 FH Key Location/Qualifiers  
 FT Modified-site 13  
 FT /note= "Optional C-terminal amide"  
 XX  
 PN WO200213851-A1.  
 XX  
 PD 21-FEB-2002.  
 XX  
 PF 17-AUG-2000; 2000WO-US22777.  
 XX  
 PR 17-AUG-2000; 2000WO-US22777.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 PI Boldogh I, Stanton JG, Hughes TK;  
 XX  
 XX WPI; 2002-269152/31.  
 DR  
 XX Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -  
 XX  
 XX Claim 7; Page 22; 37pp; English.  
 XX  
 CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in  
 CC the method of the invention.  
 XX  
 SQ Sequence 13 AA;  
 Query Match 85.7%; Score 6; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLYQE 7  
 Db |||||  
 1 FLLYQE 6  
 RESULT 30  
 ID AAU83314  
 XX AAU83314 standard; Peptide; 13 AA.  
 XX  
 AC AAU83314;  
 XX  
 DT 23-APR-2002 (first entry)  
 XX  
 DE Antiviral composition peptide-A, fragment #32.  
 XX  
 KW Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002004579-A1.  
 XX  
 PD 10-JAN-2002.  
 XX

PF 17-JAN-2001; 2001US-0764017.  
 XX 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT Disclosure; Page 8; 37pp; English.  
 XX  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 13 AA;  
 SQ Query Match 85.7%; Score 6; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQ 6  
 Db 8 AFLLYQ 13  
 |||||  
 |||||  
 RESULT 31  
 AAU83320  
 ID AAU83320 standard; Peptide; 14 AA.  
 XX  
 AC AAU83320;  
 XX  
 XX 23-APR-2002 (first entry)  
 DT  
 XX Antiviral composition peptide-A, fragment #38.  
 DE  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002004579-A1.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX 17-JAN-2001; 2001US-0764017.  
 PF  
 XX 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT Disclosure; Page 8; 37pp; English.  
 XX

CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 14 AA;  
 SQ Query Match 85.7%; Score 6; DB 23; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 4.2;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AFLLYQ 6  
 Db 9 AFLLYQ 14  
 |||||  
 |||||  
 RESULT 32  
 AAU83332  
 ID AAU83332 standard; Peptide; 15 AA.  
 XX  
 AC AAU83332;  
 XX  
 XX 23-APR-2002 (first entry)  
 DT  
 XX Antiviral composition peptide-A, fragment #50.  
 DE  
 XX Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002004579-A1.  
 PN  
 XX 10-JAN-2002.  
 PD  
 XX 17-JAN-2001; 2001US-0764017.  
 PF  
 XX 22-OCT-1996; 96US-0735236.  
 PR 25-JUN-1999; 99US-0344095.  
 XX  
 XX (ADVI-) ADVANCED VIRAL RES CORP.  
 PA Friedland B, Hirschman SZ, Taraporewala IB;  
 PI WPI; 2002-163727/21.  
 XX  
 XX New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -  
 PT Disclosure; Page 8; 37pp; English.  
 XX  
 XX The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.  
 XX  
 XX Sequence 15 AA;  
 SQ Query Match 85.7%; Score 6; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 4.4;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



XX WPI; 2002-636633/68.  
 XX New human butyrylcholinesterase variant polypeptides, useful for  
 PT treating cocaine-induced conditions -  
 PS Disclosure; Fig 8; 150pp; English.  
 XX The present invention relates to mutants of human butyrylcholinesterase.  
 CC The enzymes have an increased cocaine hydrolysis activity and can be used  
 CC for treating a cocaine-induced condition. The present sequence is a  
 CC protein shown in the exemplification of the invention.

XX Sequence 6`AA;  
 SQ

Query Match 71.4%; Score 5; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLY 5  
 |||||  
 Db 2 AFLLY 6

RESULT 36  
 AAE07190  
 ID AAE07190 standard; peptide; 7 AA.

XX AC

XX 06-NOV-2001 (first entry)

XX Colostrinin peptide 6.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral.

XX Unidentified.

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REG- ) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX Claim 1; Page 15; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurodegenerative disorders e.g., Alzheimer's disease, motor neuron  
 CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,

CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrinin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrinin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrinin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is colostrinin peptide 6 related to the invention.  
 CC Colostrinin peptide 6 corresponds to position 204-210 of beta-caesin.

XX Sequence 7 AA;  
 SQ

Query Match 71.4%; Score 5; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQE 7  
 |||||  
 Db 1 LLYQE 5

RESULT 37

AAE07200

ID AAE07200 standard; peptide; 8 AA.

XX AC AAE07200;

XX 06-NOV-2001 (first entry)

XX Modified colostrinin cyclic peptide #6.

XX Colostrinin; nootropic; neuroprotective; immunomodulatory; antibacterial;  
 KW Parkinson's disease; Alzheimer's disease; mental disorder; food additive;  
 KW central nervous system disorder; neurodegenerative disorder; weight loss;  
 KW beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;  
 KW acquired immunological deficiency; neurological disorder; dementia;  
 KW antiviral; cyclic.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl; this residue forms a cyclic  
 FT linkage with Val found at the C-terminal end"

XX WO200155199-A1.

XX 02-AUG-2001.

XX 26-JAN-2001; 2001WO-GB00329.

XX 26-JAN-2000; 2000GB-0001825.

XX (REG- ) REGEN THERAPEUTICS PLC.

XX Georgiades JA;

XX WPI; 2001-488775/53.

XX Peptide useful as an inter alia in the treatment of e.g. disorders of  
 PT the immune system and the central nervous system comprises ten  
 PT amino-terminal amino acid sequence derived from peptides present in  
 PT colostrinin -

XX Example 2; Page 9; 40pp; English.

XX The invention relates to colostrinin peptide fragments which are useful,  
 CC inter alia, in the treatment of chronic disorders of the immune system  
 CC and the central nervous system. Colostrinin peptides are used as a  
 CC medicament in the treatment of neurological disorders e.g., dementia,  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,



CC disease e.g., Parkinson's disease, mental disorders e.g. psychosis and  
 CC neurosis, in acquired immunological deficiencies, chronic bacterial and  
 CC viral infections and diseases characterised by the presence of beta-  
 CC amyloid plaques and as a dietary supplement for babies, small children,  
 CC adults and senile persons, who have been subjected to chemotherapy or  
 CC have suffered from cachexia or weight loss due to the chronic disease.  
 CC Colostrin peptides are also used as food additives and as an auxiliary  
 CC withdrawal treatment for drug addicts, after a period of detoxification  
 CC and in persons dependent on stimulants. Colostrin peptides are used to  
 CC prepare antibodies and to treat emotional disturbances, e.g. emotional  
 CC disturbances of psychiatric patients in a state of depression. These  
 CC colostrin peptides improves the development of immune system in a new  
 CC born child and to correct the immunological deficiencies in a child.  
 CC The present sequence is modified colostrin cyclic peptide #6 related to  
 CC the invention.

XX SQ Sequence 8 AA;

Query Match 71.4%; Score 5; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0;

Qy 3 LLYQE 7  
 Db 2 LLYQE 6  
 |||||

RESULT 38  
 AAU83337  
 ID AAU83337 standard; Peptide; 16 AA.

XX AC AAU83337;

DT 23-APR-2002 (first entry)

XX DE Antiviral composition peptide-A, fragment #55.

XX XN Virucide; Immunostimulant; interleukin-8; viral infection;  
 KW monocyte chemotactic protein 1; immune system.

XX OS Synthetic.

XX XN US2002004579-A1.

XX PD 10-JAN-2002.

XX PF 17-JAN-2001; 2001US-0764017.

XX PR 22-OCT-1996; 96US-0735236.

XX PR 25-JUN-1999; 99US-0344095.

XX PA (ADVI-) ADVANCED VIRAL RES CORP.

XX PI Friedland B, Hirschman SZ, Taraporewala IB;

XX DR WPI; 2002-163727/21.

XX PT New peptides compositions, useful for treating viral infections and  
 PT stimulating the immune system -

XX PS Disclosure; Page 8; 37pp; English.

XX CC The invention relates to a new peptide composition comprising a specified  
 CC peptide sequence. The composition comprises nucleotide-peptide comprising  
 CC a peptide linked through a serine residue and diphosphodiester to a  
 CC nucleotide; or peptides with about 31 amino acid residues capable of  
 CC stimulating production of interleukin-8 in cultured cells; or peptides  
 CC with about 31 amino acid residues capable of stimulating production of  
 CC monocyte chemotactic protein 1 in cultured cells. The peptides are useful  
 CC for treating viral infections and stimulating the immune system.  
 CC AAU83282-AAU83401 represent peptides used in the composition of the  
 CC invention.

XX

SQ Sequence 16 AA;

Query Match 71.4%; Score 5; DB 23; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 56;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLLY 5  
 Db 12 AFLLY 16  
 |||||

RESULT 39

AAAY16494

ID AAY16494 standard; peptide; 5 AA.

XX AC AAY16494;

XX DT 06-AUG-1999 (first entry)

XX DE Linear thrombin receptor peptide analogue.

XX KW Peptide analogue; N-terminal domain; cancer; angiogenesis; metastasis;  
 KW human G protein linked thrombin receptor; cyclic; antagonist; agonist;  
 KW cardiovascular disease; inflammatory disease; gastrointestinal disease;  
 KW osteoporosis; tissue injury; tissue repair; nerve regeneration;  
 KW thrombin-mimetic study; platelet function; myocardial infarction;  
 KW arterial plaque formation.

XX OS Synthetic.

XX XN US5516889-A.

XX PD 14-MAY-1996.

XX PF 17-MAR-1995; 95US-0405933.

XX PR 21-JUN-1993; 93US-0080643.

XX PR 17-MAR-1995; 95US-0405933.

XX PA (UYTE-) UNIV TECHNOLOGIES INT INC.

XX PI Hollenberg MD, Matsoukas JM, Moore GJ;

XX DR WPI; 1996-251084/25.

XX PT New cyclic peptide(s) derived from the protein G linked thrombin  
 PT receptor - are agonists or antagonists for treating diseases  
 PT involving this receptor, e.g. myocardial infarction

XX PS Example 1; Column 53; 36pp; English.

XX CC AAY16465-98 represent peptide analogues of the N-terminal domain of  
 CC the human G protein linked thrombin receptor sequence. The peptides,  
 CC which may be cyclic, have the formula X1-Pei-X2-X3-Omega-X4 in which  
 CC Psi = any (non-)natural aromatic amino acid (aa); Omega = any  
 CC (non-)natural basic aa or derivatives; X1 is absent or is a natural  
 CC aa, 1-3C acyl or 1-5C alkyl; X2 = any natural aa; X3 is absent or is  
 CC any natural aa; and X4 is absent or is any natural aa. The peptides  
 CC are antagonists and agonists for treating disorders involving  
 CC thrombin receptors, e.g. cardiovascular, inflammatory or  
 CC gastrointestinal diseases; osteoporosis; tissue injury and repair  
 CC (including nerve regeneration); and cancer (by inhibiting angiogenesis  
 CC and metastasis). They may also be used diagnostically and in  
 CC thrombin-mimetic studies. The peptide analogues are particularly used  
 CC to modulate platelet function (acting synergistically with aspirin-type  
 CC compounds) and so are useful in cases of myocardial infarction, as well  
 CC as to coat prostheses and to reduce arterial plaque formation.

XX SQ Sequence 5 AA;

Query Match 57.1%; Score 4; DB 17; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
 DB 1 AFLL 4

## RESULT 40

AAU08616  
 ID AAU08616 standard; Peptide; 6 AA.

XX AC AAU08616;  
 XX DT 18-DEC-2001 (first entry)  
 XX DE Human olfactory receptor PCR primer design motif #1.  
 XX KW Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;  
 XX KW food additive; cosmetic; fragrance; pharmaceutical additive.  
 XX OS Homo sapiens.  
 XX PN WO200168805-A2.  
 XX PD 20-SEP-2001.  
 XX PF 13-MAR-2001; 2001WO-US07771.  
 XX PR 13-MAR-2000; 2000US-0188914.  
 XX PR 24-MAR-2000; 2000US-0192033.  
 XX PR 12-APR-2000; 2000US-0198474.  
 XX PR 24-APR-2000; 2000US-0199335.  
 XX PR 26-MAY-2000; 2000US-0207702.  
 XX PR 23-JUN-2000; 2000US-0213849.  
 XX PR 16-AUG-2000; 2000US-0226534.  
 XX PR 07-SEP-2000; 2000US-0230732.  
 XX PR 07-FEB-2001; 2001US-0266862.  
 XX PA (SENO-) SENOMYX INC.  
 XX PI Zozulya S;  
 XX WPI; 2001-570867/64.

PT Nucleic acids encoding human olfactory G protein-coupled receptors,  
 PT useful for screening for compounds involved in olfactory sensation,  
 PT where the compounds can be used in the food, pharmaceutical and  
 PT cosmetic industries to customise odours -  
 XX PS Disclosure; Page 42; 319pp; English.

XX The invention relates to nucleic acids encoding human olfactory  
 CC receptors, OR, (a G protein-coupled receptor, GPCR). The OR's  
 CC specifically recognise molecules, odourants, that elicit specific  
 CC olfactory sensation. The human olfactory receptors and polynucleotides  
 CC encoding them are useful for screening a library of chemical compounds  
 CC for compounds that are involved in olfactory sensation. Modulators of  
 CC olfactory activity are useful for pharmacological and genetic modulation of  
 CC olfactory signalling pathways. Therefore, they can be used in the food,  
 CC pharmaceutical and cosmetic industries to customise odours and  
 CC fragrances. The present sequence is a human olfactory receptor  
 CC protein motif end used to design PCR primers against the first  
 CC transmembrane domain.  
 XX

SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
 DB 2 FLLY 5

## RESULT 41

AAG63026  
 ID AAG63026 standard; peptide; 6 AA.

XX AC AAG63026;  
 XX DT 01-OCT-2001 (first entry)  
 XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.  
 XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;  
 XX KW virus binding domain.

XX OS Unidentified.

XX PN WO200140265-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US42515.

XX PR 02-DEC-1999; 99US-0453115.

XX PA (VITE-) VI TECHNOLOGIES INC.

XX PI Hammond DJ;

XX DR WPI; 2001-475677/51.

XX PT Identifying ligands that interact with a target by Quick Assay for  
 PT Selecting Affinity Resins, involves differentiating specific or  
 PT non-specific false positive interactions from target-specific  
 PT interactions -

XX PS Claim 4; Page 27; 39pp; English.

XX CC The present sequence represents a Hepatitis A virus (HAV)-binding  
 CC domain. It was identified using the method of the invention. The method  
 CC identifies ligands that interact with a target by Quick Assay for  
 CC Selecting Affinity Resins. The method comprise differentiating false  
 CC positive interactions (either specific or non-specific) from  
 CC target-specific interaction, by distinguishing non-specific binding of  
 CC ligands to agents in the screening solution from specific binding  
 CC between a ligand and target. The method is useful for identifying  
 CC ligands that interact with the target, and for multiple screenings of  
 CC the same surface-immobilized library for a number of different ligands.  
 XX

SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
 DB 1 FLLY 4

## RESULT 42

AAG63034  
 ID AAG63034 standard; peptide; 6 AA.

XX AC AAG63034;

XX DT 01-OCT-2001 (first entry)

XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.

XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;  
 XX KW virus binding domain.

XX OS Unidentified.

```

XX PH Key Location/Qualifiers
FT FT Misc-difference 1
FT FT /note= "D-form residue"
XX XX
XX PN WO200140265-A2.
XX XX
XX PD 07-JUN-2001.
XX XX
XX PF 01-DEC-2000; 2000WO-US42515.
XX XX
XX PR 02-DEC-1999; 99US-0453115.
XX XX
XX PA (VITE-) VI TECHNOLOGIES INC.
XX XX
XX PI Hammond DJ;
XX XX
XX DR WPI; 2001-475677/51.
XX XX
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 4; Page 27; 39pp; English.
XX CC The present sequence represents a Hepatitis A virus (HAV)-binding
XX CC domain. It was identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding of
XX CC ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX SQ Sequence 6 AA;

XX PS Query Match 57.1%; Score 4; DB 22; Length 6;
XX PS Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX PS Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 2 FLLY 5
XX DB 1 FLLY 4

XX RESULT 43
XX AAG63043
XX ID AAG63043 standard; peptide; 6 AA.
XX AC AAG63043;
XX XX
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX XX (VITE-) VI TECHNOLOGIES INC.
XX XX
XX PI Hammond DJ;
XX XX
XX DR WPI; 2001-475677/51.
XX XX
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 10; Page 28; 39pp; English.
XX CC The present sequence represents a Hepatitis A virus (HAV)-binding
XX CC domain. It was identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding of
XX CC ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX SQ Sequence 6 AA;

XX PS Query Match 57.1%; Score 4; DB 22; Length 6;
XX PS Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX PS Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 2 FLLY 5
XX DB 1 FLLY 4

XX RESULT 44
XX AAG63065
XX ID AAG63065 standard; peptide; 6 AA.
XX AC AAG63065;
XX XX
XX DT 01-OCT-2001 (first entry)
XX DE Amino acid sequence of a Hepatitis A virus (HAV)-binding domain.
XX KW Hepatitis A virus; HAV; Quick Assay for Selecting Affinity Resins;
XX KW virus binding domain.
XX OS Unidentified.
XX PN WO200140265-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US42515.
XX PR 02-DEC-1999; 99US-0453115.
XX XX (VITE-) VI TECHNOLOGIES INC.
XX XX
XX PI Hammond DJ;
XX XX
XX DR WPI; 2001-475677/51.
XX XX
XX PT Identifying ligands that interact with a target by Quick Assay for
XX PT Selecting Affinity Resins, involves differentiating specific or
XX PT non-specific false positive interactions from target-specific
XX PT interactions -
XX PS Claim 10; Page 28; 39pp; English.
XX CC The present sequence represents a Hepatitis A virus (HAV)-binding
XX CC domain. It was identified using the method of the invention. The method
XX CC identifies ligands that interact with a target by Quick Assay for
XX CC Selecting Affinity Resins. The method comprise differentiating false
XX CC positive interactions (either specific or non-specific) from
XX CC target-specific interaction, by distinguishing non-specific binding of
XX CC ligands to agents in the screening solution from specific binding
XX CC between a ligand and target. The method is useful for identifying
XX CC ligands that interact with the target, and for multiple screenings of
XX CC the same surface-immobilized library for a number of different ligands.
XX SQ Sequence 6 AA;

```

CC positive interactions (either specific or non-specific) from  
 CC target-specific interaction, by distinguishing non-specific binding of  
 CC ligands to agents in the screening solution from specific binding  
 CC between a ligand and target. The method is useful for identifying  
 CC ligands that interact with the target, and for multiple screenings of  
 CC the same surface-immobilized library for a number of different ligands.

XX  
 XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
 . ||||  
 Db 1 FLLY 4

RESULT 45  
 AAG63106  
 ID AAG63106 standard; peptide; 6 AA.

AC AAG63106;

DT 01-OCT-2001 (first entry)

DE Amino acid sequence of a Poliovirus-binding domain.

KW Poliovirus; Quick Assay for Selecting Affinity Resins;  
 KW virus binding domain.

OS Unidentified.

PN W0200140265-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US42515.

PR 02-DEC-1999; 99US-0453115.

PA (VITE-) VI TECHNOLOGIES INC.

XX Hammond DJ;

XX WPI; 2001-475677/51.

XX Identifying ligands that interact with a target by Quick Assay for  
 PT Selecting Affinity Resins, involves differentiating specific or  
 PT non-specific false positive interactions from target-specific  
 PT interactions -

XX Claim 30; Page 30; 39pp; English.

XX The present sequence represents a Poliovirus-binding domain. It was  
 CC identified using the method of the invention. The method identifies  
 CC ligands that interact with a target by Quick Assay for Selecting Affinity  
 CC Resins. The method comprise differentiating false positive interactions  
 CC (either specific or non-specific) from target-specific interaction, by  
 CC distinguishing non-specific binding of ligands to agents in the  
 CC screening solution from specific binding between a ligand and target.  
 CC The method is useful for identifying ligands that interact with the  
 CC target, and for multiple screenings of the same surface-immobilized  
 CC library for a number of different ligands.

XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
 . ||||

Db 1 FLLY 4

RESULT 46

AAG63108

ID AAG63108 standard; peptide; 6 AA.

XX AAG63108;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of a Poliovirus-binding domain.

KW Poliovirus; Quick Assay for Selecting Affinity Resins;  
 KW virus binding domain.

OS Unidentified.

PN W0200140265-A2.

XX 07-JUN-2001.

XX 01-DEC-2000; 2000WO-US42515.

PR 02-DEC-1999; 99US-0453115.

XX (VITE-) VI TECHNOLOGIES INC.

XX Hammond DJ;

XX WPI; 2001-475677/51.

XX Identifying ligands that interact with a target by Quick Assay for  
 PT Selecting Affinity Resins, involves differentiating specific or  
 PT non-specific false positive interactions from target-specific  
 PT interactions -

XX Claim 30; Page 30; 39pp; English.

XX The present sequence represents a Poliovirus-binding domain. It was  
 CC identified using the method of the invention. The method identifies  
 CC ligands that interact with a target by Quick Assay for Selecting Affinity  
 CC Resins. The method comprise differentiating false positive interactions  
 CC (either specific or non-specific) from target-specific interaction, by  
 CC distinguishing non-specific binding of ligands to agents in the  
 CC screening solution from specific binding between a ligand and target.  
 CC The method is useful for identifying ligands that interact with the  
 CC target, and for multiple screenings of the same surface-immobilized  
 CC library for a number of different ligands.

XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5

Db 1 FLLY 4

RESULT 47

ABU67261

ID ABU67261 standard; Peptide; 6 AA.

XX AC ABU67261;

XX 28-MAY-2003 (first entry)

XX Olfactory receptor ligand binding region I peptide.

XX Olfactory receptor; odourant; ligand-binding region;

KW olfactory neuron; olfactory epithelium; 7 transmembrane receptor;

KW olfactory response.  
 OS Mammalia.  
 XX  
 PN US6492143-B1.  
 XX  
 PD 10-DEC-2002.  
 XX  
 PF 17-DEC-1999; 99US-0465901.  
 XX  
 PR 17-DEC-1998; 98US-112605P.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Read RR, Yau K, Krautwurst D;  
 XX  
 DR WPI; 2003-327314/31.  
 XX  
 PT Novel amplification primer sequence pair for amplifying nucleic acid  
 FT encoding an olfactory receptor ligand-binding region -  
 XX  
 PS Disclosure; Column 14; 46pp; English.  
 XX  
 CC The invention relates to an amplification primer sequence pair for  
 CC amplifying a nucleic acid encoding an olfactory receptor ligand-binding  
 CC region, comprising a primers appearing as ACA0488 and ACA0489.  
 CC Also included is a kit for amplifying olfactory receptor sequences  
 CC comprising the primers. The primers are useful for generating a nucleic  
 CC acid sequence that encodes a ligand-binding region of an olfactory  
 CC receptor. The amplified nucleic acid is genomic DNA, mRNA or cDNA derived  
 CC from olfactory neurons or the olfactory epithelium. The olfactory  
 CC receptors are 7 transmembrane receptors, manipulation of which can  
 CC modulate an animals olfactory response and can be used to generate novel  
 CC odorants. The present sequence is a olfactory receptor peptide consensus  
 CC sequence used design degenerate PCR primer used to amplify an olfactory  
 CC receptor ligand-binding region.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 FLLY 5  
 Db ||||  
 2 FLLY 5  
 RESULT 48  
 ABUS8261  
 ID ABUS8261 standard; Peptide; 6 AA.  
 XX  
 AC ABUS8261;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #7.  
 XX  
 KW Hepatitis A virus; HAV; porcine parvovirus; ppv; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002155106-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 01-DEC-2000; 2000US-0727963.  
 XX  
 PR 01-DEC-2000; 2000US-0727963.  
 XX  
 PA (HAMM/) HAMMOND D J.  
 XX  
 PI Hammond DJ;  
 XX  
 DR WPI; 2003-198483/19.  
 XX  
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A  
 FT virus-binding or prion-binding domain, useful for screening a library  
 of surface-immobilized ligands that bind to target molecules -  
 Claim 4; Page 31; 35pp; English.  
 XX  
 CC The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 FLLY 5  
 Db ||||  
 1 FLLY 4  
 RESULT 49  
 ABUS8271  
 ID ABUS8271 standard; Peptide; 6 AA.  
 XX  
 AC ABUS8271;  
 XX  
 DT 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #12.  
 XX  
 KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002155106-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 01-DEC-2000; 2000US-0727963.  
 XX  
 PR 01-DEC-2000; 2000US-0727963.  
 XX  
 PA (HAMM/) HAMMOND D J.  
 XX  
 PI Hammond DJ;  
 XX  
 DR WPI; 2003-198483/19.  
 XX  
 PT New peptide comprising a porcine parvovirus-binding, hepatitis A  
 FT virus-binding or prion-binding domain, useful for screening a library

PT of surface-immobilized ligands that bind to target molecules -  
 XX Claim 4; Page 31; 35pp; English.  
 XX  
 CC The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.  
 XX  
 XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLY 5  
 DB 1 FLLY 4

RESULT 50  
 ABUS8273  
 ID ABUS8273 standard; Peptide; 6 AA.  
 AC ABUS8273;  
 XX  
 XX 14-APR-2003 (first entry)  
 XX  
 DE Peptide binding to hepatitis A virus in the presence of fibrinogen #14.  
 XX  
 XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.  
 XX  
 XX US2002155106-A1.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 01-DEC-2000; 2000US-0727963.  
 XX  
 XX 01-DEC-2000; 2000US-0727963.  
 XX  
 XX (HAMM/) HAMMOND D J.  
 XX  
 XX Hammond DJ;  
 XX  
 XX WPI; 2003-198483/19.  
 XX  
 XX New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -  
 XX  
 XX Claim 10; Page 31; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target

CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.  
 XX  
 XX Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLLY 5  
 DB 1 FLLY 4

RESULT 51  
 ABUS8291  
 ID ABUS8291 standard; Peptide; 6 AA.

XX AC ABUS8291;  
 XX  
 XX 14-APR-2003 (first entry)  
 XX  
 DE Poliovirus-binding peptide #6.  
 XX  
 XX Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX  
 OS Synthetic.

XX US2002155106-A1.  
 XX  
 XX 24-OCT-2002.  
 XX  
 XX 01-DEC-2000; 2000US-0727963.  
 XX  
 XX 01-DEC-2000; 2000US-0727963.  
 XX  
 XX (HAMM/) HAMMOND D J.

XX Hammond DJ;  
 XX  
 XX WPI; 2003-198483/19.  
 XX  
 XX New peptide comprising a porcine parvovirus-binding, hepatitis A  
 PT virus-binding or prion-binding domain, useful for screening a library  
 PT of surface-immobilized ligands that bind to target molecules -  
 XX  
 XX Claim 30; Page 32; 35pp; English.

XX The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target

CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLLY 5  
 ||||  
 Db 1 FLLY 4

RESULT 52  
 ABUS8293  
 ID ABUS8293 standard; Peptide; 6 AA.  
 XX AC ABUS8293;  
 XX DT 14-APR-2003 (first entry)  
 XX DE Poliovirus-binding peptide #8.  
 XX KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX OS Synthetic.  
 XX FN US2002155106-A1.  
 XX PV 24-OCT-2002.  
 XX PD 01-DEC-2000; 2000US-0727963.  
 XX PF 01-DEC-2000; 2000US-0727963.  
 XX PR (HAMM/) HAMMOND D J.  
 XX PA Hammond DJ;  
 XX PI WPI; 2003-198483/19.  
 XX DR New peptide comprising a porcine parvovirus-binding, hepatitis A  
 XX PT virus-binding or prion-binding domain, useful for screening a library  
 XX PT of surface-immobilized ligands that bind to target molecules -  
 XX PS Claim 30; Page 32; 35pp; English.  
 XX CC The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLLY 5  
 ||||  
 Db 1 FLLY 4

RESULT 53  
 ABUS8312  
 ID ABUS8312 standard; Peptide; 6 AA.  
 XX AC ABUS8312;  
 XX DT 14-APR-2003 (first entry)  
 XX DE Peptide binding to hepatitis A virus in the presence of fibrinogen #23.  
 XX KW Hepatitis A virus; HAV; porcine parvovirus; PPV; pseudorabies virus;  
 KW PRV; bovine viral diarrhoea virus; BVDV; encephalomyocarditis virus;  
 KW EMCV; SV40; prion protein; alpha-1-proteinase inhibitor; API; ligand;  
 KW surface-immobilised library; blood composition.  
 XX OS Synthetic.  
 XX FN US2002155106-A1.  
 XX PV 24-OCT-2002.  
 XX PD 01-DEC-2000; 2000US-0727963.  
 XX PF 01-DEC-2000; 2000US-0727963.  
 XX PR 01-DEC-2000; 2000US-0727963.  
 XX PA (HAMM/) HAMMOND D J.  
 XX PI Hammond DJ;  
 XX DR WPI; 2003-198483/19.  
 XX PT New peptide comprising a porcine parvovirus-binding, hepatitis A  
 XX PT virus-binding or prion-binding domain, useful for screening a library  
 XX PS of surface-immobilized ligands that bind to target molecules -  
 XX CC Claim 4; Page 31; 35pp; English.  
 XX CC The invention relates to a peptide, having a sequence of less than 20  
 CC amino acids, and comprising a porcine parvovirus (PPV)-binding, hepatitis  
 CC A virus (HAV)-binding, or prion-binding domain. Also included are  
 CC a composition comprising the peptide, removing a target from a biological  
 CC fluid, identifying a ligand for a target or targets and identifying a  
 CC peptide that binds to a virus present in a blood composition. The peptide  
 CC is useful for identifying a ligand for a target or targets (Hepatitis A  
 CC virus, HAV, porcine parvovirus, PPV, pseudorabies virus, PRV, bovine  
 CC viral diarrhoea virus, BVDV, encephalomyocarditis virus, EMCV, SV40,  
 CC prion protein and alpha-1-proteinase inhibitor, API) or identifying a  
 CC peptide that binds to a virus present in a blood composition. It is used  
 CC to screen a library of surface-immobilised ligands that bind to target  
 CC molecules. The peptide allows for multiple screenings of the same  
 CC surface-immobilised library for a number of different ligands.  
 CC The present sequence is a peptide of the invention, targeting one  
 CC of the above listed targets.

XX SQ Sequence 6 AA;

Query Match 57.1%; Score 4; DB 24; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLLY 5  
 ||||  
 Db 1 FLLY 4

```

RESULT 54
AAW04280
ID AAW04280 standard; peptide; 7 AA.
AC AAW04280;
XX
DT 06-JUN-1997 (first entry)
XX
DE Milk derived non-anti-hypertensive peptide.
XX
KW Non-anti-hypertensive; fermentation; animal milk; Lactobacillus;
KW microorganism; digestion; protease; reduction; blood pressure.
XX
OS Mammalian spp.
XX
PN BP737690-A2.
XX
PD 16-OCT-1996.
XX
PF 10-APR-1996; 96EP-0302522.
XX
PR 10-APR-1995; 95JP-0084247.
XX
PA (CALV ) CALPIS FOOD IND CO LTD.
XX
PI Maeno M;
XX
DR WPI; 1996-457284/46.
XX
PT Antihypertensive compens. derived from milk - by fermentation or
PT protease digestion
XX
PS Example 1; Page 6; 10pp; English.
XX
CC The present non-anti-hypertensive (NAH) peptide was prepared by
CC fermenting an animal milk starting material with a Lactobacillus
CC microorganism, especially L. helveticus, L. delbrueckii subspecies
CC bulgaricus or L. acidophilus, or digesting it with a protease at
CC 20-50 degrees C for 3-30 hours, obtaining an eluent by
CC ultrafiltration and then fractionating the eluent by reverse phase
CC HPLC. The change in the systolic blood pressure of spontaneously
CC hypertensive rats treated intragastrically with 1 mg/kg of body
CC weight of the present NAH peptide was plus 1.2 +/- 9.8 mmHg.
XX
SQ Sequence 7 AA;
Query Match 57.1%; Score 4; DB 17; Length 7;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 55
AAV38067
ID AAV38067 standard; Peptide; 9 AA.
XX
AC AAV38067;
XX
DT 29-SEP-1999 (first entry)
XX
DE Hepatitis B virus-derived HLA-binding peptide.
XX
KW Immunogen; HLA; human leukocyte antigen; binding motif; antiviral;
KW MHC; major histocompatibility complex; viral infection; anticancer;
KW prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
XX
OS Hepatitis B virus.
XX
PN WO9403205-A1.
XX

```

```

PD 17-FEB-1994.
XX
PF 06-AUG-1993; 93WO-US07421.
XX
PR 05-MAR-1993; 93US-0027746.
PR 07-AUG-1992; 92US-0926666.
XX
PA (CYTE-) CYTEL CORP.
XX
PI Celis E, Grey HM, Kubo RT, Sette A;
XX
DR WPI; 1994-065403/08.
XX
PT Peptide which specifically binds selected MHC allele - used to
PT induce an immune response for treatment or prevention of viral
PT infection or cancer, or for diagnosis
XX
PS Disclosure; Page 106; 150pp; English.
XX
CC The sequence is a specific example of a group of new immunogenic
CC peptides having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding
CC motif. For example, the peptides having an HLA-A3.2 binding motif
CC each have 9-10 residues and contain, from the N-terminus to the
CC C-terminus, (a) a first conserved residue selected from L, M, I,
CC V, S, A, T, F, C, G, D and E and (b) a second conserved residue of
CC K, R, Y, H or F, where the first and second conserved residues are
CC separated by 6-7 residues. The peptides are capable of binding
CC selected MHC molecules and inducing an immune response. They can be
CC used to treat and/or prevent viral infection and cancer, e.g. prostate
CC cancer, lymphoma, hepatitis or AIDS. They can also be used to produce
CC antibodies for use as diagnostic or therapeutic agents. The peptides
CC can also be used as diagnostic agents.
XX
SQ Sequence 9 AA;
Query Match 57.1%; Score 4; DB 15; Length 9;
Best Local Similarity 100.0%; Pred.No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 56
AAV45635
ID AAV45635 standard; Peptide; 9 AA.
XX
AC AAV45635;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #246.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMMUNE INC.
XX

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PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI; 1999-551214/46.
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases -
PT
XX
PS Claim 1; Page 38; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 1 LLYQ 4

RESULT 57
AAY4637
ID AAY4637 standard; Peptide; 9 AA.
XX
AC AAY4637;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1248.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
DR WPI; 1999-551214/46.
DR
XX
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PT and diagnosis of cancers and viral diseases -
PT
XX
PS Claim 1; Page 38; 150pp; English.
XX
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CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 1 LLYQ 4

RESULT 57
AAY4637
ID AAY4637 standard; Peptide; 9 AA.
XX
AC AAY4637;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1248.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
DR WPI; 1999-551214/46.
DR
XX
XX New immunogenic peptides with HLA binding motif, useful in treatment
PT and diagnosis of cancers and viral diseases -
PT
XX
PS Claim 1; Page 79; 150pp; English.
XX
XX AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also
CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
CC response against the antigen from which the peptide is derived.
CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
CC normally induced by an antigen in the form of a peptide fragment bound
CC to a HLA molecule, rather than the intact foreign antigen itself, and
CC are particularly important in tumour rejection and in fighting viral
CC infections. The peptides are therefore useful therapeutically to treat
CC or prevent viral infections and cancers in mammals (especially humans)
CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
CC They can be administered as vaccines to elicit an immune response in
CC individuals susceptible or otherwise at risk of viral infection or
CC cancer, or used to treat chronic or acute conditions. They are also
CC useful diagnostically, and can be used to induce a cytotoxic T cell
CC response, by contacting a cytotoxic T cell with the peptide e.g. to
CC produce CTLs ex vivo for infusion back into a patient. The
CC polynucleotides encoding the immunogenic peptides are also useful
CC therapeutically and for immunisation as above.
XX
SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLLY 5
Db 6 FLLY 9

RESULT 58
AAY46638
ID AAY46638 standard; Peptide; 9 AA.
XX
AC AAY46638;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1249.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US05039.
XX
PR 13-MAR-1998; 98WO-US05039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
PI
DR WPI; 1999-551214/46.
DR
XX

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PT New immunogenic peptides with HLA binding motif, useful in treatment  
 PT and diagnosis of cancers and viral diseases -  
 XX  
 PS Claim 1; Page 79; 150pp; English.  
 XX  
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides  
 CC having a human major histocompatibility complex (MHC) Class I (also  
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic  
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes  
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell  
 CC response against the antigen from which the peptide is derived.  
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are  
 CC normally induced by an antigen in the form of a peptide fragment bound  
 CC to a HLA molecule, rather than the intact foreign antigen itself, and  
 CC are particularly important in tumour rejection and in fighting viral  
 CC infections. The peptides are therefore useful therapeutically to treat  
 CC or prevent viral infections and cancers in mammals (especially humans)  
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.  
 CC They can be administered as vaccines to elicit an immune response in  
 CC individuals susceptible or otherwise at risk of viral infection or  
 CC cancer, or used to treat chronic or acute conditions. They are also  
 CC useful diagnostically, and can be used to induce a cytotoxic T cell  
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to  
 CC produce CTLs ex vivo for infusion back into a patient. The  
 CC polynucleotides encoding the immunogenic peptides are also useful  
 CC therapeutically and for immunisation as above.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 20; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 FLYY 5  
 Db |||||  
 6 FLYY 9  
 RESULT 59  
 AAB09810  
 ID AAB09810 standard; Peptide; 9 AA.  
 XX  
 AC AAB09810;  
 XX  
 DT 06-SEP-2000 (first entry)  
 XX  
 DE Antiviral antibody scFv 3a-2 epitope SEQ ID NO:146.  
 XX  
 KW Molecular pathogenicide; plant disease; resistance; antibody; scFv;  
 KW gene construct; pathogen; toxin; fusion protein; antimicrobial;  
 KW deoxyribonuclease; RNase; ribosome inactivator; immunomodulator.  
 XX  
 OS Tobacco mosaic virus.  
 OS Synthetic.  
 XX  
 PN WO200023593-A2.  
 XX  
 PD 27-APR-2000.  
 XX  
 PF 15-OCT-1999; 99WO-EF07844.  
 XX  
 PR 16-OCT-1998; 98EP-0119630.  
 PR 16-OCT-1998; 98IN-0000666.  
 XX  
 PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
 XX  
 PI Fischer R, Schillberg S, Naehring J, Sack M, Monecke M, Liao Y;  
 PI Spiegel H, Zimmerman S, Emans N, Holzem A;  
 XX  
 DR WPI; 2000-339692/29.  
 XX  
 XX New fusion proteins and gene constructs for expressing agents  
 PT (antibodies, enzymes, vectors or molecular pathogenicides), useful for  
 PT

PT protecting plants against pathogens and increasing resistance to  
 PT disease -  
 XX  
 PS Example 6; Fig 25; 193pp; English.  
 XX  
 CC The present invention describes a fusion protein (I) comprising at least  
 CC one binding domain specifically recognising an epitope of a plant  
 CC pathogen and at least one further domain comprising a protein or peptide  
 CC sequence which is toxic to the pathogen or detrimental to its  
 CC replication, transmission or life cycle. Also described is a  
 CC pathogenicide (II) comprising (I) and a cellular targeting sequence  
 CC and/or membrane localisation sequence and/or motif that leads to  
 CC membrane anchoring; or at least one binding domain that specifically  
 CC recognises a viral movement and/or replicase protein. The fusion  
 CC protein, pathogenicide, polynucleotide, vectors, and compositions from  
 CC the present invention are useful for the protection of a plant against  
 CC the action of a pathogen. The kit from the present invention is useful  
 CC for carrying out the methods and may be employed in different  
 CC applications, for example in the diagnostic field or as research tools.  
 CC The kit or its components, such as the fusion protein, pathogenicide,  
 CC polynucleotides, vectors or compositions are useful in plant cell and  
 CC plant tissue culture, in agriculture. They are extremely useful for  
 CC breeding new varieties of plants that display improved properties such as  
 CC resistance to pathogens. AAB56587 to AAB56702 and AAB09774 to B097820  
 CC represent sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 57.1%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LYQE 7  
 Db |||||  
 6 LYQE 9  
 RESULT 60  
 AAY96340  
 ID AAY96340 standard; peptide; 9 AA.  
 XX  
 AC AAY96340;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE HLA-A\*0201 binding peptide hTERT W1072.  
 XX  
 KW hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;  
 KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;  
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200025813-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-US25438.  
 XX  
 PR 29-OCT-1998; 98US-0106106.  
 XX  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.  
 XX  
 PI Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;  
 XX  
 DR WPI; 2000-365402/31.  
 XX  
 XX Universal tumor-associated antigens such as telomerase catalytic  
 PT subunit capable of binding major histocompatibility complex molecule  
 PT useful for diagnosis, prevention and treatment of cancer  
 XX

PS Disclosure; Page 73; 136pp; English.

CC Human telomerase complex reverse transcriptase (hTERT) is expressed in  
 CC more than 85 percent of human cancers. hTERT is useful as a universal  
 CC tumour-associated antigen (TAA) that binds to a major histocompatibility  
 CC complex molecule (MHC). hTERT peptides were analyzed for the ability to  
 CC bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T  
 CC lymphocytes (CTL) were then generated that kill a cell expressing hTERT  
 CC or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.  
 CC Antigen presenting cells (APC) were also generated ex vivo for  
 CC presentation of a TAA peptide or hTERT. The APC can be used to activate  
 CC CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and  
 CC CTL are useful for cancer immunotherapy. Measuring the level of CTL in a  
 CC sample is useful for assessing the level of immunity of a patient to a  
 CC TAA or a peptide, where the sample is obtained before or after a cancer  
 CC treatment is given to the patient. TAA peptides (e.g. hTERT) are also  
 CC useful for diagnosis and prophylactic treatment of cancer.

SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4  
 Db |||||  
 6 APLL 9

RESULT 61  
 AAY86649

ID AAY86649 standard; Peptide; 9 AA.

XX  
 AC AAY86649;  
 XX  
 DT 05-MAY-2000 (first entry)  
 XX  
 DE Telomerase peptide #64.  
 XX  
 KW Telomerase; antigenic peptide; cancer; therapy; human; tumour cell;  
 KW malignant melanoma; leukaemia; lymphoma; biliary tract carcinoma;  
 KW telomerase T lymphocyte.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 PN WO200002581-A1.  
 XX  
 PD 20-JAN-2000.  
 XX  
 PF 30-JUN-1999; 99WO-NO00220.  
 XX  
 PR 08-JUL-1998; 98NO-0003141.  
 XX  
 PA (NHVD ) NORSK HYDRO AS.  
 XX  
 PI Gaudernack G, Eriksen JA, Moller M, Gjertsen MK, Saeterdal I;  
 PI Saeboe-Larsen S;  
 XX  
 XX WPI; 2000-145727/13.  
 XX  
 XX Protein or peptide fragments useful in the treatment and prophylaxis of  
 PT cancer in mammals -  
 XX  
 XX Claim 12; Page 35; 53pp; English.

CC This sequence represents a telomerase peptide of the invention, and can  
 CC be used in a method for the treatment or prophylaxis of cancer. The  
 CC sequences are useful in the treatment or prophylaxis of cancer  
 CC especially, breast, lung, ovarian, cervical, colorectal, prostate or  
 CC pancreatic cancers, malignant melanoma, leukemias, lymphomas, or biliary  
 CC tract carcinomas. They are useful for generating telomerase T lymphocytes  
 CC capable of recognising and destroying tumour cells in a mammal,  
 CC comprising culturing T lymphocytes obtained from the mammal with the

CC peptides. Telomerase protein is expressed only by tumour cells, hence,  
 CC other body cells are not targeted or destroyed by telomerase specific T  
 CC cells.  
 CC Note: This sequence was indexed from WO200002581, which is the first  
 CC major country equivalent to NO9803141.

SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 21; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4  
 Db |||||  
 6 APLL 9

RESULT 62  
 AAU23931

ID AAU23931 standard; Peptide; 9 AA.

XX  
 AC AAU23931;  
 XX  
 DT 17-DEC-2001 (first entry)  
 XX  
 DE Human MHC class I molecule HLA-A2 binding 103P2D6 peptide #16.  
 XX  
 KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200162925-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 26-FEB-2001; 2001WO-US05996.  
 XX  
 PR 24-FEB-2000; 2000US-0184558.  
 PR 13-JUL-2000; 2000US-0218856.  
 XX  
 PA (UROG-) UROGENESIS INC.  
 XX  
 XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid PM, Faris M, Jakobovits A;  
 XX  
 XX WPI; 2001-557705/62.

PT New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -  
 XX  
 XX Example 15; Page 83; 132pp; English.

CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.

SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
| | | |  
Db 1 LLYQ 4

RESULT 63  
AAU23957  
ID AAU23957 standard; Peptide; 9 AA.  
XX AC  
XX AAU23957;  
XX DT 17-DEC-2001 (first entry)  
XX DE Human MHC class I molecule HLA-A2 binding 103P2D6 peptide #42.  
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
KW single chain monoclonal antibody; cervix; human.  
XX OS Homo sapiens.  
XX PN WO200162925-A2.  
XX PD 30-AUG-2001.  
XX PF 26-FEB-2001; 2001WO-US05996.  
XX PR 24-FEB-2000; 2000US-0184558.  
XX PR 13-JUL-2000; 2000US-0218856.  
XX PA (UROG-) UROGENESYS INC.  
XX PI Raitano AB, Afar DRH, Rastegar GS, Mitchell SC, Hubert RS;  
PI Challita-eid PM, Faris M, Jakobovits A;  
XX DR WPI; 2001-557705/62.  
XX PT New polynucleotide for treating and diagnosing prostate cancer is the  
XX 103P2D6 gene which encodes for 103P2D6-related proteins -  
XX PS Example 15; Page 84; 132pp; English.  
XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
CC adult tissue but is aberrantly expressed in some foetal tissues and many  
CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
CC related protein and also peptide fragments of the protein are therefore  
CC useful for diagnosing and treating cancer. A vector comprising a  
CC polynucleotide which encodes a single chain monoclonal antibody, that  
CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
CC are both useful in the preparation of a composition for treating a  
CC patient with a cancer that expresses 103P2D6. The sequences can be used  
CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
CC serum, blood, urine and tissue and to thereby detect the presence of  
CC cancerous cells.  
XX SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
| | | |  
Db 2 LLYQ 5

RESULT 64  
AAU24052  
ID AAU24052 standard; Peptide; 9 AA.  
XX AC  
XX AAU24052;  
XX DT 17-DEC-2001 (first entry)  
XX DE Human MHC class I molecule HLA-A3 binding 103P2D6 peptide #37.  
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
KW single chain monoclonal antibody; cervix; human.  
XX OS Homo sapiens.  
XX PN WO200162925-A2.  
XX PD 30-AUG-2001.  
XX PF 26-FEB-2001; 2001WO-US05996.  
XX PR 24-FEB-2000; 2000US-0184558.  
XX PR 13-JUL-2000; 2000US-0218856.  
XX PA (UROG-) UROGENESYS INC.  
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;  
PI Challita-eid PM, Faris M, Jakobovits A;  
XX DR WPI; 2001-557705/62.  
XX PT New polynucleotide for treating and diagnosing prostate cancer is the  
XX 103P2D6 gene which encodes for 103P2D6-related proteins -  
XX PS Example 15; Page 87; 132pp; English.  
XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
CC adult tissue but is aberrantly expressed in some foetal tissues and many  
CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
CC related protein and also peptide fragments of the protein are therefore  
CC useful for diagnosing and treating cancer. A vector comprising a  
CC polynucleotide which encodes a single chain monoclonal antibody, that  
CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
CC are both useful in the preparation of a composition for treating a  
CC patient with a cancer that expresses 103P2D6. The sequences can be used  
CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
CC serum, blood, urine and tissue and to thereby detect the presence of  
CC cancerous cells.  
XX SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
| | | |  
Db 1 LLYQ 4

RESULT 65  
AAU24158  
ID AAU24158 standard; Peptide; 9 AA.  
XX AC  
XX AAU24158;  
XX DT 17-DEC-2001 (first entry)

```

XX DE Human MHC molecule HLA-A11 binding 103P2D6 peptide #43.
XX DE
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX PA (UROC-) UROGENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Paris M, Jakobovits A;
XX DR WPI; 2001-557705/62.
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX PS Example 15; Page 90; 132pp; English.
XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103P2D6. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103P2D6 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLYQ 6
XX ||||
XX Db 3 LLYQ 6
XX
XX RESULT 66
XX AAU24257
XX ID AAU24257 standard; Peptide; 9 AA.
XX AC AAU24257;
XX XX
XX DT 17-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #42.
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX PA (UROC-) UROGENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Paris M, Jakobovits A;
XX DR WPI; 2001-557705/62.
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX PS Example 15; Page 90; 132pp; English.
XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103P2D6. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103P2D6 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLYQ 6
XX ||||
XX Db 3 LLYQ 6
XX
XX RESULT 67
XX AAU24261
XX ID AAU24261 standard; Peptide; 9 AA.
XX AC AAU24261;
XX XX
XX DT 17-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #46.
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX

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OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX PA (UROC-) UROGENESYS INC.
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Paris M, Jakobovits A;
XX DR WPI; 2001-557705/62.
XX PT New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX PS Example 15; Page 93; 132pp; English.
XX CC Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX CC adult tissue but is aberrantly expressed in some foetal tissues and many
XX CC cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX CC related protein and also peptide fragments of the protein are therefore
XX CC useful for diagnosing and treating cancer. A vector comprising a
XX CC polynucleotide which encodes a single chain monoclonal antibody, that
XX CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX CC are both useful in the preparation of a composition for treating a
XX CC patient with a cancer that expresses 103P2D6. The sequences can be used
XX CC in diagnostic methods to monitor the level of 103P2D6 gene products in
XX CC serum, blood, urine and tissue and to thereby detect the presence of
XX CC cancerous cells.
XX SQ Sequence 9 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLYQ 6
XX ||||
XX Db 1 LLYQ 4
XX
XX RESULT 67
XX AAU24261
XX ID AAU24261 standard; Peptide; 9 AA.
XX AC AAU24261;
XX XX
XX DT 17-DEC-2001 (first entry)
XX DE Human MHC class I molecule HLA-A24 binding 103P2D6 peptide #46.
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX KW single chain monoclonal antibody; cervix; human.
XX OS Homo sapiens.
XX PN WO200162925-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US05996.
XX

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PR 24-FEB-2000; 2000US-0184558.
PR 13-JUL-2000; 2000US-0218856.
XX (UROG-) UROGENESYS INC.
XX
XX Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Faris M, Jakobovits A;
XX
XX WPI; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 93; 132pp; English.
XX
XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX adult tissue but is aberrantly expressed in some foetal tissues and many
XX cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX related protein and also peptide fragments of the protein are therefore
XX useful for diagnosing and treating cancer. A vector comprising a
XX polynucleotide which encodes a single chain monoclonal antibody, that
XX immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX are both useful in the preparation of a composition for treating a
XX patient with a cancer that expresses 103P2D6. The sequences can be used
XX in diagnostic methods to monitor the level of 103P2D6 gene products in
XX serum, blood, urine and tissue and to thereby detect the presence of
XX cancerous cells.
XX
XX Sequence 9 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLYQ 6
XX ||||
XX Db 5 LLYQ 8
XX
XX RESULT 68
XX AAU24330
XX ID AAU24330 standard; Peptide; 9 AA.
XX
XX AC AAU24330;
XX
XX DT 17-DEC-2001 (first entry)
XX
XX DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #15.
XX
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX single chain monoclonal antibody; cervix; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200162925-A2.
XX
XX PD 30-AUG-2001.
XX
XX PF 26-FEB-2001; 2001WO-US05996.
XX
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX
XX PA (UROG-) UROGENESYS INC.
XX
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Faris M, Jakobovits A;
XX
XX

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DR WPI; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 95; 132pp; English.
XX
XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and
XX peptide fragments of the polypeptide. 103P2D6 is not expressed in normal
XX adult tissue but is aberrantly expressed in some foetal tissues and many
XX cancers including tumours of the prostate, testis, bladder, bone, cervix,
XX ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its
XX related protein and also peptide fragments of the protein are therefore
XX useful for diagnosing and treating cancer. A vector comprising a
XX polynucleotide which encodes a single chain monoclonal antibody, that
XX immunospecifically binds to an 103P2D6-related protein, and a ribozyme
XX capable of cleaving a polynucleotide having the 103P2D6 coding sequence,
XX are both useful in the preparation of a composition for treating a
XX patient with a cancer that expresses 103P2D6. The sequences can be used
XX in diagnostic methods to monitor the level of 103P2D6 gene products in
XX serum, blood, urine and tissue and to thereby detect the presence of
XX cancerous cells.
XX
XX Sequence 9 AA;
XX
XX Query Match 57.1%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 LLYQ 6
XX ||||
XX Db 5 LLYQ 8
XX
XX RESULT 69
XX AAU24341
XX ID AAU24341 standard; Peptide; 9 AA.
XX
XX AC AAU24341;
XX
XX DT 17-DEC-2001 (first entry)
XX
XX DE Human MHC class I molecule HLA-B7 binding 103P2D6 peptide #26.
XX
XX KW 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;
XX tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;
XX gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;
XX single chain monoclonal antibody; cervix; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200162925-A2.
XX
XX PD 30-AUG-2001.
XX
XX PF 26-FEB-2001; 2001WO-US05996.
XX
XX PR 24-FEB-2000; 2000US-0184558.
XX PR 13-JUL-2000; 2000US-0218856.
XX
XX PA (UROG-) UROGENESYS INC.
XX
XX PI Raitano AB, Afar DEH, Rastegar GS, Mitchell SC, Hubert RS;
XX PI Challita-eid PM, Faris M, Jakobovits A;
XX
XX WPI; 2001-557705/62.
XX
XX New polynucleotide for treating and diagnosing prostate cancer is the
XX PT 103P2D6 gene which encodes for 103P2D6-related proteins -
XX
XX Example 15; Page 95; 132pp; English.
XX
XX Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and

```

CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme  
 CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.

XX SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 ||||  
 Db 1 LLYQ 4

RESULT 70  
 AAU24442  
 ID AAU24442 standard; Peptide; 9 AA.  
 AC AAU24442;  
 XX 17-DEC-2001 (first entry)  
 DT Human MHC molecule HLA-B35 binding 103P2D6 peptide #27.  
 DE 103P2D6; PCR primer; DNA adaptor; prostate; testis; foetal tissue;  
 KW tumour; cancer; bone; ovary; breast; pancreas; colon; lung; cytostatic;  
 KW gene therapy; antibody therapy; ribozyme; serum; blood; urine; bladder;  
 KW single chain monoclonal antibody; cervix; human.  
 XX Homo sapiens.  
 OS WO200162925-A2.  
 FN 30-AUG-2001.  
 PD 26-FEB-2001; 2001WO-US05996.  
 XX 24-FEB-2000; 2000US-0184559.  
 PR 13-JUL-2000; 2000US-0218856.  
 XX (UROG-) UROGENESYS INC.  
 PA Raitano AB, Afar DH, Rastegar GS, Mitchell SC, Hubert RS;  
 PI Challita-eid FM, Faris M, Jakobovits A;  
 DR WPI; 2001-557705/62.  
 XX New polynucleotide for treating and diagnosing prostate cancer is the  
 PT 103P2D6 gene which encodes for 103P2D6-related proteins -  
 XX Example 15; Page 98; 132pp; English.

Sequences AAU23815-AAU24515 represent the 103P2D6-related protein and  
 CC peptide fragments of the polypeptide. 103P2D6 is not expressed in normal  
 CC adult tissue but is aberrantly expressed in some foetal tissues and many  
 CC cancers including tumours of the prostate, testis, bladder, bone, cervix,  
 CC ovary, breast, pancreas, colon and lung. The 103P2D6 polynucleotide, its  
 CC related protein and also peptide fragments of the protein are therefore  
 CC useful for diagnosing and treating cancer. A vector comprising a  
 CC polynucleotide which encodes a single chain monoclonal antibody, that  
 CC immunospecifically binds to an 103P2D6-related protein, and a ribozyme

CC capable of cleaving a polynucleotide having the 103P2D6 coding sequence,  
 CC are both useful in the preparation of a composition for treating a  
 CC patient with a cancer that expresses 103P2D6. The sequences can be used  
 CC in diagnostic methods to monitor the level of 103P2D6 gene products in  
 CC serum, blood, urine and tissue and to thereby detect the presence of  
 CC cancerous cells.

XX SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 ||||  
 Db 5 LLYQ 8

RESULT 71  
 AAM22143  
 ID AAM22143 standard; Peptide; 9 AA.  
 AC AAM22143;  
 XX 22-OCT-2001 (first entry)  
 DT HIV peptide SEQ ID NO 28.  
 DE Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;  
 KW human immunodeficiency virus; vaccine.  
 KW Human immunodeficiency virus.  
 OS Synthetic.  
 OS WO200155177-A2.  
 FN 02-AUG-2001.  
 XX 29-JAN-2001; 2001WO-DK00059.  
 PF 28-JAN-2000; 2000EP-0610017.  
 PR 31-JAN-2000; 2000US-0179333.  
 XX (STAT-) STATENS SERUM INST.  
 FA Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;  
 XX WPI; 2001-476184/51.  
 DR The generation of cytotoxic T cell lymphocytes epitopes for use in  
 PT anti-HIV vaccines -  
 XX Claim 13; Page 49; 383pp; English.

The invention relates to identification of cytotoxic T cell lymphocyte  
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL  
 CC are a major protective mechanism against viral diseases. Antibodies may  
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or  
 CC prevent infection of cells in the host, but CTL will limit viral  
 CC production by killing the cell. The CTL epitopes are useful in medicine,  
 CC in the manufacture of vaccines or diagnostic agents.

XX SQ Sequence 9 AA;

Query Match 57.1%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 ||||  
 Db 2 LLYQ 5

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RESULT 72
ABJ15353
ID ABJ15353 standard; Peptide; 9 AA.
XX AC ABJ15353;
XX DT 16-JAN-2003 (first entry)
XX DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 7.
XX KW Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
XX KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
XX KW passive immunisation.
XX OS Unidentified.
XX PN WO200260953-A2.
XX PD 08-AUG-2002.
XX PF 17-DEC-2001; 2001WO-US49133.
XX PR 15-DEC-2000; 2000US-256210P.
XX PA (AGEN-) AGENSYS INC.
XX PI Challita-eid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
XX PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX WPI; 2002-627469/67.
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108P5H8), useful in diagnosing and treating
PT patients with cancer that express 108P5H8, such as breast, colon,
PT ovarian or lung cancer -
XX Claim 21; Page 172; 309pp; English.
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful as probes
CC or primers for the amplification or detection of 108P5H8 genes, as
CC coding sequences for directing the expression of 108P5H8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8
CC related peptide of the invention.
XX Sequence 9 AA;
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FLLY 5
Db 6 FLLY 9
RESULT 73
ABJ15391
ID ABJ15391 standard; Peptide; 9 AA.
XX AC ABJ15391;
XX DT 16-JAN-2003 (first entry)
XX DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 45.

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XX Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
KW passive immunisation.
XX OS Unidentified.
XX PN WO200260953-A2.
XX PD 08-AUG-2002.
XX PF 17-DEC-2001; 2001WO-US49133.
XX PR 15-DEC-2000; 2000US-256210P.
XX PA (AGEN-) AGENSYS INC.
XX PI Challita-eid PM, Faris M, Afar DEH, Hubert RS, Mitchell SC;
XX PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;
XX WPI; 2002-627469/67.
XX Composition comprising a substance that modulates the status of a zinc
PT transporter protein (108P5H8), useful in diagnosing and treating
PT patients with cancer that express 108P5H8, such as breast, colon,
PT ovarian or lung cancer -
XX Claim 21; Page 173; 309pp; English.
XX The invention relates to a new composition comprising a substance that
CC modulates the status of a zinc transporter protein, designated as
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is
CC useful in diagnosing, preventing, prognosticating or treating patients
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a
CC humoral or cellular immune response. The antibodies are useful as probes
CC or primers for the amplification or detection of 108P5H8 genes, as
CC coding sequences for directing the expression of 108P5H8 polypeptides, or
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.
CC The polynucleotides of the invention can be used to treat disorders by
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8
CC related peptide of the invention.
XX Sequence 9 AA;
Query Match 57.1%; Score 4; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FLLY 5
Db 1 FLLY 4
RESULT 74
ABJ15465
ID ABJ15465 standard; Peptide; 9 AA.
XX AC ABJ15465;
XX DT 16-JAN-2003 (first entry)
XX DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 119.
XX KW Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;
XX KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;
XX KW passive immunisation.
XX OS Unidentified.
XX PN WO200260953-A2.

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PD 08-AUG-2002.  
XX  
XX  
PF 17-DEC-2001; 2001WO-US49133.  
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PR 15-DEC-2000; 2000US-256210P.  
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XX  
PA (AGEN-) AGENSYS INC.  
XX  
XX  
PI Challita-eid PM, Paris M, Afar DEH, Hubert RS, Mitchell SC;  
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;  
XX  
XX  
DR WPI; 2002-627469/67.  
XX  
XX  
CC Composition comprising a substance that modulates the status of a zinc  
PT transporter protein (108P5H8), useful in diagnosing and treating  
PT patients with cancer that express 108P5H8, such as breast, colon,  
PT ovarian or lung cancer -  
XX  
XX  
PS Claim 21; Page 177; 309pp; English.  
XX  
XX  
CC The invention relates to a new composition comprising a substance that  
CC modulates the status of a zinc transporter protein, designated as  
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is  
CC useful in diagnosing, preventing, prognosticating or treating patients  
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or  
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a  
CC humoral or cellular immune response. The antibodies are useful in active  
CC or passive immunisation. The 108P5H8 polynucleotides are useful as probes  
CC and primers for the amplification or detection of 108P5H8 genes, as  
CC coding sequences for directing the expression of 108P5H8 polypeptides, or  
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.  
CC The polynucleotides of the invention can be used to treat disorders by  
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8  
CC related peptide of the invention.  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 57.1%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 FLLY 5  
Db |||||  
5 FLLY 8  
Search completed: November 25, 2003, 19:27:17  
Job time : 19.8663 secs

PD 08-AUG-2002.  
XX  
XX  
PF 17-DEC-2001; 2001WO-US49133.  
XX  
XX  
PR 15-DEC-2000; 2000US-256210P.  
XX  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
XX  
PI Challita-eid PM, Paris M, Afar DEH, Hubert RS, Mitchell SC;  
PI Levin E, Morrison KJM, Raitano AB, Jakobovits A;  
XX  
XX  
DR WPI; 2002-627469/67.  
XX  
XX  
CC Composition comprising a substance that modulates the status of a zinc  
PT transporter protein (108P5H8), useful in diagnosing and treating  
PT patients with cancer that express 108P5H8, such as breast, colon,  
PT ovarian or lung cancer -  
XX  
XX  
PS Claim 21; Page 177; 309pp; English.  
XX  
XX  
CC The invention relates to a new composition comprising a substance that  
CC modulates the status of a zinc transporter protein, designated as  
CC 108P5H8, or a molecule that is modulated by 108P5H8. The composition is  
CC useful in diagnosing, preventing, prognosticating or treating patients  
CC with cancer that expresses 108P5H8, such as breast, colon, ovarian or  
CC lung cancer. The 108P5H8 gene or its fragment can be used to elicit a  
CC humoral or cellular immune response. The antibodies are useful in active  
CC or passive immunisation. The 108P5H8 polynucleotides are useful as probes  
CC and primers for the amplification or detection of 108P5H8 genes, as  
CC coding sequences for directing the expression of 108P5H8 polypeptides, or  
CC as tools for modulating or inhibiting the expression of 108P5H8 genes.  
CC The polynucleotides of the invention can be used to treat disorders by  
CC gene therapy. This sequence represents a zinc transporter protein 108P5H8  
CC related peptide of the invention.  
XX  
XX  
SQ Sequence 9 AA;  
Query Match 57.1%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 FLLY 5  
Db |||||  
4 FLLY 7  
RESULT 75  
ABJ15482  
ID ABJ15482 standard; Peptide; 9 AA.  
XX  
XX  
AC ABJ15482;  
XX  
DT 16-JAN-2003 (first entry)  
XX  
DE Zinc transporter protein 108P5H8 related HLA peptide SEQ ID No 136.  
XX  
KW Cytostatic; gene therapy; vaccine; zinc transporter protein 108P5H8;  
KW cancer; breast; colon; ovarian; lung; humoral; cellular immune response;  
KW passive immunisation.  
XX  
OS Unidentified.  
XX  
PN WO200260953-A2.  
XX  
PD 08-AUG-2002.  
XX  
XX  
PF 17-DEC-2001; 2001WO-US49133.  
XX  
XX  
PR 15-DEC-2000; 2000US-256210P.  
XX  
XX  
PA (AGEN-) AGENSYS INC.  
XX  
XX  
PI Challita-eid PM, Paris M, Afar DEH, Hubert RS, Mitchell SC;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 11.2326 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-28

Perfect score: 7

Sequence: 1 AFLLYQE 7

Scoring table: OIIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	6	85.7	13	15	US-10-281-652-32
3	6	85.7	19	12	US-10-280-833-7
4	4	57.1	6	10	US-09-727-963A-15
5	4	57.1	6	10	US-09-727-963A-25
6	4	57.1	6	10	US-09-727-963A-27
7	4	57.1	6	10	US-09-727-963A-45
8	4	57.1	6	10	US-09-727-963A-47
9	4	57.1	6	11	US-09-804-291-519
10	4	57.1	6	12	US-10-259-423-49
11	4	57.1	6	15	US-10-259-430-49
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Sequence 99, App  
Sequence 9, App  
Sequence 84, App  
Sequence 221, App  
Sequence 4, App  
Sequence 4, App

89 4 57.1 19 15 US-10-153-344-18 Sequence 18, Appl  
90 4 57.1 20 9 US-09-759-143-500 Sequence 500, App  
91 4 57.1 20 9 US-09-780-669-500 Sequence 500, App  
92 4 57.1 20 9 US-09-822-827-500 Sequence 500, App  
93 4 57.1 20 10 US-09-895-793-500 Sequence 500, App  
94 4 57.1 20 10 US-09-895-844-500 Sequence 500, App  
95 4 57.1 20 11 US-09-798-889-118 Sequence 118, App  
96 4 57.1 20 12 US-10-144-678A-500 Sequence 500, App  
97 4 57.1 20 12 US-10-196-394-61 Sequence 61, Appl  
98 4 57.1 20 12 US-10-294-025-500 Sequence 500, App  
99 4 57.1 20 14 US-10-012-896-500 Sequence 500, App  
100 4 57.1 20 15 US-10-000-823-13 Sequence 13, Appl

## ALIGNMENTS

RESULT 1  
US-10-281-652-28  
; Sequence 28, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-28

Query Match 100.0%; Score 7; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQE 7  
Db 1 AFLLYQE 7

RESULT 2  
US-10-281-652-32  
; Sequence 32, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281,652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 32  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-32

Query Match 85.7%; Score 6; DB 15; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLYQE 7  
Db 1 FLLYQE 6

RESULT 3  
US-10-280-833-7  
; Sequence 7, Application US/10280833  
; Publication No. US20030195150A1  
; GENERAL INFORMATION:  
; APPLICANT: Reynolds, Charles Eric  
; APPLICANT: Dasher, Stuart Geoffrey  
; APPLICANT: O'Brien-Simpson, Neil Martin  
; APPLICANT: Talbo, Gert Hoy  
; APPLICANT: Malkoski, Marina  
; TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES  
; FILE REFERENCE: EDWP-001CON  
; CURRENT APPLICATION NUMBER: US/10/280,833  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 09/554,997  
; PRIOR FILING DATE: 2000-08-09  
; PRIOR APPLICATION NUMBER: PP 0514  
; PRIOR FILING DATE: 1997-11-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: bovine  
; OTHER INFORMATION:  
US-10-280-833-7

Query Match 85.7%; Score 6; DB 12; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.4; Indels 0; Gaps 0;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLLYQ 6  
Db 6 AFLLYQ 11

RESULT 4  
US-09-727-963A-15  
; Sequence 15, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
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; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-15

Query Match 57.1%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5  
|||  
Db 1 FLYY 4

RESULT 5  
US-09-727-963A-25  
; Sequence 25, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-25

Query Match 57.1%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5  
|||  
Db 1 FLYY 4

RESULT 6  
US-09-727-963A-27  
; Sequence 27, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 27  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence : peptide  
; OTHER INFORMATION: ligand  
US-09-727-963A-27

Query Match 57.1%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5  
|||  
Db 1 FLYY 4

RESULT 7  
US-09-727-963A-45  
; Sequence 45, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand  
US-09-727-963A-45

Query Match 57.1%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5  
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Db 1 FLYY 4

RESULT 8  
US-09-727-963A-47  
; Sequence 47, Application US/09727963A  
; Patent No. US20020155106A1  
; GENERAL INFORMATION:  
; APPLICANT: V.I. Technologies, Inc.  
; APPLICANT: Hammond, David J.  
; TITLE OF INVENTION: METHOD OF IDENTIFYING A LIGAND FOR A TARGET MOLECULE  
; FILE REFERENCE: 18242-505  
; CURRENT APPLICATION NUMBER: US/09/727,963A  
; CURRENT FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/327,557  
; PRIOR FILING DATE: 1999-12-02  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 47  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide Ligand  
US-09-727-963A-47

Query Match 57.1%; Score 4; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLYY 5  
|||  
Db 1 FLYY 4

RESULT 9  
US-09-804-291-519  
; Sequence 519, Application US/09804291

Publication No. US20030088059A1  
; GENERAL INFORMATION:  
; APPLICANT: ZOZULA, SERGEY  
; TITLE OF INVENTION: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME  
; FILE REFERENCE: P 0278005  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: 60/188,914  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/192,033  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/198,474  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/199,335  
; PRIOR FILING DATE: 2000-04-24  
; PRIOR APPLICATION NUMBER: 60/207,702  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/213,849  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: 60/226,534  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: 60/230,732  
; PRIOR FILING DATE: 2000-09-07  
; PRIOR APPLICATION NUMBER: 60/266,862  
; PRIOR FILING DATE: 2001-02-07  
; NUMBER OF SEQ ID NOS: 529  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 519  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-804-291-519

Query Match 57.1%; Score 4; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
|||  
DB 2 FLLY 5

RESULT 10  
US-10-259-423-49  
; Sequence 49, Application US/10259423  
; Publication No. US20030175744A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Randall  
; APPLICANT: Yau, King-Wai  
; APPLICANT: Krautwurst, Dietmar  
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries  
; FILE REFERENCE: 001107.00105  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 60/192,033  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/112,605  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-259-423-49

Query Match 57.1%; Score 4; DB 12; Length 6;

Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 FLLY 5  
|||  
DB 2 FLLY 5  
RESULT 11  
US-10-259-430-49  
; Sequence 49, Application US/10259430  
; Publication No. US20030082615A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, Randall  
; APPLICANT: Yau, King-Wai  
; APPLICANT: Krautwurst, Dietmar  
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries  
; FILE REFERENCE: 001107.00105  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: 60/192,033  
; PRIOR FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/112,605  
; PRIOR FILING DATE: 1998-12-17  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 49  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Mus musculus  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-259-430-49

Query Match 57.1%; Score 4; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLY 5  
|||  
DB 2 FLLY 5

RESULT 12  
US-10-305-346-12  
; Sequence 12, Application US/10305346  
; Publication No. US20030130195A1  
; GENERAL INFORMATION:  
; APPLICANT: AMIOT, Jean  
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS  
; FILE REFERENCE: 6013-57"US"-1  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk proteins  
US-10-305-346-12

Query Match 57.1%; Score 4; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7  
|||  
DB 1 LYQE 4

RESULT 13  
 US-09-793-451-130  
 ; Sequence 130, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 130  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-130

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 Db 1 LLYQ 4

RESULT 14  
 US-09-793-451-156  
 ; Sequence 156, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 156  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-156

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 LLYQ 6  
 Db 2 LLYQ 5

RESULT 15  
 US-09-793-451-251  
 ; Sequence 251, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 251  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-251

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 Db 1 LLYQ 4

RESULT 16  
 US-09-793-451-357  
 ; Sequence 357, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 357  
 ; LENGTH: 9  
 ; TYPE: PRT

; ORGANISM: homo sapiens  
US-09-793-451-357

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|||  
Db 3 LLYQ 6

## RESULT 17

US-09-793-451-456  
; Sequence 456, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 456  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-456

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|||  
Db 1 LLYQ 4

## RESULT 18

US-09-793-451-460  
; Sequence 460, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 460

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|||  
Db 5 LLYQ 8

## RESULT 19

US-09-793-451-529  
; Sequence 529, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 529  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-529

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred.No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|||  
Db 5 LLYQ 8

## RESULT 20

US-09-793-451-540  
; Sequence 540, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/09/793,451

; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184, 558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218, 856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 540  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-540

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
|||  
Db 1 LLYQ 4

RESULT 21  
US-09-793-451-641  
; Sequence 641, Application US/09793451  
; Publication No. US20030157597A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Bid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129, 2USU2  
; CURRENT APPLICATION NUMBER: US/09/793, 451  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184, 558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218, 856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 641  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-793-451-641

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
|||  
Db 5 LLYQ 8

RESULT 22  
US-09-935-384-127  
; Sequence 127, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO

; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935, 384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227, 098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 127  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-127

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 3 AFLL 6

RESULT 23  
US-09-935-384-145  
; Sequence 145, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935, 384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227, 098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 145  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-145

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 2 AFLL 5

RESULT 24  
US-09-935-384-318  
; Sequence 318, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL



; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: GE, WANGMAO  
 ; APPLICANT: JAKOBOVITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; FILE REFERENCE: 51158-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/935,384  
 ; CURRENT FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 783  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 318  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-935-384-318

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
 Db 1 AFLL 4

RESULT 25  
 US-09-935-384-402  
 ; Sequence 402, Application US/09935384  
 ; Publication No. US20030166526A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHALLITA-BID, PIA  
 ; APPLICANT: HUBERT, RENE  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: GE, WANGMAO  
 ; APPLICANT: JAKOBOVITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; FILE REFERENCE: 51158-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/935,384  
 ; CURRENT FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 783  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 402  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-935-384-402

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
 Db 6 AFLL 9

RESULT 26  
 US-09-935-384-433  
 ; Sequence 433, Application US/09935384  
 ; Publication No. US20030166526A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHALLITA-BID, PIA

; APPLICANT: HUBERT, RENE  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: GE, WANGMAO  
 ; APPLICANT: JAKOBOVITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; FILE REFERENCE: 51158-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/935,384  
 ; CURRENT FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 783  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 433  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-935-384-433

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
 Db 2 AFLL 5

RESULT 27  
 US-09-935-384-510  
 ; Sequence 510, Application US/09935384  
 ; Publication No. US20030166526A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHALLITA-BID, PIA  
 ; APPLICANT: HUBERT, RENE  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: GE, WANGMAO  
 ; APPLICANT: JAKOBOVITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; FILE REFERENCE: 51158-20033.00  
 ; CURRENT APPLICATION NUMBER: US/09/935,384  
 ; CURRENT FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; NUMBER OF SEQ ID NOS: 783  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 510  
 ; LENGTH: 9  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-935-384-510

Query Match 57.1%; Score 4; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 6e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
 Db 2 AFLL 5

RESULT 28  
 US-09-935-384-630  
 ; Sequence 630, Application US/09935384

```

; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: PARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 630
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-384-630

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFL 4
Db 2 AFL 5

RESULT 29
US-10-283-722-130
; Sequence 130, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-283-722-130

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 31
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-283-722-251

Query Match      57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6
Db 2 LLYQ 5

RESULT 31
US-10-283-722-251
; Sequence 251, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Paris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 251
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-283-722-251

```

```
; ORGANISM: homo sapiens
US-10-283-722-251

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 1 LLYQ 4

RESULT 32
US-10-283-722-357
; Sequence 357, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-357

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 3 LLYQ 6

RESULT 33
US-10-283-722-456
; Sequence 456, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-456

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 3 LLYQ 6

RESULT 34
US-10-283-722-460
; Sequence 460, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/10/283,722
; PRIOR FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/793,451
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 460
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-283-722-460

Query Match          57.1%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
   ||||
Db 1 LLYQ 4

RESULT 35
US-10-283-722-529
; Sequence 529, Application US/10283722
; Publication No. US20030194407A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
```

; APPLICANT: Mary Faris  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 529  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-529

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
|||  
Db 5 LLYQ 8

RESULT 36  
US-10-283-722-540  
; Sequence 540, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 540  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-540

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
|||  
Db 1 LLYQ 4

RESULT 37  
US-10-283-722-641

; Sequence 641, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 641  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-641

Query Match 57.1%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
|||  
Db 5 LLYQ 8

RESULT 38  
US-09-572-404B-1212  
; Sequence 1212, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human Patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 1212  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in SCN4A at 835-844 and may interact with Sequ  
; OTHER INFORMATION: in this patent.  
US-09-572-404B-1212

Query Match 57.1%; Score 4; DB 11; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 4 AFLL 7

RESULT 39  
US-09-572-404B-2701  
; Sequence 2701, Application US/09572404B  
; Publication No. US20030078374A1

; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
 ; FILE REFERENCE: Human patent  
 ; CURRENT APPLICATION NUMBER: US/09/572,404B  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 4203  
 ; SOFTWARE: ProtPatent version 1.0  
 ; SEQ ID NO 2701  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: sequence located in CRRP2 OR CRP2R OR CRH2R at 132-141 and may interact with  
 ; OTHER INFORMATION: with Sequence 2702 in this patent.  
 US-09-572-404B-2701

Query Match 57.1%; Score 4; DB 11; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4  
 Db 3 APLL 6

RESULT 40  
 US-09-572-270A-350  
 ; Sequence 350, Application US/09572270A  
 ; Publication No. US20030148368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Inter- complementary peptide listing  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/09/572,270A  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 1144  
 ; SOFTWARE: ProtPatent version 1.0  
 ; SEQ ID NO 350  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis Thaliana  
 ; OTHER INFORMATION: Sequence located in ATJ. at 649-658 and may interact with  
 US-09-572-270A-350

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4  
 Db 5 APLL 8

RESULT 41  
 US-09-572-270A-585  
 ; Sequence 585, Application US/09572270A  
 ; Publication No. US20030148368A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Proteom Ltd  
 ; TITLE OF INVENTION: Inter- complementary peptide listing  
 ; FILE REFERENCE:  
 ; CURRENT APPLICATION NUMBER: US/09/572,270A  
 ; CURRENT FILING DATE: 2000-05-17  
 ; NUMBER OF SEQ ID NOS: 1144  
 ; SOFTWARE: ProtPatent version 1.0  
 ; SEQ ID NO 585  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis Thaliana  
 ; OTHER INFORMATION: Sequence located in ATJ. at 653-662 and may interact with  
 US-09-572-270A-585

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APLL 4  
 Db 1 APLL 4

RESULT 42  
 US-09-793-451-183  
 ; Sequence 183, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 183  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-09-793-451-183

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LIXQ 6  
 Db 2 LIXQ 5

RESULT 43  
 US-09-793-451-206  
 ; Sequence 206, Application US/09793451  
 ; Publication No. US20030157597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/09/793,451  
 ; CURRENT FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 206

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-206

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 6 LLYQ 9

RESULT 44
US-09-793-451-272
; Sequence 272, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-272

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 1 LLYQ 4

RESULT 45
US-09-793-451-303
; Sequence 303, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
```

```
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-303

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 2 LLYQ 5

RESULT 46
US-09-793-451-474
; Sequence 474, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-474

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6
Db 2 LLYQ 5

RESULT 47
US-09-793-451-502
; Sequence 502, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; FILE REFERENCE: 129.2USU2
```

```

; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-502

```

```

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 LLYQ 6
        ||||
Db       6 LLYQ 9

```

## RESULT 48

```

US-09-793-451-594
; Sequence 594, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-594

```

```

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 LLYQ 6
        ||||
Db       2 LLYQ 5

```

## RESULT 49

```

US-09-793-451-596
; Sequence 596, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert

```

```

; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 596
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-596

```

```

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 LLYQ 6
        ||||
Db       6 LLYQ 9

```

## RESULT 50

```

US-09-793-451-691
; Sequence 691, Application US/09793451
; Publication No. US20030157597A1
; GENERAL INFORMATION:
; APPLICANT: Arthur B. Raitano
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Gazelle S. Rastegar
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Rene S. Hubert
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY
; TITLE OF INVENTION: EXPRESSED IN VARIOUS CANCERS
; FILE REFERENCE: 129.2USU2
; CURRENT APPLICATION NUMBER: US/09/793,451
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,558
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/218,856
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 752
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 691
; LENGTH: 10
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-793-451-691

```

```

Query Match      57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 LLYQ 6
        ||||
Db       5 LLYQ 8

```

## RESULT 51

```

US-09-935-384-159
; Sequence 159, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:

```

```

; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 159
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-159

```

```

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 7 AFLL 10

```

```

RESULT 52
US-09-935-384-180
; Sequence 180, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 180
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-180

```

```

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 3 AFLL 6

```

```

RESULT 53
US-09-935-384-278

```

```

; Sequence 278, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 278
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-278

```

```

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 2 AFLL 5

```

```

RESULT 54
US-09-935-384-283
; Sequence 283, Application US/09935384
; Publication No. US20030166526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; TITLE OF INVENTION: OTHER CANCERS
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 283
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-384-283

```

```

Query Match          57.1%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 7 AFLL 10

```



RESULT 55  
US-09-935-384-358  
; Sequence 358, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 358  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-358

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 1 AFLL 4

RESULT 56  
US-09-935-384-360  
; Sequence 360, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 360  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-360

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best-Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4

Db 2 AFLL 5  
RESULT 57  
US-09-935-384-459  
; Sequence 459, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 459  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-459

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 3 AFLL 6

RESULT 58  
US-09-935-384-475  
; Sequence 475, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOWITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PIH4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; CURRENT FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 475  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-475

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 6 AFLL 9

## RESULT 59

US-09-935-384-493  
; Sequence 493, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 493  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-493

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 7 AFLL 10

## RESULT 60

US-09-935-384-574  
; Sequence 574, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 574  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-574

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 6 AFLL 9

## RESULT 59

US-09-935-384-493  
; Sequence 493, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 493  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-493

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 7 AFLL 10

## RESULT 60

US-09-935-384-574  
; Sequence 574, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 574  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-574

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 7 AFLL 10

## RESULT 61

US-09-935-384-575  
; Sequence 575, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 575  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-575

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 3 AFLL 6

## RESULT 62

US-09-935-384-691  
; Sequence 691, Application US/09935384  
; Publication No. US20030166526A1  
; GENERAL INFORMATION:  
; APPLICANT: CHALLITA-EID, PIA  
; APPLICANT: HUBERT, RENE  
; APPLICANT: RAITANO, ARTHUR  
; APPLICANT: AFAR, DANIEL  
; APPLICANT: LEVIN, ELANA  
; APPLICANT: FARIS, MARY  
; APPLICANT: GE, WANGMAO  
; APPLICANT: JAKOBOVITZ, AYA  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4  
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
; TITLE OF INVENTION: OTHER CANCERS  
; FILE REFERENCE: 51158-20033.00  
; CURRENT APPLICATION NUMBER: US/09/935,384  
; PRIOR FILING DATE: 2001-08-22  
; PRIOR APPLICATION NUMBER: 60/227,098  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 691  
; LENGTH: 10

; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-935-384-691

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4  
|  
|  
|  
|  
Db 3 AFL 6

## RESULT 63

US-10-283-722-183  
; Sequence 183, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 183  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-183

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|  
|  
|  
|  
Db 2 LLYQ 5

## RESULT 64

US-10-283-722-206  
; Sequence 206, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451

; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 206  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-206

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|  
|  
|  
|  
Db 6 LLYQ 9

## RESULT 65

US-10-283-722-272  
; Sequence 272, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Aya Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 272  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-272

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
|  
|  
|  
|  
Db 1 LLYQ 4

## RESULT 66

US-10-283-722-303  
; Sequence 303, Application US/10283722  
; Publication No. US20030194407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert

; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 303  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-303

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 Db 2 LLYQ 5

RESULT 67  
 US-10-283-722-474  
 ; Sequence 474, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 474  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-474

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 Db 2 LLYQ 5

RESULT 68

Query Match 57.1%; Score 4; DB 12; Length 10;

US-10-283-722-502  
 ; Sequence 502, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 502  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-502

Query Match 57.1%; Score 4; DB 12; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
 Db 6 LLYQ 9

RESULT 69  
 US-10-283-722-594  
 ; Sequence 594, Application US/10283722  
 ; Publication No. US20030194407A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Arthur B. Raitano  
 ; APPLICANT: Daniel E.H. Afar  
 ; APPLICANT: Gazelle S. Rastegar  
 ; APPLICANT: Steve Chappell Mitchell  
 ; APPLICANT: Rene S. Hubert  
 ; APPLICANT: Pia M. Challita-Eid  
 ; APPLICANT: Mary Faris  
 ; APPLICANT: Aya Jakobovits  
 ; TITLE OF INVENTION: 103PD6: TISSUE SPECIFIC PROTEIN HIGHLY  
 ; FILE REFERENCE: 129.2USU2  
 ; CURRENT APPLICATION NUMBER: US/10/283,722  
 ; CURRENT FILING DATE: 2003-02-03  
 ; PRIOR FILING DATE: 2001-02-26  
 ; PRIOR APPLICATION NUMBER: US/09/793,451  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/184,558  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/218,856  
 ; PRIOR FILING DATE: 2000-07-13  
 ; NUMBER OF SEQ ID NOS: 752  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 594  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: homo sapiens  
 US-10-283-722-594

Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 3 LLYQ 6  
Db 2 LLYQ 5

RESULT 70  
US-10-283-722-596  
; Sequence 596, Application US/10283722  
; Publication No. US2003019407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2 EXPRESSED IN VARIOUS CANCERS  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13  
; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 596  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-596

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 3 LLYQ 6  
Db 6 LLYQ 9

RESULT 71  
US-10-283-722-691  
; Sequence 691, Application US/10283722  
; Publication No. US2003019407A1  
; GENERAL INFORMATION:  
; APPLICANT: Arthur B. Raitano  
; APPLICANT: Daniel E.H. Afar  
; APPLICANT: Gazelle S. Rastegar  
; APPLICANT: Steve Chappell Mitchell  
; APPLICANT: Rene S. Hubert  
; APPLICANT: Pia M. Challita-Eid  
; APPLICANT: Mary Faris  
; APPLICANT: Ava Jakobovits  
; TITLE OF INVENTION: 103P2D6: TISSUE SPECIFIC PROTEIN HIGHLY  
; FILE REFERENCE: 129.2USU2 EXPRESSED IN VARIOUS CANCERS  
; CURRENT APPLICATION NUMBER: US/10/283,722  
; CURRENT FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US/09/793,451  
; PRIOR FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: 60/184,558  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/218,856  
; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 752  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 691  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-283-722-691

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 3 LLYQ 6  
Db 5 LLYQ 8

RESULT 72  
US-09-573-822C-734  
; Sequence 734, Application US/09573822C  
; Publication No. US20030199011A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome  
; FILE REFERENCE: Microbe patent  
; CURRENT APPLICATION NUMBER: US/09/573,822C  
; CURRENT FILING DATE: 2000-05-18  
; NUMBER OF SEQ ID NOS: 804  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 734  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: mycoplasma genitalium  
; FEATURE:  
; OTHER INFORMATION: Sequence located in MG468 at 1655-1664 and may interact with S  
; OTHER INFORMATION: 733 in this patent.  
US-09-573-822C-734

Query Match 57.1%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0;

QY 1 AFLL 4  
Db 5 AFLL 8

RESULT 73  
US-10-001-546-18  
; Sequence 18, Application US/10001546  
; Publication No. US20030027766A1  
; GENERAL INFORMATION:  
; APPLICANT: IOANNIDES, CONSTANTIN G.  
; APPLICANT: FISK, BRYAN A.  
; APPLICANT: IOANNIDES, MARIA G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; FILE REFERENCE: T-LYMPHOCYTES  
; FILE REFERENCE: UTSC:390USC2  
; CURRENT APPLICATION NUMBER: US/10/001,546  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: 08/403,459  
; PRIOR FILING DATE: 1995-03-14  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: PatentIn-Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-001-546-18

Query Match 57.1%; Score 4; DB 15; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LYQ 6  
Db 2 LYQ 5

RESULT 74  
US-09-983-802-439  
; Sequence 439, Application US/09983802  
; Publication No. US20030022185A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: P2010P1  
; CURRENT APPLICATION NUMBER: US/09/983,802  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360  
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18

Query Match 57.1%; Score 4; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5  
Db 7 FLY 10

RESULT 75  
US-10-350-405-197  
; Sequence 197, Application US/10350405  
; Publication No. US20030215894A1  
; GENERAL INFORMATION:  
; APPLICANT: Niman, Henry L.  
; TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors  
; FILE REFERENCE: TSRI 35, 5 CON 7/LIG  
; CURRENT APPLICATION NUMBER: US/10/350,405  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/427,576  
; PRIOR FILING DATE: 1999-10-26  
; PRIOR APPLICATION NUMBER: 08/461,583  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: 08/294,879  
; PRIOR FILING DATE: 1994-08-23  
; PRIOR APPLICATION NUMBER: 08/054,864  
; PRIOR FILING DATE: 1993-04-28  
; PRIOR APPLICATION NUMBER: 07/900,502  
; PRIOR FILING DATE: 1992-06-16  
; PRIOR APPLICATION NUMBER: 07/780,415  
; PRIOR FILING DATE: 1991-10-22  
; NUMBER OF SEQ ID NOS: 227  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 197  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: retrovirus  
US-10-350-405-197

Query Match 57.1%; Score 4; DB 12; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 7  
Db 8 LYQ 11

Search completed: November 25, 2003, 20:37:05  
Job time : 12.2326 secs







## ALIGNMENTS

RESULT 1  
US-09-641-803-28  
; Sequence 28, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEROF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR FILING DATE: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 28  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-28

Query Match 100.0%; Score 7; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLVQE 7  
|||||  
Db 1 AFLVQE 7

RESULT 2  
US-09-641-803-32  
; Sequence 32, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRIN, CONSTITUENT PEPTIDES THEROF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-641-803-32

Query Match 85.7%; Score 6; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 0.81;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLLVQE 7  
|||||  
Db 1 FLLVQE 6

RESULT 3  
US-08-617-929-14  
; Sequence 14, Application US/08617929  
; Patent No. 5885771  
; GENERAL INFORMATION:  
; APPLICANT: KUMAZAWA, Toshiaki  
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND  
; TITLE OF INVENTION: IMMUNOASSAY  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/617,929  
; FILING DATE: 24-APR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/JP94/01823  
; FILING DATE: 28-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6/207695  
; FILING DATE: 31-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 5/272864  
; FILING DATE: 29-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Bernhard D.  
; REGISTRATION NUMBER: 28,665  
; REFERENCE/DOCKET NUMBER: 77384/109  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-617-929-14  
Query Match 71.4%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 7.9;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQE 7  
|||||  
Db 3 LLYQE 7

RESULT 4  
US-08-617-929-16  
; Sequence 16, Application US/08617929  
; Patent No. 5885771  
; GENERAL INFORMATION:  
; APPLICANT: KUMAZAWA, Toshiaki  
; TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND  
; TITLE OF INVENTION: IMMUNOASSAY  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,929
; FILING DATE: 24-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/01823
; FILING DATE: 28-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: JP 6/207695
; FILING DATE: 31-AUG-1994
; APPLICATION DATA:
; APPLICATION NUMBER: JP 5/272864
; FILING DATE: 29-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 77384/109
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-617-929-16

Query Match
Best Local Similarity 71.4%; Score 5; DB 2; Length 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQE 7
Db 10 LLYQE 14

RESULT 5
US-08-405-933-41
; Sequence 41, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillabuntz, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-405-933-41

Query Match
Best Local Similarity 57.1%; Score 4; DB 1; Length 5;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4
Db 1 AFL 4

RESULT 6
US-09-465-901-49
; Sequence 49, Application US/09465901
; Patent No. 6492143
; GENERAL INFORMATION:
; APPLICANT: Reed, Randall
; APPLICANT: Yau, King-Wai
; APPLICANT: Krautwurst, Dietmar
; TITLE OF INVENTION: Olfactory Receptor Expression Libraries
; TITLE OF INVENTION: ad Methods of Making and Using Them
; FILE REFERENCE: 001107.00105
; CURRENT APPLICATION NUMBER: US/09/465,901
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/112,605
; PRIOR FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: PCR primer
; US-09-465-901-49

Query Match
Best Local Similarity 57.1%; Score 4; DB 4; Length 6;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLY 5
Db 2 FLY 5

RESULT 7
US-09-492-766-12
; Sequence 12, Application US/09492766
; Patent No. 6506732
; GENERAL INFORMATION:
; APPLICANT: AMLOT, Jean
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
; FILE REFERENCE: 6013-57"US"
; CURRENT APPLICATION NUMBER: US/09/492,766
; CURRENT FILING DATE: 2000-01-27
; EARLIER APPLICATION NUMBER: 60/117,661
; EARLIER FILING DATE: 1999-01-28

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NUMBER OF SEQ ID NOS: 13  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 12  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
OTHER INFORMATION: proteins  
US-09-492-766-12

Query Match 57.1%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LLYQ 7  
Db 1 LLYQ 4

RESULT 8  
US-08-159-339A-366  
Sequence 366, Application US/08159339A  
Patent No. 6037135  
GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 366:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-366

Query Match 57.1%; Score 4; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
Db 1 LLYQ 4

RESULT 9  
US-08-159-339A-375  
Sequence 375, Application US/08159339A  
Patent No. 6037135  
GENERAL INFORMATION:  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Sette, Alessandro  
APPLICANT: Celis, Esteban  
TITLE OF INVENTION: HLA Binding peptides and Their  
TITLE OF INVENTION: Uses  
NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 375:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-375

Query Match 57.1%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LLYQ 6  
Db 2 LLYQ 5

RESULT 10  
US-08-403-459-18  
Sequence 18, Application US/08403459  
Patent No. 6514942

GENERAL INFORMATION:  
; APPLICANT: Ioannides, Constantin G.  
; APPLICANT: Fisk, Bryan A.  
; APPLICANT: Ioannides, Maria G.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING  
; TITLE OF INVENTION: T-LYMPHOCYTES  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403,459  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; TELEX: 79-0924  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-403-459-18

Query Match 57.1%; Score 4; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLYQ 6  
Db 2 LLYQ 5

RESULT 11  
US-08-443-568B-1  
; Sequence 1, Application US/08443568B  
; Patent No. 5759807  
; GENERAL INFORMATION:  
; APPLICANT: Breece, Tim  
; APPLICANT: Hayenga, Kirk  
; APPLICANT: Rindersknecht, Ernst  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Daniel, Yansura  
; TITLE OF INVENTION: Process for Producing Relaxin  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,568B  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/080,354  
; FILING DATE: 21-JUNE-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Abrams, Samuel B.  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 7842-037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-5556  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-443-568B-1

Query Match 57.1%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLI 4  
Db 6 AFLI 9

RESULT 12  
US-08-443-568B-19  
; Sequence 19, Application US/08443568B  
; Patent No. 5759807  
; GENERAL INFORMATION:  
; APPLICANT: Breece, Tim  
; APPLICANT: Hayenga, Kirk  
; APPLICANT: Rindersknecht, Ernst  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Daniel, Yansura  
; TITLE OF INVENTION: Process for Producing Relaxin  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,568B  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/080,354  
; FILING DATE: 21-JUNE-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Abrams, Samuel B.  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 7842-037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-5556  
; TELEFAX: 650-493-5556

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-443-568B-19

Query Match 57.1%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 6 AFLL 9

RESULT 13  
US-08-443-568B-20  
; Sequence 20, Application US/08443568B  
; Patent No. 5759807  
; GENERAL INFORMATION:  
; APPLICANT: Breece, Tim  
; APPLICANT: Hayenga, Kirk  
; APPLICANT: Rindersknecht, Ernst  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Daniel, Yansura  
; TITLE OF INVENTION: Process for Producing Relaxin  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,568B  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/080,354  
; FILING DATE: 21-JUNE-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Abrams, Samuel B.  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 7842-037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-443-568B-20

Query Match 57.1%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4

Db 6 AFLL 9

RESULT 14  
US-08-443-568B-21  
; Sequence 21, Application US/08443568B  
; Patent No. 5759807  
; GENERAL INFORMATION:  
; APPLICANT: Breece, Tim  
; APPLICANT: Hayenga, Kirk  
; APPLICANT: Rindersknecht, Ernst  
; APPLICANT: Vandlen, Richard  
; APPLICANT: Daniel, Yansura  
; TITLE OF INVENTION: Process for Producing Relaxin  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,568B  
; FILING DATE: 22-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/080,354  
; FILING DATE: 21-JUNE-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Abrams, Samuel B.  
; REGISTRATION NUMBER: 30,605  
; REFERENCE/DOCKET NUMBER: 7842-037  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-443-568B-21

Query Match 57.1%; Score 4; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 6 AFLL 9

RESULT 15  
PCT-US94-06997-1  
; Sequence 1, Application PC/TUS9406997  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: 460 Point San Bruno Boulevard  
; APPLICANT: South San Francisco, California  
; APPLICANT: United States of America  
; TITLE OF INVENTION: Process for Producing Relaxin  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06997  
FILING DATE: 20-JUN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7842-025-228  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US94-06997-1

Query Match 57.1%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 6 AFLL 9

RESULT 16  
PCT-US94-06997-19  
Sequence 19, Application PC/TUS9406997  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: 460 Point San Bruno Boulevard  
APPLICANT: South San Francisco, California  
APPLICANT: United States of America  
TITLE OF INVENTION: Process for Producing Relaxin  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06997  
FILING DATE: 20-JUN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7842-025-228  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660

TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US94-06997-19

Query Match 57.1%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 6 AFLL 9

RESULT 17  
PCT-US94-06997-20  
Sequence 20, Application PC/TUS9406997  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: 460 Point San Bruno Boulevard  
APPLICANT: South San Francisco, California  
APPLICANT: United States of America  
TITLE OF INVENTION: Process for Producing Relaxin  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/06997  
FILING DATE: 20-JUN-1994  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 7842-025-228  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
PCT-US94-06997-20

Query Match 57.1%; Score 4; DB 5; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFLL 4  
Db 6 AFLL 9

RESULT 18

```

PCT-US94-06997-21
; Sequence 21, Application PC/TUS9406997
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: 460 Point San Bruno Boulevard
; APPLICANT: South San Francisco, California
; APPLICANT: United States of America
; TITLE OF INVENTION: Process for Producing Relaxin
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06997
; FILING DATE: 20-JUN-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7842-025-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA
PCT-US94-06997-21

```

```

Query Match      57.1%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AFLL 4
        ||||
Db      6 AFLL 9

```

```

RESULT 19
US-07-789-184-139
; Sequence 139, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,184
; FILING DATE: 19911107
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-789-184-139

```

```

Query Match      57.1%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AFLL 4
        ||||
Db      1 AFLL 4

```

```

RESULT 20
US-08-475-263-139
; Sequence 139, Application US/08475263
; Patent No. 5759994
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,263
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-475-263-139

```

```

Query Match      57.1%; Score 4; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;

```

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 1 AFLL 4

## RESULT 21

US-08-485-886-139  
; Sequence 139, Application US/08485886  
; Patent No. 5798248  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,886  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 139:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-485-886-139

Query Match 57.1%; Score 4; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 1 AFLL 4

## RESULT 22

US-08-477-362-139  
; Sequence 139, Application US/08477362  
; Patent No. 5849507  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,362  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,184  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
INFORMATION FOR SEQ ID NO: 139:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-477-362-139

Query Match 57.1%; Score 4; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 1 AFLL 4

## RESULT 23

US-08-477-134-139  
; Sequence 139, Application US/08477134  
; Patent No. 5856448  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,134  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.



Query Match: 57.1%; Score 4; DB 2; Length 12;

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; TEL#FAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 9
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 12 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: peptide
; US-08-750-856A-9

```

RESULT 26  
US-08-473-489A-139  
; Sequence 139, Application US/08473489A  
; Patent No. 6024936  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.

APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/473,489A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,184  
FILING DATE: 1991-11-07  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-473-489A-139  
Query Match 57.1%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 APLL 4  
Db 1 AFLL 4  
RESULT 27  
US-08-485-695-139  
Sequence 139, Application US/08485695  
Patent No. 6124101  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,695  
FILING DATE: 07-JUN-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,184  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-485-695-139  
Query Match 57.1%; Score 4; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
QY 1 APLL 4  
Db 1 AFLL 4  
RESULT 28  
US-08-018-760-139  
Sequence 139, Application US/08018760  
Patent No. 6197541  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/018,760  
FILING DATE: 17-FEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/789,184  
FILING DATE: 07-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 34-0154  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-018-760-139

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Query Match      57.1%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 1 AFLL 4

RESULT 29
US-08-064-400B-16
; Sequence 16, Application US/08064400B
; Patent No. 5559028
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: Regulation of Antigen Presentation
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/064.400B
; FILING DATE: May 19, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH93-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 207-363-0558
; TELEFAX: 207-363-0528
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-064-400B-16

Query Match      57.1%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQE 7
Db 1 LYQE 4

RESULT 30
US-08-291-601-1
; Sequence 1, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-2

Query Match      57.1%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQE 7
Db 1 LYQE 4

RESULT 31
US-08-291-601-2
; Sequence 2, Application US/08291601
; Patent No. 5679527
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: Maine
; COUNTRY: US
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,601
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M.
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9401M
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-291-601-2
```

Query Match 57.1%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LYQE 7  
 Db 1 LYQE 4

## RESULT 32

US-08-291-601-3  
 ; Sequence 3, Application US/08291601  
 ; Patent No. 5679527  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Humphreys, Robert E.  
 ; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE STRUCTURE  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kevin M. Farrell, P.C.  
 ; STREET: P.O. Box 999  
 ; CITY: York Harbor  
 ; STATE: Maine  
 ; COUNTRY: US  
 ; ZIP: 03911  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/291,601  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Farrell, Kevin M.  
 ; REGISTRATION NUMBER: 35,505  
 ; REFERENCE/DOCKET NUMBER: REH-9401M  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (207) 363-0558  
 ; TELEFAX: (207) 363-0528  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 13 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-291-601-3

Query Match 57.1%; Score 4; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 4 LYQE 7  
 Db 1 LYQE 4

## RESULT 33

US-09-227-357-439  
 ; Sequence 439, Application US/09227357  
 ; Patent No. 6342581  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer et al.  
 ; TITLE OF INVENTION: 123 Human Secreted Proteins  
 ; FILE REFERENCE: P2010P1  
 ; CURRENT APPLICATION NUMBER: US/09/227,357  
 ; CURRENT FILING DATE: 1999-01-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/13684  
 ; EARLIER FILING DATE: 1998-07-07  
 ; EARLIER APPLICATION NUMBER: 60/051,926  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,793  
 ; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,925  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,929  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,803  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,732  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,931  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,932  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,916  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,930  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,918  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,920  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,733  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/052,795  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,919  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/051,928  
 ; EARLIER FILING DATE: 1997-07-08  
 ; EARLIER APPLICATION NUMBER: 60/055,722  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,723  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,948  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,949  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,953  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,950  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,947  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,964  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/056,360  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,684  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,984  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/055,954  
 ; EARLIER FILING DATE: 1997-08-18  
 ; EARLIER APPLICATION NUMBER: 60/058,785  
 ; EARLIER FILING DATE: 1997-09-12  
 ; EARLIER APPLICATION NUMBER: 60/058,664  
 ; EARLIER FILING DATE: 1997-09-12  
 ; EARLIER APPLICATION NUMBER: 60/058,660  
 ; EARLIER FILING DATE: 1997-09-12  
 ; EARLIER APPLICATION NUMBER: 60/058,661  
 ; EARLIER FILING DATE: 1997-09-12  
 ; NUMBER OF SEQ ID NOS: 672  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 439  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-227-357-439

Query Match 57.1%; Score 4; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 2 FLY 5

```
Db          |||||
            7 FLLY 10

RESULT 34
US-08-637-759B-246
; Sequence 246, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/637,759B
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-246

Query Match          57.1%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 AFLL 4
Db          |||||
            3 AFLL 6

RESULT 35
US-09-201-945-246
; Sequence 246, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/637,759
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
```

;; REFERENCE/DOCKET NUMBER: RPMS 101  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (404) 873-8794  
;; TELEFAX: (404) 873-8795  
;; INFORMATION FOR SEQ ID NO: 246:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 15 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; HYPOTHETICAL: NO  
US-09-201-945-246

Query Match 57.1%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 3 AFLL 6

RESULT 37  
US-08-205-697A-42  
; Sequence 42, Application US/08205697A  
; Patent No. 6218510  
; GENERAL INFORMATION:  
; APPLICANT: Sharpe, Arlene H.  
; APPLICANT: Bortello, Francescopaolo  
; APPLICANT: Freeman, Gordon J.  
; APPLICANT: Nadler, Lee M.  
; TITLE OF INVENTION: and Uses Therefor  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/205.697A  
; FILING DATE: 02-Mar-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: BWI-120  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-205-697A-42

Query Match 57.1%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 11 AFLL 14

RESULT 38  
US-08-702-525-42  
; Sequence 42, Application US/08702525  
; Patent No. 6294660  
; GENERAL INFORMATION:  
; APPLICANT: Sharpe, Sharpe  
; APPLICANT: Bortello, Francescopaolo  
; APPLICANT: Freeman, Gordon  
; APPLICANT: Nadler, Lee  
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory  
; TITLE OF INVENTION: Molecules and Uses Therefor  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/702,525  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/205,697  
; FILING DATE: 02-Mar-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: BWI-120CPUS  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-702-525-42

Query Match 57.1%; Score 4; DB 3; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|||  
Db 11 AFLL 14

RESULT 39  
US-09-340-620A-47  
; Sequence 47, Application US/09340620A  
; Patent No. 6482933  
; GENERAL INFORMATION:  
; APPLICANT: Bertin, John  
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THE  
; FILE REFERENCE: 07334-124001  
; CURRENT APPLICATION NUMBER: US/09/340,620A  
; CURRENT FILING DATE: 1999-06-28  
; PRIOR APPLICATION NUMBER: US 09/245,281  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: US 09/207,359  
; PRIOR FILING DATE: 1998-12-08  
; PRIOR APPLICATION NUMBER: US 09/099,041  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: US 09/019,942  
; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-340-620A-47

Query Match 57.1%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4  
Db 13 AFL 16

RESULT 40  
PCT-US95-02576-42  
; Sequence 42, Application PC/TUS9502576  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street, suite 510  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/02576  
; FILING DATE:  
; PRIOR APPLICATION DATA: US 08/205,697  
; FILING DATE: 02-Mar-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mandragouras, Amy E.  
; REGISTRATION NUMBER: 36,207  
; REFERENCE/DOCKET NUMBER: BWI-120CPPC  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 42:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US95-02576-42

Query Match 57.1%; Score 4; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4  
Db 11 AFL 14

RESULT 41  
US-08-401-512-64  
; Sequence 64, Application US/08401512  
; Patent No. 5595673  
; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.

; APPLICANT: Curran, Mark E.  
; APPLICANT: Wang, Qing  
; TITLE OF INVENTION: Long QT Syndrome Genes  
; NUMBER OF SEQUENCES: 81  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3917  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/401,512  
; FILING DATE: 09-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Saxe, Stephen A.  
; REGISTRATION NUMBER: 38,609  
; REFERENCE/DOCKET NUMBER: 19780-113879  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4848  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 64:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-401-512-64

Query Match 57.1%; Score 4; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4  
Db 13 AFL 16

RESULT 42  
US-08-244-116B-9  
; Sequence 9, Application US/08244116B  
; Patent No. 5763159  
; GENERAL INFORMATION:  
; APPLICANT: Simmonds, Peter  
; APPLICANT: Chan, Shiu-Wan  
; APPLICANT: Yap, Peng L.  
; TITLE OF INVENTION: Hepatitis-C Virus Testing  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson, P.A.  
; STREET: 1211 East Morehead Street  
; CITY: Charlotte  
; STATE: No. 5763159th Carolina  
; COUNTRY: United States  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,116B  
; FILING DATE: 15-JUL-1994  
; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02143
; FILING DATE: 20-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 1749-125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 704-377-1561
; TELEFAX: 704-334-2014
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Hepatitis-C virus
; US-08-244-1168-9

Query Match 57.1%; Score 4; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQE 7
Db 11 LYQE 14

RESULT 43
US-09-226-012-99
; Sequence 99, Application US/09226012
; Patent No. 6207383
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Splawski, Igor
; TITLE OF INVENTION: MUTATIONS IN AND GENOMIC STRUCTURE OF HERG - A LONG QT
; TITLE OF INVENTION: SYNDROME GENE
; FILE REFERENCE: 2323-136
; CURRENT APPLICATION NUMBER: US/09/226,012
; CURRENT FILING DATE: 1999-01-06
; EARLIER APPLICATION NUMBER: 09/122,847
; EARLIER FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; TYPE: PRT
; LENGTH: 18
; ORGANISM: Homo sapiens
; US-09-226-012-99

Query Match 57.1%; Score 4; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4
Db 13 AFLL 16

RESULT 44
US-08-507-124-5
; Sequence 5, Application US/08507124
; Patent No. 5670618
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Maureen A.
; TITLE OF INVENTION: Insulin-Like Peptide
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolasch & Birch

```

```

; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,124
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/956,342
; FILING DATE: 05-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1828-102P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Geodia cydonium
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..19
; OTHER INFORMATION: /label= peptide
; OTHER INFORMATION: /note= "Amino-terminal sequence of insulin-like
; OTHER INFORMATION: peptide from Geodia cydonium."
; US-08-507-124-5

Query Match 57.1%; Score 4; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LYQE 7
Db 12 LYQE 15

RESULT 45
US-08-451-472-12
; Sequence 12, Application US/08451472
; Patent No. 5770192
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 5770192th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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US-08-451-472-46  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,472  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,125  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 117-187  
TELEPHONE: (703) 816 4000  
TELEFAX: (703) 816 4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-451-472-12

Query Match 57.1%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFLL 4  
DB 9 AFLL 12

RESULT 46  
US-08-451-472-46  
Sequence 46, Application US/08451472  
Patent No. 5770192  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS  
NUMBER OF SEQUENCES: 73  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon & Vanderhye PC  
STREET: 8th Floor, 1100 No. 5770192th Glebe Road  
CITY: Arlington  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/451,472  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/117,125  
FILING DATE: 24-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary J Wilson  
REGISTRATION NUMBER: 32,955  
REFERENCE/DOCKET NUMBER: 117-187  
TELEPHONE: (703) 816 4000  
TELEFAX: (703) 816 4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 46:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-451-472-46  
Query Match 57.1%; Score 4; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AFLL 4  
DB 9 AFLL 12

RESULT 47  
US-08-928-213B-35  
Sequence 35, Application US/08928213B  
Patent No. 6238905  
GENERAL INFORMATION:  
APPLICANT: McHenry, Charles S.  
Seville, Mark  
Cull, Millard G.  
TITLE OF INVENTION: NOVEL THERMOPHILIC POLYMERASE III  
HOLENZYME  
NUMBER OF SEQUENCES: 195  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,213B  
FILING DATE: 12-Sep-1997  
CLASSIFICATION: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: MacKnight, Kamrin T.  
REGISTRATION NUMBER: 38,230  
REFERENCE/DOCKET NUMBER: ENZYCO-02550  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-705-8410  
TELEFAX: 415-397-8338  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-08-928-213B-35

Query Match 57.1%; Score 4; DB 3; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LYQE 7  
DB 10 LYQE 13

RESULT 48  
US-09-486-580A-4  
Sequence 4, Application US/09486580A  
Patent No. 6329340  
GENERAL INFORMATION:  
APPLICANT: GENSET SA  
TITLE OF INVENTION: HUMAN DEFENSIN DEF-X GENE AND DNAC  
COMPOSITION CONTAINING SAME AND DIAGNOSTIC AND  
THERAPEUTIC APPLICATIONS

NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 550 West C Street  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/486,580A  
FILING DATE: FEBRUARY 25, 2000  
ATTORNEY/AGENT INFORMATION:  
NAME: Hart, Daniel  
REGISTRATION NUMBER: 40,637  
REFERENCE/DOCKET NUMBER: GENSET.064C1  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: SIGNAL PEPTIDE  
ORGANISM: Homo sapiens  
US-09-486-580A-4

Query Match 57.1%; Score 4; DB 4; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 4  
|||  
Db 9 AFL 12

RESULT 49  
US-08-617-929-1  
Sequence 1, Application US/08617929  
Patent No. 5885771  
GENERAL INFORMATION:  
APPLICANT: KUMAZAWA, Toshiaki  
TITLE OF INVENTION: ANTIGENIC PEPTIDE COMPOUND AND  
METHOD OF INVENTION: IMMUNOASSAY  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/617,929  
FILING DATE: 24-APR-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/JP94/01823  
FILING DATE: 28-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6/207695  
FILING DATE: 31-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5/272864

FILING DATE: 29-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Saxe, Bernhard D.  
REGISTRATION NUMBER: 28,665  
REFERENCE/DOCKET NUMBER: 77384/109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-617-929-1

Query Match 57.1%; Score 4; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQE 7  
|||  
Db 14 LYQE 17

RESULT 50  
US-08-460-576-15  
Sequence 15, Application US/08460576  
Patent No. 6033903  
GENERAL INFORMATION:  
APPLICANT: Sisk, William P.  
TITLE OF INVENTION: A METHOD OF EXPRESSING AND SECRETING  
TITLE OF INVENTION: SOLUBLE EXTRACELLULAR DOMAINS OF HUMAN GONADOTROPIN  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,576  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: YUN, Allen C.  
REGISTRATION NUMBER: 37,971  
REFERENCE/DOCKET NUMBER: SISK=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-460-576-15

Query Match 57.1%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 5 AFLL 8

## RESULT 51

US-09-439-313-500  
; Sequence 500, Application US/09439313  
; Patent No. 6329505  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Devin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan Louise  
; APPLICANT: Jiang Yuqui  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Kalos, Michael  
; APPLICANT: Fanger, Gary  
; APPLICANT: Retter, Mark  
; APPLICANT: Solk, John  
; APPLICANT: Day, Craig  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.427C9  
; CURRENT APPLICATION NUMBER: US/09/439,313  
; CURRENT FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 575  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 500  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Made in a lab  
US-09-439-313-500

Query Match 57.1%; Score 4; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AFLL 4  
|  
|  
|  
|  
Db 4 AFLL 7

## RESULT 52

US-07-657-769B-14  
; Sequence 14, Application US/07657769B  
; Patent No. 5256766  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED  
; PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IRELL & MANELLA  
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/657,769B  
; FILING DATE: 19910219  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959

; REFERENCE/DOCKET NUMBER: 2000-0502.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-327-7250  
; TELEFAX: 415-327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-657-769B-14

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
|  
|  
|  
|  
Db 2 FLL 4

## RESULT 53

US-07-657-769B-54  
; Sequence 54, Application US/07657769B  
; Patent No. 5256766  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; TITLE OF INVENTION: RECOMBINANT RECEPTOR AND RELATED  
; PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 69  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: IRELL & MANELLA  
; STREET: 545 MIDDLEFIELD ROAD, SUITE 200  
; CITY: MENLO PARK  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94025  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/657,769B  
; FILING DATE: 19910219  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 2000-0502.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-327-7250  
; TELEFAX: 415-327-2951  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 54:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: AMINO ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-07-657-769B-54

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
|  
|  
|  
|  
Db 2 FLL 4

## RESULT 54

```

US-08-405-933-4
; Sequence 4, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-405-933-4

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 55
US-08-405-933-6
; Sequence 6, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /label= Arg
; OTHER INFORMATION: /note= "Arg is acetylated"
US-08-405-933-6

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 56
US-08-405-933-14
; Sequence 14, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275

```

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/ INFORMATION FOR SEQ ID NO: 14:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-405-933-14

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 57
US-08-405-933-38
; Sequence 38, Application US/08405933
; Patent No. 5516889
; GENERAL INFORMATION:
; APPLICANT: Hollenberg, Morley D.
; APPLICANT: Matsoukas, John M.
; APPLICANT: Moore, Graham J.
; TITLE OF INVENTION: Synthetic Thrombin Receptor Peptides
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: Washington & Prince Streets, P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/405,933
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/080,643
; FILING DATE: 21-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dillahunty, Mary Ann
; REGISTRATION NUMBER: 34,576
; REFERENCE/DOCKET NUMBER: 028722-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)854-7400
; TELEFAX: (415)854-8275
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= Phe
; OTHER INFORMATION: /note= "Phe is n-propionyl Phe"
US-08-405-933-38

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 1 FLL 3

RESULT 59
US-07-789-184-35
; Sequence 35, Application US/07789184
; Patent No. 5688768
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
```

;; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
;; NUMBER OF SEQUENCES: 223  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/789,184  
;; FILING DATE: 19911107  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 22000-20502.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 813-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 34-0154  
;; INFORMATION FOR SEQ ID NO: 35:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 1  
;; OTHER INFORMATION: /note= "This position is Mpr,  
;; US-07-789-184-35

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 2 FLL 4

RESULT 60  
US-07-789-184-109  
;; Sequence 109, Application US/07789184  
;; Patent No. 5688768  
;; GENERAL INFORMATION:  
;; APPLICANT: COUGHLIN, SHAUN R.  
;; APPLICANT: SCARBOROUGH, ROBERT M.  
;; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
;; RELATED PHARMACEUTICALS  
;; NUMBER OF SEQUENCES: 223  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/789,184  
;; FILING DATE: 19911107

;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 22000-20502.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 813-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 34-0154  
;; INFORMATION FOR SEQ ID NO: 109:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-07-789-184-109  
Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 2 FLL 4

RESULT 61  
US-07-789-184-117  
;; Sequence 117, Application US/07789184  
;; Patent No. 5688768  
;; GENERAL INFORMATION:  
;; APPLICANT: COUGHLIN, SHAUN R.  
;; APPLICANT: SCARBOROUGH, ROBERT M.  
;; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
;; RELATED PHARMACEUTICALS  
;; NUMBER OF SEQUENCES: 223  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/789,184  
;; FILING DATE: 19911107  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: MURASHIGE, KATE H.  
;; REGISTRATION NUMBER: 29,959  
;; REFERENCE/DOCKET NUMBER: 22000-20502.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 813-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 34-0154  
;; INFORMATION FOR SEQ ID NO: 117:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4 amino acids  
;; TYPE: AMINO ACID  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 4  
;; OTHER INFORMATION: /note= "This position is L-NH2."  
;; US-07-789-184-117

Query Match 42.9%; Score 3; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
Db 2 FLL 4

RESULT 62  
US-08-549-008-29  
; Sequence 29, Application US/08549008  
; Patent No. 5714342  
; GENERAL INFORMATION:  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of  
; TITLE OF INVENTION: Protease in Biological Samples and Methods of Use Thereof  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/549,008  
; FILING DATE: 27-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,383  
; FILING DATE: 28-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 016865-000110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-549-008-29

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AFL 3  
Db 2 AFL 4

RESULT 63  
US-08-475-263-35  
; Sequence 35, Application US/08475263  
; Patent No. 5759994  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,263  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.

ADDRESSEE: MORRISON & FOERSTER  
STREET: 2000 Pennsylvania Ave., NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,263  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.03  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /note= "This position is Mpr,  
OTHER INFORMATION: S-Me Mpr or Mba."  
US-08-475-263-35

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
Db 2 FLL 4

RESULT 64  
US-08-475-263-109  
; Sequence 109, Application US/08475263  
; Patent No. 5759994  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/475,263  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.03  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 109:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-475-263-109

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
DB 2 FLL 4

RESULT 65  
US-08-475-263-117  
Sequence 117, Application US/08475263  
Patent No. 5759994  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.  
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
TITLE OF INVENTION: RELATED PHARMACEUTICALS  
NUMBER OF SEQUENCES: 223  
CORRESPONDENCE ADDRESS:  
ADDRESSES: MORRISON & FORSTER  
STREET: 2000 Pennsylvania Ave., NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006-1812  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,263  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: MURASHIGE, KATE H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 22000-20502.03  
TELEPHONE: (202) 887-1500  
TELEFAX: (202) 887-0763  
TELEX: 90-4030  
INFORMATION FOR SEQ ID NO: 117:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /note= "this position is L-NH2."  
US-08-475-263-117

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
DB 2 FLL 4  
RESULT 66  
US-08-205-511-1  
Sequence 1, Application US/08205511  
Patent No. 5792451  
GENERAL INFORMATION:  
APPLICANT: Sarubbi, Donald J.  
APPLICANT: Leone-Bay, Andrea  
APPLICANT: Paton, Duncan R.  
TITLE OF INVENTION: ORAL DRUG DELIVERY COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Darby & Darby, P.C.  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/205,511  
FILING DATE: 02-MAR-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Robinson, Joseph R.  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 1946/09323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1  
OTHER INFORMATION: /product= "ACETYL-PHENYLALANINE"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 4  
OTHER INFORMATION: /product= "ARGININE ALDEHYDE"  
US-08-205-511-1

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
DB 1 FLL 3

RESULT 67  
US-08-485-886-35  
Sequence 35, Application US/08485886  
Patent No. 5798248  
GENERAL INFORMATION:  
APPLICANT: COUGHLIN, SHAUN R.  
APPLICANT: SCARBOROUGH, ROBERT M.



```

; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr Or Mba."
US-08-485-886-35

```

```

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 FLL 4
   |||
Db 2 FLL 4

```

```

RESULT 68
US-08-485-886-109
; Sequence 109, Application US/08/485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-485-886-109

```

```

Query Match 42.9%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 FLL 4
   |||
Db 2 FLL 4

```

```

RESULT 69
US-08-485-886-117
; Sequence 117, Application US/08/485886
; Patent No. 5798248
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids

```

;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; FEATURE:  
;; NAME/KEY: Modified-site  
;; LOCATION: 4  
;; OTHER INFORMATION: /note= "This position is L-NH2."  
US-08-485-886-117

Query Match 42.9%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 2 FLL 4

RESULT 70  
US-08-477-362-35  
; Sequence 35, Application US/08477362  
; Patent No. 5849507  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,362  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1  
; OTHER INFORMATION: /note= "This position is Mpr,  
; OTHER INFORMATION: S-Me Mpr or Mba."  
US-08-477-362-35

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4

Db 2 FLL 4

RESULT 71  
US-08-477-362-109  
; Sequence 109, Application US/08477362  
; Patent No. 5849507  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,362  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-477-362-109

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FLL 4  
Db 2 FLL 4

RESULT 72  
US-08-477-362-117  
; Sequence 117, Application US/08477362  
; Patent No. 5849507  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California

```

; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,362
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is L-NH2."
; US-08-477-362-117

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4
Db 2 FLL 4

RESULT 73
US-08-188-583-37
; Sequence 37, Application US/08188583
; Patent No. 5851813
; GENERAL INFORMATION:
; APPLICANT: Desrosiers, Ronald C.
; TITLE OF INVENTION: PRIMATE LENTIVIRUS VACCINES
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: Wordperfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/188,583
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/727,494
; FILING DATE: July 9, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/551,945
; FILING DATE: July 12, 1990

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; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: Reg. No. 5851813 29,066
; REFERENCE/DOCKET NUMBER: 00246/079002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-188-583-37

Query Match 42.9%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LYQ 6
Db 1 LYQ 3

RESULT 74
US-08-477-134-35
; Sequence 35, Application US/08477134
; Patent No. 5856448
; GENERAL INFORMATION:
; APPLICANT: COUGHLIN, SHAUN R.
; APPLICANT: SCARBOROUGH, ROBERT M.
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
; TITLE OF INVENTION: RELATED PHARMACEUTICALS
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,134
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/789,184
; FILING DATE: 07-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 22000-20502.20
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 34-0154
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /note= "This position is Mpr,
; OTHER INFORMATION: S-Me Mpr or Mba."

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US-08-477-134-35

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|  
|  
|  
Db 2 FLL 4

RESULT 75

US-08-477-134-109  
; Sequence 109, Application US/08477134  
; Patent No. 5856448  
; GENERAL INFORMATION:  
; APPLICANT: COUGHLIN, SHAUN R.  
; APPLICANT: SCARBOROUGH, ROBERT M.  
; TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
; TITLE OF INVENTION: RELATED PHARMACEUTICALS  
; NUMBER OF SEQUENCES: 223  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,134  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/789,184  
; FILING DATE: 07-NOV-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MURASHIGE, KATE H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 22000-20502.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 34-0154  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-477-134-109

Query Match 42.9%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FLL 4  
|  
|  
|  
Db 2 FLL 4

Search completed: November 25, 2003, 20:30:04  
Job time : 6.65698 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 5.48837 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFFILV 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

PIR 76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	75.0	15	2	PS0452
2	4	50.0	15	2	A56970
3	3	37.5	6	2	A61049
4	3	37.5	8	2	A61328
5	3	37.5	9	2	S15850
6	3	37.5	9	2	S66419
7	3	37.5	10	2	S26506
8	3	37.5	11	2	S33782
9	3	37.5	11	2	PA0028
10	3	37.5	11	2	FU0029
11	3	37.5	11	2	I33098
12	3	37.5	12	4	PC2390
13	3	37.5	11	4	PC2391
14	3	37.5	11	4	PC2392
15	3	37.5	11	4	PC2393
16	3	37.5	12	2	S11298
17	3	37.5	12	2	S67528
18	3	37.5	12	2	PQ0696
19	3	37.5	12	2	S43957
20	3	37.5	12	2	PN0046
21	3	37.5	12	4	JX0315
22	3	37.5	13	2	PQ0700
23	3	37.5	13	2	A61514
24	3	37.5	13	2	S33273
25	3	37.5	13	2	C53275
26	3	37.5	14	2	B61309
27	3	37.5	14	2	S09721
28	3	37.5	14	2	B28018
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30	3	37.5	15	1	LFTWL
31	3	37.5	15	2	A28497
32	3	37.5	15	2	PW0004
33	3	37.5	15	2	S20410
34	3	37.5	15	2	PA0024
35	3	37.5	15	2	PS0455
36	3	37.5	16	2	A42411
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39	3	37.5	16	2	S78415
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41	3	37.5	17	2	G85956
42	3	37.5	18	2	S09722
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44	3	37.5	18	2	S13974
45	3	37.5	18	2	S40502
46	3	37.5	19	1	BWSMCN
47	3	37.5	19	2	T30825
48	3	37.5	20	2	S65399
49	3	37.5	20	2	S61278
50	3	37.5	20	2	S09720
51	3	37.5	20	2	B30208
52	3	37.5	20	2	S58382
53	3	37.5	20	2	B53283
54	3	37.5	20	2	A60801
55	2	25.0	3	3	PQ0010
56	2	25.0	4	2	B43848
57	2	25.0	4	2	T46627
58	2	25.0	4	2	S53508
59	2	25.0	4	2	P70675
60	2	25.0	4	2	S47552
61	2	25.0	5	2	C41225
62	2	25.0	5	2	B60274
63	2	25.0	5	2	B37988
64	2	25.0	5	2	J50319
65	2	25.0	5	2	P70267
66	2	25.0	5	2	J70520
67	2	25.0	5	2	P70525
68	2	25.0	5	2	P70608
69	2	25.0	5	2	P70669
70	2	25.0	5	2	P70695
71	2	25.0	5	2	P70700
72	2	25.0	6	2	A60986
73	2	25.0	6	2	PQ0008
74	2	25.0	6	2	I51317
75	2	25.0	6	2	I51434
76	2	25.0	6	2	A41946
77	2	25.0	7	2	S71867
78	2	25.0	7	2	S71870
79	2	25.0	7	2	PH1408
80	2	25.0	7	2	PQ0663
81	2	25.0	7	2	A44428
82	2	25.0	7	2	A25269
83	2	25.0	7	2	A30812
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85	2	25.0	7	2	PQ0728
86	2	25.0	7	2	A33098
87	2	25.0	7	2	P70246
88	2	25.0	7	2	S42620
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90	2	25.0	7	2	P70515
91	2	25.0	7	2	P70620
92	2	25.0	7	2	P70556
93	2	25.0	7	2	P70542
94	2	25.0	7	2	P70676
95	2	25.0	7	2	P70671
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97	2	25.0	7	2	B48394
98	2	25.0	7	4	I55382
99	2	25.0	7	4	S15597
100	2	25.0	8	2	PH1407

leu leader peptide  
neurotensin-relate  
chlorophyll a/b-bi  
protein kinase (BC  
protein QA300050 -  
superoxide dismuta  
myosin light chain  
T cell receptor al  
hemoglobin beta-x  
ribosomal protein  
gene R81 protein -  
hypothetical prote  
2S albumin small c  
2S albumin small c  
chlorophyll a/b-bi  
20-alpha-hydroxyat  
cinnamycin - Strep  
RNA polymerase bet  
immunodeficiency v  
nikkomycin synthe  
2S albumin small c  
hypothetical prote  
hypothetical prote  
major cat allergen  
acrosome stabilizi  
angiotensin-conver  
cell surface adhes  
hypothetical prote  
starvation-induced  
T-cell receptor be  
ubiquitin - rat  
copper resistance  
major protein anti  
acid proteinase li  
subesophageal gang  
Ig heavy chain CRD  
Ig kappa chain V-I  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
T-cell receptor be  
N-formyl oligopept  
angiotensin-conver  
bHLH transcription  
H4 histone - Afri  
T-cell receptor ga  
glutathione transf  
glutathione transf  
Ig heavy chain V r  
membrane protein -  
platelet aggregati  
sex pheromone CAM3  
sex pheromone cCF1  
omega-gliadine 1,  
unidentified 5.0/1  
244k exoantigen -  
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aggreacan - bovine  
Ig mu chain D regi  
T-cell receptor be  
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T-cell receptor be  
glucuronosyltransf  
major fat-globule  
hypothetical pepti  
orf 4 xara 5-regi  
Ig heavy chain V r

## ALIGNMENTS

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RESULT 1
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C;Species: Oryza sativa (rice)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C;Accession: PS0452
R;Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PS0452
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Experimental source: bran, strain Nihonbare
C;Comment: molecular weight 32K, pI 5.3.

Query Match 75.0%; Score 6; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPFIL 7
DB 5 GPPFIL 10

RESULT 2
A56970
GLYMA1 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 02-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 08-Sep-1995
C;Accession: A56970
R;Codina, M.R.
submitted to the Protein Sequence Database, September 1995
A;Reference number: A56970
A;Accession: A56970
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <COD>

Query Match 50.0%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 11 RGPF 14

RESULT 3
A61049
halo-toxin - Pseudomonas syringae pv. mori
C;Species: Pseudomonas syringae pv. mori
A;Note: host mulberry tree
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
C;Accession: A61049
R;Kajimoto, T.; Yokomizo, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata, M.
Chem. Lett. 00, 679-680, 1989
A;Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas syri
A;Reference number: A61049
A;Accession: A61049
A;Molecule type: protein
A;Residues: 1-6 <KAJ>
A;Note: sequence confirmed by synthesis
C;Comment: This toxin is one of the etiological agents of halo bright disease in mulberry
C;Keywords: toxin

Query Match 37.5%; Score 3; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5

```

DB 1 PFP 3

## RESULT 4

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A61328
trypsin (EC 3.4.21.4) precursor - minke whale (fragment)
C;Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C;Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C;Accession: A61328
R;Bricteux-Gregoire, S.; Schyns, R.; Florquin, M.; Emmens, M.; Welling, G.W.; Beintema
Biochim. Biophys. Acta 386, 244-255, 1975
A;Title: N-terminal amino acid sequence of trypsinogen from the lesser rorqual, Balaen
creas.
A;Reference number: A61328; MUID:75146765; PMID:1125273
A;Accession: A61328
A;Molecule type: protein
A;Residues: 1-8 <BRI>
C;Keywords: hydrolase; protein digestion; serine proteinase; zymogen
F;1-8/Domain: activation peptide #status experimental <APT>

Query Match 37.5%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
DB 1 FPI 3

RESULT 5
S15850
vitamin D3 26-monoxygenase (EC 1.14.14.-) cytochrome P450 27 - pig (fragment)
N;Alternate names: cytochrome P450(26); vitamin D3 26-hydroxylase
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
C;Accession: S15850
R;Bergman, T.; Postlind, H.
Biochem. J. 276, 427-432, 1991
A;Title: Characterization of mitochondrial cytochromes P-450 from pig kidney and liver
A;Reference number: S15850; MUID:91264797; PMID:2049072
A;Accession: S15850
A;Molecule type: protein
A;Residues: 1-9 <BIO>
C;Genetics:
A;Gene: CYP27
C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C;Keywords: heme; mitochondrion; monooxygenase; oxidoreductase; transmembrane protein

Query Match 37.5%; Score 3; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
DB 6 GPF 8

RESULT 6
S66419
tetrameric proteinase precursor, 60K, dithiothreitol-sensitive - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997
C;Accession: S66419
R;Kuwabara, T.
FEBS Lett. 371, 195-198, 1995
A;Title: The 60-kDa precursor to the dithiothreitol-sensitive tetrameric protease of
A;Reference number: S66419; MUID:95402209; PMID:7672127
A;Accession: S66419
A;Molecule type: protein
A;Residues: 1-9 <KUW>

Query Match 37.5%; Score 3; DB 2; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7  
|||  
Db 2 PIL 4

RESULT 7  
S26506  
collagen alpha 1(VI) chain - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Dec-1998  
C;Accession: S26506  
R;Jander, R.; Rautenberg, J.; Glanville, R.W.  
Eur. J. Biochem. 133, 39-46, 1983  
A;Title: Further characterization of the three polypeptide chains of bovine and human skin  
A;Reference number: S26506; MUID:83203648; PMID:6852033  
A;Accession: S26506  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <JAN>  
C;Keywords: hydroxyproline  
F;9/Modified site: hydroxyproline (Pro) #status experimental

Query Match 37.5%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3  
|||  
Db 6 RGP 8

RESULT 8  
S33782  
acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcescens  
C;Species: Serratia marcescens  
C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C;Accession: S33782  
R;Yang, J.H.; Kim, S.S.  
Biochim. Biophys. Acta 1157, 178-184, 1993  
A;Title: Purification and characterization of the valine sensitive acetolactate synthase  
A;Reference number: S33781; MUID:93283409; PMID:8507653  
A;Accession: S33782  
A;Molecule type: protein  
A;Residues: 1-11 <YAN>  
A;Experimental source: ATCC 25419  
C;Complex: heterotetramer; two small and two large chains  
C;Function:  
A;Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alp  
A;Pathway: valine, leucine, and isoleucine biosynthesis  
A;Note: this isoenzyme exhibits homotropic allosterism with pyruvate  
C;Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; h

Query Match 37.5%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
|||  
Db 2 ILV 4

RESULT 9  
PA0028  
Protein QA300042 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0028  
R;Kano, M.; Kawakami, T.; Miyatake, N.; Taugita, A.  
submitted to JPIID, July 1994  
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional

A;Reference number: PA0001  
A;Accession: PA0028  
A;Molecule type: protein  
A;Residues: 1-11 <KAM>  
A;Experimental source: seed  
C;Keywords: seed

Query Match 37.5%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5  
|||  
Db 6 PFP 8

RESULT 10  
PU0029  
33K protein 3218 - rice (strain Nohonbare) (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
C;Accession: PU0029  
R;Taugita, A.; Miyatake, N.  
submitted to JPIID, April 1993  
A;Reference number: PS0208  
A;Accession: PU0029  
A;Molecule type: protein  
A;Residues: 1-11 <TSU>  
A;Experimental source: bran  
C;Comment: molecular weight 33K, pI 6.0.

Query Match 37.5%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GFP 4  
|||  
Db 5 GFP 7

RESULT 11  
I33098  
173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
C;Accession: I33098  
R;Nichols, J.H.; Hager, L.P.  
submitted to the Protein Sequence Database, May 1990  
A;Reference number: A33098  
A;Accession: I33098  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <NIC>

Query Match 37.5%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6  
|||  
Db 9 FPI 11

RESULT 12  
PC2390  
trichorozin I - fungus (Trichoderma harzianum)  
C;Species: Trichoderma harzianum  
C;Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000  
C;Accession: PC2390  
R;Iida, A.; Sanekata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai  
Chem. Pharm. Bull. 43, 392-397, 1995  
A;Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichorozins I-IV  
A;Reference number: PC2390; MUID:95292356; PMID:7539721

A:Accession: PC2390  
A:Status: unencoded polypeptide  
A:Molecule type: protein  
A:Residues: 1-11 <IID>  
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.  
C:Keywords: antibiotic; unencoded polypeptide  
F:1/Modified site: acetylated amino end #status experimental  
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental  
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
Db 6 PIL 8

RESULT 13  
PC2391  
trichoroxin II - fungus (Trichoderma harzianum)  
C:Species: Trichoderma harzianum  
C:Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000  
C:Accession: PC2391  
R:Ida, A.; Saneakata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995  
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichoroxins I-IV, A:Reference number: PC2390; MUID:95292356; PMID:7539721  
A:Accession: PC2391  
A:Status: unencoded polypeptide  
A:Molecule type: protein  
A:Residues: 1-11 <IID>  
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.  
C:Keywords: antibiotic; unencoded polypeptide  
F:1/Modified site: acetylated amino end #status experimental  
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental  
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
Db 6 PIL 8

RESULT 14  
PC2392  
trichoroxin III - fungus (Trichoderma harzianum)  
C:Species: Trichoderma harzianum  
C:Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000  
C:Accession: PC2392  
R:Ida, A.; Saneakata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995  
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichoroxins I-IV, A:Reference number: PC2390; MUID:95292356; PMID:7539721  
A:Accession: PC2392  
A:Status: unencoded polypeptide  
A:Molecule type: protein  
A:Residues: 1-11 <IID>  
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.  
C:Keywords: antibiotic; unencoded polypeptide  
F:1/Modified site: acetylated amino end #status experimental  
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental  
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
Db 6 PIL 8

Db 6 PIL 8

RESULT 15  
PC2393  
trichoroxin IV - fungus (Trichoderma harzianum)  
C:Species: Trichoderma harzianum  
C:Date: 17-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Oct-2000  
C:Accession: PC2393  
R:Ida, A.; Saneakata, M.; Wada, S.; Fujita, T.; Tanaka, H.; Enoki, A.; Fuse, G.; Kanai, Chem. Pharm. Bull. 43, 392-397, 1995  
A:Title: Fungal metabolites. XVIII. New membrane-modifying peptides, trichoroxins I-IV, A:Reference number: PC2390; MUID:95292356; PMID:7539721  
A:Accession: PC2393  
A:Status: unencoded polypeptide  
A:Molecule type: protein  
A:Residues: 1-11 <IID>  
C:Comment: This peptide exhibits voltage-dependent ion channel-like activity in lipid bilayers.  
C:Keywords: antibiotic; unencoded polypeptide  
F:1/Modified site: acetylated amino end #status experimental  
F:1,5,9/Modified site: 2-amino-2-methylpropanoic acid #status experimental  
F:11/Modified site: valinol #status experimental

Query Match 37.5%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
Db 6 PIL 8

RESULT 16  
S11298  
hemagglutinin precursor - influenza A virus (strain A/FPV/Rostock/34 [H7N1]) (fragment)  
C:Species: influenza A virus  
C:Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 08-Apr-1994  
C:Accession: S11298  
R:Robertson, J.S.  
Nucleic Acids Res. 6, 3745-3757, 1979  
A:Title: 5' and 3' terminal nucleotide sequences of the RNA genome segments of influenza A virus  
A:Reference number: S11286; MUID:80034428; PMID:493121  
A:Accession: S11298  
A:Molecule type: genomic RNA  
A:Residues: 1-12 <ROB>  
A:Cross-references: GB:J02111  
C:Genetics:  
A:Map position: segment 4  
A:Superfamily: influenza virus hemagglutinin  
C:Keywords: homotrimer

Query Match 37.5%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8  
Db 5 ILV 7

RESULT 17  
S67528  
napin - rape (fragments)  
C:Species: Brassica napus (rape)  
C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S67528  
R:Murn, E.; Ek, B.; Rask, L.  
Eur. J. Biochem. 227, 316-321, 1995  
A:Title: Processing of the 2S storage protein pronapin in Brassica napus and in transgenic Arabidopsis thaliana  
A:Reference number: S67528; MUID:95154306; PMID:7851402  
A:Accession: S67528  
A:Status: preliminary



A:Molecule type: protein  
A:Residues: 1-6;7-12 <WUR>

Query Match 37.5%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 3 GPF 5

## RESULT 18

PQ0696

1,4-alpha-glucan branching enzyme (EC 2.4.1.18) [imported] - rice (fragment)

C:Species: Oryza sativa (rice)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PQ0696  
R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension  
A:Reference number: PQ0696

A:Accession: PQ0696

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <KOM>

C:Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase

Query Match 37.5%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 5 GPF 7

## RESULT 19

S43957

Ig mu chain V region (clone 3) - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C:Accession: S43957  
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A:Reference number: S43956; PMID:94248036; PMID:8190629

A:Accession: S43957

A:Molecule type: DNA

A:Residues: 1-12 <WAG>

C:Keywords: immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 4 GPF 6

## RESULT 20

PN0046

ATP synthase D chain, mitochondrial - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 29-Oct-1997 #sequence\_revision 29-Oct-1997 #text\_change 23-Jan-1998  
C:Accession: PN0046  
R:Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A:Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro  
A:Reference number: PN0041

A:Accession: PN0046

A:Molecule type: protein

A:Residues: 1-12 <KAT>  
A:Experimental source: neuroblastoma cell  
C:Comment: The molecular mass is 24,400 and the pI is 5.37. The amino-terminus is blo  
C:Keywords: brain; mitochondrion

Query Match 37.5%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
|||  
Db 8 PIL 10

## RESULT 21

JX0315

aminotransferase chimera DY18 - synthetic (fragment)

C:Species: synthetic  
C:Date: 28-May-1999 #sequence\_revision 28-May-1999 #text\_change 28-May-1999  
C:Accession: JX0315  
R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.  
J. Biochem. 115, 568-577, 1994

A:Title: Construction of aminotransferase chimeras and analysis of their substrate sp  
A:Reference number: JX0315; MUID:94334304; PMID:8056774

A:Accession: JX0315

A:Molecule type: DNA

A:Residues: 1-12 <MIY>

C:Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransf  
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction  
C:Keywords: aminotransferase

Query Match 37.5%; Score 3; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
|||  
Db 5 PIL 7

## RESULT 22

PQ0700

unidentified 6.3/40K protein [imported] - rice (fragment)

C:Species: Oryza sativa (rice)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: PQ0700  
R:Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimens  
A:Reference number: PQ0696

A:Accession: PQ0700

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <KOM>

Query Match 37.5%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8  
|||  
Db 11 ILV 13

## RESULT 23

AG1514

glutathione transferase (EC 2.5.1.18), 26k - fluke (Schistosoma japonicum) (fragment)

C:Species: Schistosoma japonicum  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 07-May-1999  
C:Accession: AG1514  
R:Mitchell, G.F.

Mol. Biochem. Parasitol. 27, 249-256, 1988

A:Title: Expression of an enzymatically active parasite molecule in Escherichia coli:

A;Reference number: A61514; MUID:88142994; PMID:3278228  
A;Accession: A61514  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <MIT>  
C;Keywords: transférase

Query Match 37.5%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGP 7  
|||  
DB 2 RGP 4

## RESULT 24

S33273  
85K glycoprotein - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 07-May-1999  
C;Accession: S33273; S33274  
R;Cunningham, H.B.; Yazaki, P.J.; Domingo, R.C.; Oades, K.V.; Bohlen, H.; Sabbadini, R.A.  
Arch. Biochem. Biophys. 303, 32-43, 1993  
A;Title: The skeletal muscle transverse tubular Mg-ATPase: identity with Mg-ATPases of S  
A;Reference number: S33272; MUID:93256569; PMID:8489264  
A;Accession: S33273  
A;Molecule type: protein  
A;Residues: 1-13 <CUN>  
A;Experimental source: gizzard  
A;Accession: S33274  
A;Molecule type: protein  
A;Residues: 1-13 <CUW>  
A;Experimental source: brain  
C;Keywords: glycoprotein

Query Match 37.5%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGP 7  
|||  
DB 6 RGP 8

## RESULT 25

C53275  
Ig kappa-1 chain J3 segment b95 allotype - rabbit (fragment)  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 16-Aug-1996  
C;Accession: C53275  
R;Ayadi, H.; Marche, P.N.; Cazenave, P.A.  
Immunogenetics 34, 201-207, 1991  
A;Title: Evolution of the rabbit immunoglobulin kappa chain genes.  
A;Reference number: A53275; MUID:91372868; PMID:1909995  
A;Accession: C53275  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-13 <AYA>  
A;Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:56164)  
C;Comment: This J3 segment may not be functional because of substitutions in the 7 mer a  
C;Keywords: heterotetramer; immunoglobulin

Query Match 37.5%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
DB 3 RGP 5

## RESULT 26

B61309  
lutropin beta chain - hamster (fragment)  
N;Alternate names: luteinizing hormone beta chain  
C;Species: Cricetinae gen. sp. (hamster)  
C;Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 07-May-1999  
C;Accession: B61309  
R;Glenn, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.  
Endocrinology 111, 1263-1269, 1982  
A;Title: Isolation and characterization of hamster luteinizing hormone.  
A;Reference number: A61309; MUID:83003498; PMID:6889489  
A;Accession: B61309  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <GDE>  
C;Superfamily: pituitary glycoprotein hormone beta chain  
C;Keywords: glycoprotein

Query Match 37.5%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
DB 2 RGP 4

## RESULT 27

S09721  
2S albumin small chain nIII - rape (fragments)  
C;Species: Brassica napus (rape)  
C;Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C;Accession: S09721  
R;Monbalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263, 209-212, 1990  
A;Title: beta-Turns as structural motifs for the proteolytic processing of seed prote  
A;Reference number: S09720; MUID:90242974; PMID:21855951  
A;Accession: S09721  
A;Molecule type: protein  
A;Residues: 1-9;10-14 <MON>  
A;Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RGP 4  
|||  
DB 3 RGP 5

## RESULT 28

B28018  
very late antigen-2 alpha chain - human (fragment)  
N;Alternate names: VLA-2 alpha chain  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994  
C;Accession: B28018  
R;Takada, Y.; Strominger, J.L.; Hemler, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987  
A;Title: The very late antigen family of heterodimers is part of a superfamily of mol  
A;Reference number: A94151; MUID:87204112; PMID:3033641  
A;Accession: B28018  
A;Molecule type: protein  
A;Residues: 1-14 <TAK>  
C;Keywords: duplication; heterodimer; membrane protein

Query Match 37.5%; Score 3; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
DB 12 RGP 14

```

RESULT 29
S36678
dodecenoyl-CoA Delta-isomerase (EC 5.3.3.8) / enoyl-CoA hydratase (EC 4.2.1.17) / 3-hydroxyacyl-CoA lyase (EC 1.1.1.41)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 24-Jul-1998
C;Accession: S36678
R;Chen, N.; Crane, D.I.
Biochem. J. 283, 605-610, 1992
A;Title: Induction of the major integral membrane protein of mouse liver peroxisomes by
A;Reference number: S21285; MUID:92246895; PMID:1575703
A;Accession: S36678
A;Molecule type: protein
A;Residues: 1-14 <CHE>
A;Experimental source: liver
C;Function:
A;Pathway: fatty acid beta-oxidation
C;Keywords: carbon-oxygen lyase; fatty acid beta-oxidation; hydro-lyase; intramolecular

Query Match 37.5%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4
Db 6 GPF 8

RESULT 30
LFTWL
leu leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
C;Accession: S00901
R;Croft, J.E.; Love, D.R.; Bergquist, P.L.
Mol. Gen. Genet. 210, 490-497, 1987
A;Title: Expression of leucine genes from an extremely thermophilic bacterium in Escheri
A;Reference number: S00901; MUID:88121725; PMID:3323845
A;Accession: S00901
A;Molecule type: DNA
A;Residues: 1-15 <CRO>
A;Cross-references: EMBL:X06604; NID:G48244; PID:CAA29823.1; PID:G48245
A;Note: the source is designated as Thermus thermophilus
C;Superfamily: Thermus aquaticus leu leader peptide

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 6 ILV 8

RESULT 31
A28497
neurotensin-related protein - turkey (fragment)
C;Species: Meleagris gallopavo (common turkey)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 23-May-1997
C;Accession: A28497
R;Carraway, R.E.; Cochrane, D.E.; Ruane, S.E.
J. Biol. Chem. 262, 15886-15889, 1987
A;Title: Isolation, structures, and biologic activity of neurotensin-related peptides ge
A;Reference number: A28497; MUID:88058942; PMID:2445741
A;Accession: A28497
A;Molecule type: protein
A;Residues: 1-15 <CAR>
C;Superfamily: collagen alpha 3(VI) chain; animal Kunitz-type proteinase inhibitor homol
C;Keywords: neuropeptide

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 10 RGP 12

RESULT 32
PW0004
chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment)
N;Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein
C;Species: Dunaliella tertiolecta
C;Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C;Accession: PW0004
R;Laroche, J.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from t
A;Reference number: JW0040; MUID:91065528; PMID:2249775
A;Accession: PW0004
A;Molecule type: protein
A;Residues: 1-15 <LAR>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4
Db 13 GPF 15

RESULT 33
S20410
protein kinase (EC 2.7.1.37) - spinach chloroplast (fragment)
N;Alternate names: LHCII protein kinase
C;Species: Chloroplast Spinacia oleracea (spinach)
C;Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C;Accession: S20410
R;Gal, A.; Herrmann, R.G.; Lottspeich, F.; Ohad, I.
PEBS Lett. 298, 33-35, 1992
A;Title: Phosphorylation of cytochrome b6 by the LHC II kinase associated with the cyt
A;Reference number: S20410; MUID:92183823; PMID:1544419
A;Accession: S20410
A;Molecule type: protein
A;Residues: 1-15 <GAL>
C;Genetics:
A;Genome: chloroplast
C;Function:
A;Description: is responsible for the regulation of energy distribution between photo
A;Note: does not exhibit redox-controlled activation
C;Keywords: chloroplast; light-harvesting complex; membrane-associated complex; phospi

Query Match 37.5%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 2 PIL 4

RESULT 34
PA0024
protein QA300050 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0024
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A;Reference number: PA0001

```

A:Accession: PA0024  
 A:Molecule type: protein  
 A:Residues: 1-15 <RAM>  
 A:Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPP 5  
 ||||  
 Db 6 PPP 8

RESULT 35  
 PS0455  
 superoxide dismutase (EC 1.15.1.1) (Mn) - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 05-Mar-1999  
 C:Accession: PS0455  
 R:Tsuigita, A.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0206  
 A:Accession: PS0455  
 A:Molecule type: protein  
 A:Residues: 1-15 <TSU>  
 A:Experimental source: germ  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: metalloprotein; oxidoreductase

Query Match 37.5%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
 ||||  
 Db 7 PIL 9

RESULT 36  
 A42411  
 myosin light chain kinase - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 03-Mar-1995  
 C:Accession: A42411  
 R:Leachman, S.A.; Gallagher, P.J.; Herring, B.P.; McPhaul, M.J.; Stull, J.T.  
 J. Biol. Chem. 267, 4930-4938, 1992  
 A:Title: Biochemical properties of chimeric skeletal and smooth muscle myosin light chain  
 A:Reference number: A42411; MUID:92165861; PMID:1371510  
 A:Accession: A42411  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid; protein  
 A:Residues: 1-16 <LEA>  
 A:Experimental source: skeletal muscle  
 A:Note: sequence extracted from NCBI backbone (NCBIP:84332)

Query Match 37.5%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
 ||||  
 Db 1 RGP 3

RESULT 37  
 PH1790  
 T cell receptor alpha chain V region (clone 2PBL V alpha 24-c) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 C:Accession: PH1790  
 R:Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood lymphocytes

A:Reference number: PH1754; MUID:93301585; PMID:8391057  
 A:Accession: PH1790  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-16 <POR>

Query Match 37.5%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
 ||||  
 Db 6 RGP 8

RESULT 38  
 I46275  
 hemoglobin beta-x chain - goat (fragment)  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 05-Nov-1999  
 C:Accession: I46275  
 R:Haynes, J.R.; Rostock, P.R.; Schon, E.A.; Gallagher, P.M.; Burks, D.J.; Smith, K.; J. Biol. Chem. 255, 6355-6367, 1980  
 A:Title: The isolation of the beta-a-, beta-c-, and gamma-globin genes and a presumpt  
 A:Reference number: I46273; MUID:80227766; PMID:6248519  
 A:Accession: I46275  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-16 <HAY>  
 A:Cross-references: GB:K00659; NID:gl64151; PIDN:AAA30919.1; PID:gl64156

Query Match 37.5%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8  
 ||||  
 Db 5 ILV 7

RESULT 39  
 S78415  
 ribosomal protein RL27, mitochondrial [validated] - rat (tentative sequence) (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jul-2000  
 C:Accession: S78415  
 R:Goldschmidt-Reisin, S.; Graack, H.R.  
 submitted to the Protein Sequence Database, February 1998  
 A:Reference number: S78411  
 A:Accession: S78415  
 A:Molecule type: protein  
 A:Residues: 1-16 <GOL>  
 A:Note: L-Val was also found  
 A:Note: the protein is designated as mitochondrial ribosomal protein L27  
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 37.5%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
 ||||  
 Db 12 RGP 14

RESULT 40  
 I78870  
 gene Rb1 protein - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C:Accession: I78870  
 R:Hogg, A.; Onadim, Z.; Baird, P.N.; Cowell, J.K.  
 Oncogene 7, 1445-1451, 1992  
 A:Title: Detection of heterozygous mutations in the RB1 gene in retinoblastoma patients  
 A:Reference number: I58362; MUID:92319557; PMID:1352398  
 A:Accession: I78870

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-17 <RES>

A:Cross-references: GB:L41911; NID:G794004; PIDN:AAB59483.1; PID:G794005

C:Genetics:

A:Gene: GDB:RB1

A:Cross-references: GDB:I18734; OMIM:180200

A:Map position: 13q14.3-13q14.3

Query Match 37.5%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

Db 1 ILV 3

#### RESULT 41

G85956  
 hypothetical protein Z4331 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C:Species: Escherichia coli

C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001

A:Accession: G85956

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grobeck, E.J.; Davis, N.W.; Lhm, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: G85956

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17 <STO>

A:Cross-references: GB:AE005174; NID:g12517539; PIDN:AAG58115.1; GSPDB:GN00145; UWGP:Z43

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z4331

Query Match 37.5%; Score 3; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFF 5

Db 6 PFF 8

#### RESULT 42

S09722  
 2S albumin small chain 1 nIV - rape (fragments)

C:Species: Brassica napus (rape)

C>Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998

A:Accession: S09722

R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.

FEBS Lett. 263, 209-212, 1990

A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins

A:Reference number: S09720; MUID:90242974; PMID:2185951

A:Accession: S09722

A:Molecule type: protein

A:Residues: 1-9;10-18 <MON>

A:Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

Db |||  
 3 GPF 5

#### RESULT 43

S09723  
 2S albumin small chain 2 nIV - rape (fragments)

C:Species: Brassica napus (rape)

C>Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998

A:Accession: S09723

R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.

FEBS Lett. 263, 209-212, 1990

A:Title: beta-Turns as structural motifs for the proteolytic processing of seed prote

A:Reference number: S09720; MUID:90242974; PMID:2185951

A:Accession: S09723

A:Molecule type: protein

A:Residues: 1-9;10-18 <MON>

A:Experimental source: seed

Query Match 37.5%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

Db 3 GPF 5

#### RESULT 44

S13974  
 chlorophyll a/b-binding protein type I - garden pea (fragment)

C:Species: Pisum sativum (garden pea)

C>Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999

A:Accession: S13974

R:Jahn, P.; Junge, W.

Eur. J. Biochem. 193, 731-736, 1990

A:Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of th.

A:Reference number: S13973; MUID:91065379; PMID:2174365

A:Accession: S13974

A:Molecule type: protein

A:Residues: 1-18 <JAH>

C:Genetics:

A:Genome: nuclear

C:Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylak.

Query Match 37.5%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

Db 6 ILV 8

#### RESULT 45

S40502  
 20-alpha-hydroxysteroid dehydrogenase - Tetrahymena pyriformis

C:Species: Tetrahymena pyriformis

C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 07-Dec-1999

A:Accession: S40502

R:Inazu, A.; Sato, K.; Nakayama, T.; Deyashiki, Y.; Hara, A.; Nozawa, Y.

Biochem. J. 297, 195-200, 1994

A:Title: Purification and characterization of a novel dimeric 20-alpha-hydroxysteroid

A:Reference number: S40502; MUID:94107273; PMID:8280099

A:Accession: S40502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <INA>

C:Genetics:

A:Genetic code: SGC5

Query Match 37.5%; Score 3; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
|||  
Db 13 FPI 15

RESULT 46  
EWSMNCN  
cinnamycin - Streptovorticillium cinnamoneum  
N:Alternate names: lanthiopeptin; lantibiotic Ro 09-0198  
C:Species: Streptovorticillium cinnamoneum  
C>Date: 30-Sep-1993 #sequence\_revision 12-May-1994 #text\_change 07-May-1999  
C:Accession: A45767  
R:Naruse, N.; Temmyo, O.; Tomita, K.; Konishi, M.; Miyaki, H.; Kawaguchi, K.; Fukase, K.  
J. Antibiot. 42, 837-845, 1989  
A:Title: Lanthiopeptin, a new peptide antibiotic. Production, isolation and properties of Tetrahedron Lett. 29, 4771-4772, 1988  
A:Reference number: A45767; MUID:89291558; PMID:2544544  
A:Accession: A45767  
A:Molecule type: protein  
A:Residues: 1-19 <NAR>  
R:Wakamiya, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.  
A:Title: Lanthiopeptin, a new peptide effective against Herpes simplex virus: structural A:Reference number: A53359  
A:Contents: annotation; strain L337-2  
C:Superfamily: cinnamycin precursor  
C:Keywords: antibiotic; beta-hydroxyaspartic acid; lanthionine  
F:1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:4-14/Cross-link: sn-(2S,6R)-lanthionine (Ser-Cys) #status experimental  
F:5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental  
F:6-19/Cross-link: (2xi,9S)-lysinoalanine (Ser-Lys) #status experimental  
F:15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 37.5%; Score 3; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 8 GPF 10

RESULT 47  
T30825  
RNA polymerase beta' chain - Neisseria meningitidis (fragment)  
C:Species: Neisseria meningitidis  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: T30825  
R:Noite, O.J.  
A:Description: Cloning and sequencing of the rpoB gene of Neisseria meningitidis which submitted to the EMBL Data Library, October 1995  
A:Reference number: Z20888  
A:Accession: T30825  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-19 <NOL>  
A:Cross-references: EMBL:Z54353; NID:gl325954; PID:e244319; PIDN:CAA91165.1  
C:Genetics:  
A>Note: rpoC

Query Match 37.5%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
|||  
Db 15 FPI 17

RESULT 48  
S65399  
immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)

C:Species: Homo sapiens (man)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 17-Mar-1999  
C:Accession: S65399  
R:Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.  
Eur. J. Biochem. 237, 64-70, 1996  
A:Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immun immunodeficiency virus type 1 inhibit cleavage of gp120.  
A:Reference number: S65399; MUID:96203909; PMID:8620895  
A:Accession: S65399  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10;11-20 <NIW>  
C:Superfamily: type E retrovirus env polyprotein

Query Match 37.5%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
Db 1 RGP 3

RESULT 49  
S61278  
nikkomycin synthesis protein P4 - Streptomyces tendae (fragment)  
C:Species: Streptomyces tendae  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S61278  
R:Moehle, V.; Roos, U.; Bormann, C.  
Mol. Microbiol. 15, 561-571, 1995  
A:Title: Identification of cellular proteins involved in nikkomycin production in Streptomyces tendae  
A:Reference number: S61278; MUID:95302967; PMID:7783626  
A:Accession: S61278  
A:Molecule type: protein  
A:Residues: 1-20 <MOE>

Query Match 37.5%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 6 GPF 8

RESULT 50  
S09720  
2S albumin small chain nII - rape (fragments)  
C:Species: Brassica napus (rape)  
C>Date: 19-Mar-1997 #sequence\_revision 13-Mar-1998 #text\_change 13-Mar-1998  
C:Accession: S09720  
R:Monsalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.  
FEBS Lett. 263, 209-212, 1990  
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins  
A:Reference number: S09720; MUID:90242974; PMID:2185951  
A:Accession: S09720  
A:Molecule type: protein  
A:Residues: 1-9;10-20 <MON>  
A:Experimental source: seed  
A>Note: 1-Ser was also found

Query Match 37.5%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4  
|||  
Db 3 GPF 5

RESULT 51  
B30208

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hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 18-Jun-1993
C;Accession: B30208
R;Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988
A;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a protein s
A;Reference number: A30208; MUID:80234499; PMID:2967496
A;Accession: B30208
A;Molecule type: DNA
A;Residues: 1-20 <PAL>
A;Cross-references: GB:J03262

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 6 PFP 8

RESULT 52
S58382
hypothetical protein 1 - human
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
C;Accession: S58382
R;Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.
Nucleic Acids Res. 23, 2815-2822, 1995
A;Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron
A;Reference number: S58382; MUID:95388493; PMID:7659502
A;Accession: S58382
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-20 <DIR>
A;Cross-references: ENBL:X83705; NID:g951023; PIDN:CAA58678.1; PID:g951024

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 12 PFP 14

RESULT 53
B53283
major cat allergen Fel d I beta chain - cat (fragment)
C;Species: Felis silvestris catus (domestic cat)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 12-May-1994
C;Accession: B53283
R;Duffort, O.A.; Garreira, J.; Nitti, G.; Polo, F.; Lombardero, M.
Mol. Immunol. 28, 301-309, 1991
A;Title: Studies on the biochemical structure of the major cat allergen Felis domesticus
A;Reference number: A53283; MUID:91287714; PMID:1712068
A;Accession: B53283
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <DUF>

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PFI 6
Db 7 PFI 9

RESULT 54
A60801
acrosome stabilizing factor large chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: A60801
R;Wilson, W.L.; Oliphant, G.
Biol. Reprod. 37, 159-169, 1987
A;Title: Isolation and biochemical characterization of the subunits of the rabbit sper
A;Reference number: A60801; MUID:88000873; PMID:3651543
A;Accession: A60801
A;Molecule type: protein
A;Residues: 1-20 <WIL>
C;Comment: spermatozoa must undergo capacitation and the acrosome reaction to become c
C;Keywords: glycoprotein; semen

Query Match 37.5%; Score 3; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 16 PIL 18

RESULT 55
PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
A;Alternate names: ficus latex peptide 3
C;Species: Ficus carica (common fig)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: PQ0010
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A;Reference number: PQ0008
A;Accession: PQ0010
A;Molecule type: protein
A;Residues: 1-3 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 2; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
Db 1 LV 2

RESULT 56
B43848
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995
C;Accession: B43848
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
Infect. Immun. 60, 899-906, 1992
A;Title: Binding of heparan sulfate to Staphylococcus aureus.
A;Reference number: A43848; MUID:92176005; PMID:1541563
A;Accession: B43848
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-4 <LIA>
A;Note: sequence extracted from NCBI backbone (NCBIF:85444)

Query Match 25.0%; Score 2; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
Db 2 LV 3

```

## RESULT 57

T46627  
 hypothetical protein c4 - loblolly pine  
 C:Species: Pinus taeda (loblolly pine)  
 C>Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
 C:Accession: T46627  
 R:Chang, S.; Puryear, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.  
 submitted to the EMBL Data Library, July 1995  
 A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do  
 A:Reference number: Z23105  
 A:Accession: T46627  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-4 <CHA>  
 A:Cross-references: EMBL:U31309; NID:g974285; PID:g974292  
 A:Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 25.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8  
 ||  
 3 LV 4

Db

## RESULT 58

S53508  
 starvation-induced ribonuclease - tomato  
 C:Species: Lycopersicon esculentum (tomato)  
 C>Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 C:Accession: S53508  
 R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.  
 Plant Mol. Biol. 27, 477-485, 1995  
 A>Title: cDNA structure and regulatory properties of a family of starvation-induced ribo  
 A:Reference number: S53506; MUID:95201242; PMID:7894013  
 A:Accession: S53508  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <KOE>

Query Match 25.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EP 5  
 ||  
 1 FP 2

Db

## RESULT 59

PT0675  
 T-cell receptor beta chain V-D-J region (140-IAC) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0675  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0675  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-4 <PEE>  
 A:Experimental source: day 18 fetal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3  
 ||

Db

||  
 3 GP 4

## RESULT 60

S47552  
 ubiquitin - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 17-Mar-1999  
 C:Accession: S47552  
 R:Hubbard, M.J.; Carne, A.  
 Biochim. Biophys. Acta 1200, 191-196, 1994  
 A>Title: Differential feeding-related regulation of ubiquitin and calbindin(9kDa) in  
 A:Reference number: S47552; MUID:94304928; PMID:8031840  
 A:Accession: S47552  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-4 <HUB>

Query Match 25.0%; Score 2; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2  
 ||  
 2 RG 3

Db

## RESULT 61

C41225  
 copper resistance protein - Pseudomonas syringae pv. tomato (fragment)  
 C:Species: Pseudomonas syringae pv. tomato  
 C>Date: 19-Jun-1992 #sequence\_revision 19-Jun-1992 #text\_change 24-Jun-1993  
 C:Accession: C41225  
 R:Cha, J.S.; Cooksey, D.A.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991  
 A>Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer  
 A:Reference number: A41225; MUID:92020961; PMID:1924351  
 A:Accession: C41225  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <CHA>

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8  
 ||  
 4 LV 5

Db

## RESULT 62

E60274  
 major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)  
 C:Species: Mycobacterium tuberculosis  
 C>Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C:Accession: E60274  
 R:Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A>Title: Isolation and partial characterization of major protein antigens in the cult  
 A:Reference number: A60274; MUID:91099989; PMID:1898899  
 A:Accession: E60274  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <NAG>

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6  
 ||



Db 3 PI 4

## RESULT 63

B37986  
 C:Species: Physarum polycephalum  
 C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
 C:Accession: B37988  
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og  
 J. Biol. Chem. 265, 19898-19903, 1990  
 A:Title: Purification and characterization of a novel intracellular acid proteinase from  
 A:Reference number: A37988; MUID:91060608; PMID:2246266  
 A:Accession: B37988  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-5 <MUR>

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PI 6

Db 4 PI 5

## RESULT 64

JS0319  
 C:Species: Acheta domesticus (house cricket)  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
 C:Accession: JS0319  
 R:Wicker, C.; Wicker, C.  
 Comp. Biochem. Physiol. C 88, 185-187, 1987  
 A:Title: Isolation and structure of a peptide isolated from the subesophageal ganglion  
 A:Reference number: JS0319  
 A:Accession: JS0319  
 A:Molecule type: protein  
 A:Residues: 1-5 <WIC>

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4

Db 4 PF 5

## RESULT 65

PT0267  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C:Accession: PT0267  
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
 A:Reference number: PT0222; MUID:91108337; PMID:1899102  
 A:Accession: PT0267  
 A:Molecule type: DNA  
 A:Residues: 1-5 <YAM>  
 A:Experimental source: B lymphocyte  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3

Db 3 GP 4

## RESULT 66

JT0520  
 C:Species: Homo sapiens (man)  
 C:Date: 23-Oct-1992 #sequence\_revision 23-Oct-1992 #text\_change 16-Aug-1996  
 C:Accession: JT0520  
 R:Anker, R.; Conley, M.E.; Pollok, B.A.  
 J. Exp. Med. 169, 2109-2119, 1989  
 A:Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglob  
 A:Reference number: JT0511; MUID:89279157; PMID:2786547  
 A:Accession: JT0520  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <ANK>  
 A>Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangeme  
 A:Note: a stop codon terminates the sequence in the V region  
 C:Keywords: heterotetramer; immunoglobulin  
 P:1-5/Domain: V kappa region <VRE>

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3

Db 4 GP 5

## RESULT 67

PT0525  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0525  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0525  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FEE>  
 A:Experimental source: adult thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RG 2

Db 3 RG 4

## RESULT 68

PT0608  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C:Accession: PT0608  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0608  
 A>Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-5 <FEE>  
 A:Experimental source: newborn thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 1 RG 2  
Db 4 RG 5

RESULT 69  
PT0669  
T-cell receptor beta chain V-D-J region (121-3BH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0669  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0669  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-5 <P>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 2 GP 3  
Db 4 GP 5

RESULT 70  
PT0695  
T-cell receptor beta chain V-D-J region (135-1D) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0695  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0695  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-5 <P>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 1 RG 2  
Db 4 RG 5

RESULT 71  
PT0700  
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0700  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0700  
A;Status: translation not shown  
A;Molecule type: DNA

A;Residues: 1-5 <P>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 25.0%; Score 2; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 1 RG 2  
Db 4 RG 5

RESULT 72  
A60986  
N-formyl oligopeptide - Escherichia coli (fragment)  
C;Species: Escherichia coli  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 31-Dec-1993  
C;Accession: A60986  
R;Broom, M.F.; Mellor, D.M.; Chadwick, V.S.  
Experientia 45, 1097-1099, 1989  
A;Title: Purification and amino acid sequencing of naturally occurring N-formyl-methionine  
A;Reference number: A60986; MUID:90092408; PMID:2689204  
A;Accession: A60986  
A;Molecule type: protein  
A;Residues: 1-6 <P>  
C;Comment: This hexapeptide was the longest of several N-formyl oligopeptides reported.  
F;1/Modified site: N-formylmethionine #status experimental

Query Match 25.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 6 IL 7  
Db 4 IL 5

RESULT 73  
PQ0008  
angiotensin-converting enzyme inhibitor (FLP-1) - common fig  
N;Alternate names: ficus latex peptide 1  
C;Species: Ficus carica (common fig)  
C;Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
C;Accession: PQ0008  
R;Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A;Reference number: PQ0008  
A;Accession: PQ0008  
A;Molecule type: protein  
A;Residues: 1-6 <MAR>  
A;Experimental source: latex  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
QY 5 PI 6  
Db 4 PI 5

RESULT 74  
I51317  
bHLH transcription factor inhibitor - African clawed frog (fragment)  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C;Accession: I51317  
R;Zhang, H.; Reynaud, S.; Kloc, M.; Etkin, L.D.; Spohr, G.  
Mech. Dev. 50, 119-130, 1995  
A;Title: Id gene activity during Xenopus embryogenesis.

A:Reference number: I51316; MUID:95344988; PMID:7619724  
A:Accession: I51317  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <ZHA>  
A:Cross-references: GB:S79038; NID:g1042006; PIDN:AAD14294.1; PID:g4361994  
C:Genetics:  
A:Gene: Xid1b

Query Match 25.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
||  
Db 5 PF 6

RESULT 75  
I51434  
H4 histone - African clawed frog (fragment)  
C:Species: Xenopus laevis (African clawed frog)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51434  
R:Woodland, H.R.; Warrington, J.R.; Ballantine, J.E.M.; Turner, P.C.  
Nucleic Acids Res. 12, 4939-4958, 1984  
A>Title: Are there major developmentally regulated H4 gene classes in Xenopus?  
A:Reference number: I51391; MUID:84247348; PMID:6330691  
A:Accession: I51434  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-6 <WOO>  
A:Cross-references: GB:K02304; NID:g214227; PIDN:AAA49738.1; PID:g555517

Query Match 25.0%; Score 2; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2  
||  
Db 4 RG 5

Search completed: November 25, 2003, 19:36:12  
Job time : 5.48837 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 2.83721 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPPFLLV 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	37.5	9	1 MGMT_BOVIN	P29177 bos taurus
2	3	37.5	13	1 CREB_VESTR	P17231 vespa tropi
3	3	37.5	13	1 TENC_RANTIE	P56918 rana tempor
4	3	37.5	14	1 JAPI_RANJA	P83305 rana japoni
5	3	37.5	15	1 AFIL_MALPA	P83141 malva parvi
6	3	37.5	15	1 LPL_TRETH	P21234 thermus the
7	3	37.5	15	1 UC06_MAIZE	P80612 zea mays (m
8	3	37.5	16	1 AFIS_MALPA	P83140 malva parvi
9	3	37.5	16	1 TRYP_FELCA	P81071 felis silve
10	3	37.5	18	1 AHD2_TETPY	P35430 tetrahymena
11	3	37.5	19	1 DURA_STRGV	P36504 streptover
12	2	25.0	5	1 PAP2_PARMA	P81864 pardachirus
13	2	25.0	5	1 SUGA_ACHDO	P19991 acheta dome
14	2	25.0	6	1 ET01_LITRU	P82096 litoria rub
15	2	25.0	7	1 CCF1_ENTFA	P20104 enterococu
16	2	25.0	7	1 CIA_ENTFA	P11932 enterococu
17	2	25.0	7	1 FARI_HELTI	P41871 helisoma tr
18	2	25.0	7	1 MNP1_LEPDE	P42984 leptinotars
19	2	25.0	7	1 UF04_MOUSE	P38642 mus musculu
20	2	25.0	7	1 UN06_PINPS	P81675 pinus pinas
21	2	25.0	8	1 ALL5_CARMA	P81818 carcinus ma
22	2	25.0	8	1 ALL6_CARMA	P81819 carcinus ma
23	2	25.0	8	1 ALL5_CALVO	P41841 calliphora
24	2	25.0	8	1 ALL5_CYDPO	P82156 cydia pomon
25	2	25.0	8	1 ALL8_CARMA	P81811 carcinus ma
26	2	25.0	8	1 ALL9_CARMA	P81812 carcinus ma
27	2	25.0	8	1 ANG2_BOTJA	Q10582 bothrops ja
28	2	25.0	8	1 CADI_ENTFA	P13268 enterococu
29	2	25.0	8	1 CPD1_ENTFA	P13269 enterococu
30	2	25.0	8	1 FAR7_ASCSU	P43171 ascaris suu
31	2	25.0	8	1 PKK2_PERAM	P82692 periplaneta
32	2	25.0	8	1 PKK3_PERAM	P82618 periplaneta
33	2	25.0	8	1 RS7_MYCIT	P33564 mycobacteri

## ALIGNMENTS

RESULT 1

34	2	25.0	8	1	RT34_BOVIN	P82929 bos taurus
35	2	25.0	8	1	UPAA_HUMAN	P30096 homo sapien
36	2	25.0	8	1	VGLG_HSV2B	P81780 herpes simp
37	2	25.0	9	1	CCAP_CARMA	P38556 carcinus ma
38	2	25.0	9	1	CONO_CONST	P05487 conus stria
39	2	25.0	9	1	DNFL_LOCMI	P13339 locusta mig
40	2	25.0	9	1	FAR5_PANRE	P82661 panagrellus
41	2	25.0	9	1	FAR9_ASCSU	P41172 ascaris suu
42	2	25.0	9	1	FIBB_PAPAN	P19344 papio anubi
43	2	25.0	9	1	ISOT_CYPCA	P42993 cyprinus ca
44	2	25.0	9	1	KNL3_BOMVA	P83058 bomina var
45	2	25.0	9	1	LMT3_LOCMI	P41489 locusta mig
46	2	25.0	9	1	OXYT_EUPRE	P42995 bufo regula
47	2	25.0	9	1	OXYT_CYPCA	P23879 cyprinus ca
48	2	25.0	9	1	OXYT_OCTVU	P80027 octopus vul
49	2	25.0	9	1	PGLR_DIAAB	P81179 diaprepes a
50	2	25.0	9	1	RE42_LITRU	P82075 litoria rub
51	2	25.0	9	1	SAMP_MUSCA	P19095 mustelus ca
52	2	25.0	9	1	TKL1_LOCMI	P12223 locusta mig
53	2	25.0	9	1	ULAD_HUMAN	P31929 homo sapien
54	2	25.0	9	1	UPA3_HUMAN	P30089 homo sapien
55	2	25.0	9	1	UPA7_HUMAN	P30093 homo sapien
56	2	25.0	10	1	AH3_PRUSE	P29261 prunus sero
57	2	25.0	10	1	ANG1_BOTJA	Q10581 bothrops ja
58	2	25.0	10	1	ANGT_BOVIN	P01017 bos taurus
59	2	25.0	10	1	ANGT_CHICK	P01018 gallus gall
60	2	25.0	10	1	BPP_VIPAS	P13351 vipera aspi
61	2	25.0	10	1	COXO_RAT	P80432 rattus norv
62	2	25.0	10	1	COXO_THUOB	P80982 thunnus obe
63	2	25.0	10	1	ESTA_SCHGA	P81012 schizaphis
64	2	25.0	10	1	FAR6_PANRE	P82660 panagrellus
65	2	25.0	10	1	NS1_MYCTU	P81135 mycobacteri
66	2	25.0	10	1	PVK_LOCMI	P83382 locusta mig
67	2	25.0	10	1	Q20B_COMTE	P80465 comamonas t
68	2	25.0	10	1	RCA_PINPS	P81084 pinus pinas
69	2	25.0	10	1	REPL_PHODV	P35946 phocine dis
70	2	25.0	10	1	SLAP_BACTG	P49325 bacillus th
71	2	25.0	10	1	TRP8_LEOWA	P81740 leucophaea
72	2	25.0	10	1	UPA5_HUMAN	P30091 homo sapien
73	2	25.0	10	1	UXA2_CHLTR	P38003 chlamydia t
74	2	25.0	10	1	XVNB_DICB4	P80717 dictyoglomu
75	2	25.0	11	1	ANGT_CRIGE	P09037 crinia geor
76	2	25.0	11	1	BPP3_BOTIN	P30423 bothrops in
77	2	25.0	11	1	BPP4_BOTIN	P30424 bothrops in
78	2	25.0	11	1	BPP_AGRHP	P04562 agkistrodon
79	2	25.0	11	1	BRK_MEGFL	P12797 magascolia
80	2	25.0	11	1	CORZ_PERAM	P11496 periplaneta
81	2	25.0	11	1	CS15_BACSU	P81095 bacillus su
82	2	25.0	11	1	CSA5_CONAL	P58848 conus aulic
83	2	25.0	11	1	ES1_RAT	P56571 rattus norv
84	2	25.0	11	1	MORN_HUMAN	P01163 homo sapien
85	2	25.0	11	1	RE41_LITRU	P82074 litoria rub
86	2	25.0	11	1	TIN1_HOPTI	P82651 hoplobatr
87	2	25.0	11	1	TIN4_HOPTI	P82654 hoplobatr
88	2	25.0	12	1	FAR7_PENMO	P83322 penaeus mon
89	2	25.0	12	1	FRE1_LITIN	P82021 litoria inf
90	2	25.0	12	1	GRAR_RANRU	P40754 rana rugosa
91	2	25.0	12	1	NUDM_CANFA	P54713 canis famil
92	2	25.0	12	1	PA2B_VIPBO	P31859 vipera beru
93	2	25.0	12	1	RF1_CONSP	P38805 conus spuri
94	2	25.0	12	1	TIN2_HOPTI	P82652 hoplobatr
95	2	25.0	12	1	TIN3_HOPTI	P82653 hoplobatr
96	2	25.0	12	1	V14K_WSSV	P82606 white spot
97	2	25.0	12	1	XYLA_STRVN	P14405 streptomyc
98	2	25.0	13	1	ACT7_SOYBN	P15987 glycine max
99	2	25.0	13	1	AH4_PRUSE	P29262 prunus sero
100	2	25.0	13	1	BLAC_STRGR	P81173 streptomyc

MGMT\_BOVIN  
 ID MGMT\_BOVIN STANDARD; PRT; 9 AA.  
 AC P29177;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Methylated-DNA-protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).  
 DE MGMT.  
 GN Bos taurus (Bovine).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Thymus;  
 RX MEDLINE=90174912; PubMed=2308822;  
 RA Rydberg B., Hall J., Karan P.;  
 RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase.";  
 RL Nucleic Acids Res. 18:17-21(1990).  
 CC -|- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS IRREVERSIBLY INACTIVATED.  
 CC -|- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.  
 CC -|- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
 CC InterPro; IPR001497; Methyltransf\_1.  
 DR PROSITE; PS00374; MGMT; PARTIAL.  
 KW DNA repair; Transferase; Methyltransferase.  
 FT NON\_TER 1 1  
 FT ACT\_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;  
 Query Match 37.5%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PIL 7  
 DB 4 PIL 6  
 RESULT 2  
 CBRL\_VESTR  
 ID CBRL\_VESTR STANDARD; PRT; 13 AA.  
 AC P17231;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Vespid chemotactic peptide T (VSCP-T).  
 DE Vespa tropica (Hornet).  
 OS Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Vespidae; Vespinae; Vespa.  
 OC NCBI\_TaxID=7450;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Yasuhara T., Nakajima T., Erspaer V.;  
 RL (in) Sakakibara S. (eds.);  
 RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation, Osaka (1983).  
 CC -|- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis of neutrophils.  
 CC Mast cell degranulation; Chemotaxis; Amidation.  
 KW MOD\_RES 13 13 AMIDATION.  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PIL 7  
 DB 3 PIL 5  
 RESULT 3  
 TEMC\_RANTZ  
 ID TEMC\_RANTZ STANDARD; PRT; 13 AA.  
 AC F56918;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Temporin C.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OC NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=9022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L., Barra D.;  
 RT "Temporins, antimicrobial peptides from the European red frog Rana temporaria.";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -|- FUNCTION: Has antibacterial activity against Gram-positive bacteria.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Skin.  
 CC -|- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 13 13 AMIDATION.  
 SQ SEQUENCE 13 AA; 1363 MW; 2201403A655B2448 CRC64;  
 Query Match 37.5%; Score 3; DB 1; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PIL 7  
 DB 3 PIL 5  
 RESULT 4  
 JAPI\_RANJA  
 ID JAPI\_RANJA STANDARD; PRT; 14 AA.  
 AC F83305;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Japonicin-1.  
 OS Rana japonica (Japanese reddish frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.  
 OC NCBI\_TaxID=8402;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=21826910; PubMed=11835990;  
 RA Isaacson T., Soto A., Iwamuro S., Knoop F.C., Conlon J.M.;  
 RT "Antimicrobial peptides with atypical structural features from the skin of the Japanese brown frog Rana japonica.";  
 RL Peptides 23:419-425(2002).  
 CC -|- FUNCTION: Antibacterial activity against the Gram-negative bacterium E.coli and the Gram-positive bacterium S.aureus.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.

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CC -!- MASS SPECTROMETRY: MW=2715.4; METHOD=Electrospray.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 8 14 BY SIMILARITY.
SQ SEQUENCE 14 AA; 1650 MW; C278625186DBE0B9 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6
   |||
Db 2 FPI 4

RESULT 5
AFIL_MALPA STANDARD; PRT; 15 AA.
AC P83141;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Antifungal protein 1 large subunit (CW-1) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1] _TAXINE=145753;
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseweed (Malva
parviflora)".;
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
not F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
concentration.
DR GO: GO:0003799; F:antifungal peptide activity; IDA.
KW Fungicide; Antibiotic.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1783 MW; 2CB3079F53C70F9 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
   |||
Db 3 GPF 5

RESULT 6
LPL_THETH STANDARD; PRT; 15 AA.
AC P21234;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Leu leader peptide.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=88121725; PubMed=3323845;
RA Croft J.E., Love D.R., Bergquist P.L.;
RT "Expression of leucine genes from an extremely thermophilic bacterium
in Escherichia coli".;

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RL Mol. Gen. Genet. 210:490-497(1987).
CC -!- FUNCTION: Involved in control of the biosynthesis of leucine.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; X06604; CAA29823.1; -.
KW Leucine biosynthesis; Leader peptide.
SQ SEQUENCE 15 AA; 1666 MW; C2F107A386D7620B CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
   |||
Db 6 ILV 8

RESULT 7
UC06_MAIZE STANDARD; PRT; 15 AA.
ID UC06_MAIZE
AC P80612;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 1131)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1] _
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.8, ITS MW IS: 71.0 kDa.
DR Maize-2DPAGE; P80612; COLEOPTILE.
DR MaizeDB; 123930; -.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1390 MW; 7005E22830F23D61 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
   |||
Db 8 RGP 10

RESULT 8
AFIS_MALPA STANDARD; PRT; 16 AA.
ID AFIS_MALPA
AC P83140;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 1 small subunit (CW-1) (fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatozoa; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 [1]  
 RN SEQUENCE, AND FUNCTION.  
 RC TISSUE=Seed;  
 RX MEDLINE=20568734; PubMed=11118343;  
 RA Wang X., Bunkers G.J.;  
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva  
 parviflora).";  
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).  
 CC -1- FUNCTION: Possesses antifungal activity against F.graminearum.  
 CC -1- SUBUNIT: Heterodimer of a large and a small subunit.  
 CC -1- MISCELLANEOUS: Antimicrobial activity is not affected by salt  
 concentration.  
 DR GO:0003799; F:antifungal peptide activity; IDA.  
 KW Fungicide; Antibiotic.  
 FT NON TER 16 16  
 FT SEQUENCE 16 AA; 1888 MW; 2893A1C66F5D3F57 CRC64;  
 QY 2 GPF 4 37.5%; Score 3; DB 1; Length 16;  
 Db 3 GPF 5 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPF 4 37.5%; Score 3; DB 1; Length 16;  
 Db 3 GPF 5 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 9  
 TRYP\_FELCA STANDARD; PRT; 16 AA.  
 ID -TRYP\_FELCA  
 AC P81071;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Trypsin precursor (EC 3.4.21.4) (Fragment).  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=97235546; PubMed=9080665;  
 RA Steiner J.M., Medinger T.L., Williams D.A.;  
 RT "Purification and partial characterization of feline trypsin.";  
 RL Comp. Biochem. Physiol. 116B:87-93(1997).  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.  
 DR InterPro; IPR001254; Ser\_protease\_Try.  
 DR PROSITE; PS00240; TRYPSIN\_DOM; PARTIAL.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; PARTIAL.  
 DR PROSITE; PS00135; TRYPSIN\_SER; PARTIAL.  
 KW Hydrolase; Serine protease; Digestion; Pancreas; Zymogen.  
 FT PROPEP 1 8  
 FT CHAIN 9 >16 ACTIVATION PEPTIDE.  
 FT NON TER 16 16 TRYPSIN.  
 FT SEQUENCE 16 AA; 1825 MW; A6D751BB58760A86 CRC64;  
 QY 4 FPI 6 37.5%; Score 3; DB 1; Length 16;  
 Db 1 FPI 3 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FPI 6 37.5%; Score 3; DB 1; Length 16;  
 Db 1 FPI 3 Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 10  
 AHD2\_TETPY STANDARD; PRT; 18 AA.  
 ID -AHD2\_TETPY

AC P35430;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE 20-alpha-hydroxysteroid dehydrogenase (EC 1.1.1.149) (20-alpha-HSD)  
 DE (Fragment).  
 OS Tetrahymena pyriformis.  
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;  
 OC Tetrahymenina; Tetrahymena.  
 OX NCBI\_TaxID=5908;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC STRAIN=W;  
 RX MEDLINE=94107273; PubMed=8280099;  
 RA Inazu A., Sato K., Nakayama Y., Hara A., Nozawa Y.;  
 RT "Purification and characterization of a novel dimeric 20 alpha-  
 RT hydroxysteroid dehydrogenase from Tetrahymena pyriformis.";  
 RL Biochem. J. 297:195-200(1994).  
 CC -1- FUNCTION: SPECIFIC FOR THE OXIDATION OF THE 20-ALPHA HYDROXY  
 CC GROUP OF 17-ALPHA-HYDROXYPROGESTERONE AND 17-ALPHA-  
 CC HYDROXYPREGNOLONE.  
 CC -1- CATALYTIC ACTIVITY: 17-alpha,20-alpha-dihydroxyprog-4-en-3-one +  
 CC NAD(P)(+) = 17-alpha-hydroxyprogesterone + NAD(P)H.  
 CC -1- SUBUNIT: Homodimer.  
 DR PIR; S40502; S40502.  
 KW Oxidoreductase; NADP.  
 FT NON TER 18 18  
 FT SEQUENCE 18 AA; 1861 MW; 16DF6B287E3B0A0D CRC64;  
 QY 4 FPI 6 37.5%; Score 3; DB 1; Length 18;  
 Db 13 FPI 15 Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 11  
 DURA\_STRGV STANDARD; PRT; 19 AA.  
 ID -DURA\_STRGV  
 AC P36504;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Lantibiotic duramycin (Leucopeptin) (Antibiotic PA48009).  
 OS Streptococcus griseoviriditatum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.  
 OX NCBI\_TaxID=68215;  
 RN [1]  
 RP SEQUENCE, AND STRUCTURE BY NMR.  
 RC STRAIN=PA-48009;  
 RX MEDLINE=91107438; PubMed=2272918;  
 RA Hayaishi P., Negashima K., Terui Y., Kawamura Y., Matsumoto K.,  
 RA Itazaki H.;  
 RT "The structure of PA48009: the revised structure of duramycin.";  
 RL J. Antibiot. 43:1421-1430(1990).  
 RN [2]  
 RP SEQUENCE.  
 RX MEDLINE=91107436; PubMed=2125590;  
 RA Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J.,  
 RA Raschdorf F., Peter H.H.;  
 RT "Duramycins B and C, two new lanthionine containing antibiotics as  
 RT inhibitors of phospholipase A2. Structural revision of duramycin and  
 RT cinnamycin.";  
 RL J. Antibiot. 43:1403-1412(1990).  
 CC -1- FUNCTION: ACTS AS INHIBITOR OF PHOSPHOLIPASE A2.  
 CC -1- FTM: Maturation of lantibiotics involves the enzymic conversion of  
 CC Thr, and Ser into dehydrated AA and the formation of thioether  
 CC bonds with cysteine or the formation of dialkylamine bonds with  
 CC lysine. This is followed by membrane translocation and cleavage of  
 CC the modified precursor.

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CC -!- SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
KW Antibiotic; Bacteriocin; Lantibiotic; D-amino acid; Thioether bond.
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;

Query Match 37.5%; Score 3; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
DB 8 GPF 10

RESULT 12
PAP2_PAP2 PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea moose sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea moose sole (Pardachirus
RT marmoratus).";
RL J. Biol. Chem. 261:16704-16713(1986).
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant
CC properties. Forms voltage-dependent, ion-permeable channels
CC in membranes. At high concentration causes cell membrane lysis.
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON TER
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5
DB 4 FP 5

RESULT 13
SUGA_ACHDO
ID SUGA_ACHDO STANDARD; PRT; 5 AA.
AC P19991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxID=6997;
RN [1]

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RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Acheta domesticus (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -!- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC CC GANGLIA. JS0319.
DR PIR; JS0319; JS0319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 4 PF 5

RESULT 14
EI01_LITRU
ID EI01_LITRU STANDARD; PRT; 6 AA.
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hyliidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD RES 6
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6
DB 3 PI 4

RESULT 15
CCF1_ENTFA
ID CCF1_ENTFA STANDARD; PRT; 7 AA.
AC P20104;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone cCF10.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=89008313; PubMed=3139658;
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,
RA Adait J.C., Dunny G.M., Suzuki A.;
RT "Structure of cCF10, a peptide sex pheromone which induces
RT conjugative transfer of the Streptococcus faecalis tetracycline

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RT resistance plasmid, pCF10."
RL J. Biol. Chem. 263:14574-14578 (1988).
CC -1- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PCF10.
DR PIR; A30812; A30812.
KW Pheromone.
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 1 LV 2

RESULT 16
CIA_ENTFA
ID_CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373."
RL FEBS Lett. 206:69-72 (1986).
CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC -1- HARBORING PAM373.
CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 4 IL 5

RESULT 17
FAR1_HELTI
ID_FAR1_HELTI STANDARD; PRT; 7 AA.
AC P41871;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRamide-like neuropeptide GDFPLRP-amide.
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Planorbidae; Helisoma.
OX NCBI_TaxID=27815;
RN [1]
RP SEQUENCE
RX TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."

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RL Peptides 15:31-36 (1994).
CC -1- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
CC THE KIDNEY, MANTLE AND SKIN.
CC -1- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 3 PF 4

RESULT 18
MNP1_LEPDE
ID_MNP1_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotropic neuropeptide 1 (Led-MNP-I).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Phytophaga; Chrysomeloidea; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxID=7539;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Head.
RX MEDLINE=95380343; PubMed=7651886;
RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., van Leeuwen F., de Loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotropic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata."
RL Peptides 16:365-374 (1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
FT MOD RES 7 7
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 4 GP 5

RESULT 19
UF04_MOUSE
ID_UF04_MOUSE STANDARD; PRT; 7 AA.
AC P38642;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P46) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RC TISSUE=Fibroblast;

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RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.0, ITS MW IS: 46 kDa.
FT NON TER
FT MOD RES 7
SQ SEQUENCE 7 AA; 766 MW; 68640AB777632700 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2
DB 6 RG 7

RESULT 20
UN06 PINPS STANDARD; PRT; 7 AA.
AC P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OC NCB1_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins";
RL Electrophoresis 20:1098-1108(1999).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
FT NON TER 1
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 6 PF 7

RESULT 21
AL15 CARMA STANDARD; PRT; 8 AA.
AC P81818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 15.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OC NCB1_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,

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RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8
FT MOD RES 8
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 2 GP 3

RESULT 22
AL16 CARMA STANDARD; PRT; 8 AA.
AC P81819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 16.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OC NCB1_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8
FT MOD RES 8
SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 2 GP 3

RESULT 23
ALL5 CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calliostatin 5 (Met-calliostatin 1) {Hyp3}Met-calliostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OC NCB1_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=93211980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,

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RA Thorpe A.;  
RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
with sequence homology to cockroach allatostatins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RP CHARACTERIZATION, AND HYDROXYLATION.  
RC TISSUE=Head;  
RX MEDLINE=94342269; PubMed=8063725;  
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
RT "[Hyp3]Met-callatostatin. Identification and biological properties of  
a novel neuropeptide from the blowfly Calliphora vomitoria.";  
RL J. Biol. Chem. 269:21059-21066(1994)  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
CC -!- TISSUE SPECIFICITY: NEURONS WITHIN BRAIN AND ABDOMINAL GANGLION.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
DR FIR; E47393;  
KW Neuropeptide; Amidation; Hydroxylation.  
FT MOD RES 3 3 HYDROXYLATION (20%).  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GP 3  
DB 1 GP 2  
RESULT 24  
ALL5\_CVDPO STANDARD; PRT; 8 AA.  
ID ALL5\_CVDPO  
AC P82156;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Cydiastatin 5.  
OS Cydia pomonella (Codling moth).  
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
OX NCBI\_TaxID=82600;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larva;  
RX MEDLINE=98054539; PubMed=9392829;  
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Winstanley D.,  
RA Davey M., East P.D., Thorpe A.;  
RT "Lepidopteran peptides of the allatostatin superfamily.";  
RL Peptides 18:1301-1309(1997).  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RG 2  
DB 2 RG 3  
RESULT 25  
ALL8\_CARMA STANDARD; PRT; 8 AA.  
ID ALL8\_CARMA  
AC P81811;

DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 8.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 795 MW; 922879CDB47687D CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GP 3  
DB 2 GP 3  
RESULT 26  
ALL9\_CARMA STANDARD; PRT; 8 AA.  
ID ALL9\_CARMA  
AC P81812;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Carcinustatin 9.  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;  
RX MEDLINE=98121193; PubMed=9461295;  
RA Duve H., Johnsen A.H., Maestros J.-L., Scott A.G., Jaros P.P.,  
RA Thorpe A.;  
RT "Isolation and identification of multiple neuropeptides of the  
allatostatin superfamily in the shore crab Carcinus maenas.";  
RL Eur. J. Biochem. 250:727-734(1997).  
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
KW Neuropeptide; Amidation; Multigene family.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 781 MW; 7C2879CDB476878 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GP 3  
DB 2 GP 3  
RESULT 27  
ANG2\_BOTJA STANDARD; PRT; 8 AA.  
ID ANG2\_BOTJA

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AC Q10582;
AD 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8929801;
RA Borgheresi R.A.M.B., Dalle Luca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca."
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasconstrictor; Plasma; Serpin.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PF 4
Db 7 PF 8

RESULT 28
CADI_ENTFA
ID -CADI_ENTFA STANDARD; PRT; 8 AA.
AC P13268;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CADI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85051889; PubMed=6437872;
RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the bacterial sex pheromone, cADI, that
RT induces plasmid transfer in Streptococcus faecalis."
RL FEBS Lett. 178:97-100(1984).
CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC HEMOLYSIN PLASMID PAD1.
KW Pheromone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
Db 4 LV 5

RESULT 29
CPDI_ENTFA
ID -CPDI_ENTFA STANDARD; PRT; 8 AA.
AC P13269;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)

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DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CPDI.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=85040388; PubMed=6436978;
RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
RA Craig R.A., Clewell D.B.;
RT "Isolation and structure of bacterial sex pheromone, cPDI."
RL Science 226:849-850(1984).
CC -!- FUNCTION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
CC BACTERIOICIN PLASMID PPDI.
KW Pheromone.
SQ SEQUENCE 8 AA; 913 MW; 8665B729C682C729 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LV 8
Db 2 LV 3

RESULT 30
FAR7_ASCSU
ID -FAR7_ASCSU STANDARD; PRT; 8 AA.
AC P43171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF7.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3
Db 2 GP 3

RESULT 31
PPK2_PERAM
ID -PPK2_PERAM STANDARD; PRT; 8 AA.
AC P82692;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;

```

RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=97353923; PubMed=9210163;  
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;  
 RT "Isolation and structural elucidation of two pyrokinins from the  
 RL retrocerebral complex of the American cockroach.";  
 RN Peptides 18:473-478(1997).  
 [2]  
 RN TISSUE SPECIFICITY.  
 RP MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
 RL the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -1- MASS SPECTROMETRY: MW=883; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 DR InterPro: IPR001484; Pyrokinin.  
 DR PROSITE: PS00539; PYROKININ; FALSE NEG.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D7775 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PF 4  
 DB 3 PF 4  
 RESULT 32  
 PK3 PERAM STANDARD; PRT; 8 AA.  
 AC P82618; 2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).  
 OS Pariplaneta americana (American cockroach).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
 CC Blattidae; Periplaneta.  
 CC NCBI\_TaxID=6978;  
 [1]  
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC TISSUE=Retrocerebral complex.  
 RX MEDLINE=99212469; PubMed=10196736;  
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;  
 RT "Differential distribution of pyrokinin-isoforms in cerebral and  
 RL abdominal neurohemal organs of the American cockroach.";  
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).  
 [2]  
 RN TISSUE SPECIFICITY.  
 RP MEDLINE=20189894; PubMed=10723010;  
 RA Predel R., Eckert M.;  
 RT "Tagma-specific distribution of FXPRlamides in the nervous system of  
 RL the American cockroach.";  
 RL J. Comp. Neurol. 419:352-363(2000).  
 CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 CC (MYOTROPIC ACTIVITY).  
 CC -1- TISSUE SPECIFICITY: CORPORA CARDIACA.  
 CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
 KW Neuropeptide; Amidation; Pyrokinin.  
 FT MOD RES 8  
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LV 8  
 DB 1 LV 2  
 RESULT 33  
 RS7 MYCIT STANDARD; PRT; 8 AA.  
 AC P33564;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE 30S ribosomal protein S7 (Fragment).  
 GN .RPSG.  
 OS Mycobacterium intracellulare.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
 CC NCBI\_TaxID=1767;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93197130; PubMed=8451173;  
 RA Nair J., Rouse D.A., Morris S.L.;  
 RT "Nucleotide sequence analysis of the ribosomal S12 gene of  
 RL Mycobacterium intracellulare.";  
 RL Nucleic Acids Res. 21:1039-1039(1993).  
 CC -1- FUNCTION: One of the primary rRNA binding proteins, it binds  
 CC directly to 16S rRNA where it nucleates assembly of the head  
 CC domain of the 30S subunit. Is located at the subunit interface  
 CC close to the decoding center, probably blocks exit of the E-site  
 CC tRNA (By similarity).  
 CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9  
 CC and S11 (By similarity).  
 CC -1- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; L08171; AAA25376.1; -  
 CC PIR; S35538; S35538.  
 CC HAMAP; MF 00480; -; 1.  
 CC InterPro: IPR000235; Ribosomal S7.  
 CC PROSITE: PS00052; RIBOSOMAL\_S7; PARTIAL.  
 KW Ribosomal protein; RNA-binding; tRNA-binding.  
 FT INIT MET 0 0 BY SIMILARITY.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GP 3  
 DB 4 GP 5  
 RESULT 34  
 RT34 BOVIN STANDARD; PRT; 8 AA.  
 ID RT34 BOVIN  
 AC P82929;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).  
 GN MRPS34.

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OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrial.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 4 IL 5

RESULT 35
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25; Created)
DT 01-APR-1993 (Rel. 25; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93029337; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1
FT VARIANT 5 1 F -> P.
FT VARIANT 5 5 /FTID=VAR_000004.
FT NON_TER 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 2 IL 3

RESULT 36
VGLG_HSV2B
ID VGLG_HSV2B STANDARD; PRT; 8 AA.
AC P81780;

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DT 15-JUL-1999 (Rel. 38; Created)
DT 15-JUL-1999 (Rel. 38; Last sequence update)
DT 15-JUL-1999 (Rel. 38; Last annotation update)
DE Glycoprotein G (Fragment).
OS Herpes simplex virus (type 2 / strain B4327UR).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=103921;
RN [1]
RP SEQUENCE.
RL Liljeqvist J.-A., Svennerholm B., Bergstrom T.;
RA Submitted (APR-1999) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
CC 2: GH, GB, GC, GG, GD, GI, AND GE.
CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV-2 THAN IN
CC HSV-1.
KW Glycoprotein.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 683 MW; 7B47686772C865B8 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred.No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3
DB 6 GP 7

RESULT 37
CCAP_CARMA
ID CCAP_CARMA STANDARD; PRT; 9 AA.
AC P38556;
DT 01-OCT-1994 (Rel. 30; Created)
DT 01-OCT-1994 (Rel. 30; Last sequence update)
DT 15-DEC-1998 (Rel. 37; Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -!- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
CC INTO THE HEMOLYPH.
DR PIR; A26363; A26363.

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DR PIR; S27233; S27233.  
 KW Neuropeptide; Amidation.  
 FT DISULFID 3 9  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
 ||  
 Db 1 PF 2

RESULT 38  
 CONO CONST STANDARD; PRT; 9 AA.  
 AC P05487;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-NOV-1988 (Rel. 09, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Arg-conopressin S.  
 OS Conus striatus (Striated cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6493;  
 RN [1]  
 RP SEQUENCE.

RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,  
 RA Gray W.R., Olivera B.M.;  
 RT "Invertebrate vasopressin/oxytocin homologs. Characterization of  
 RT peptides from Conus geographus and Conus striatus venoms.";  
 RL J. Biol. Chem. 262:15821-15824 (1987).  
 RN [2]

RP REVIEW.  
 RX MEDLINE=89024586; PubMed=3052286;  
 RA Gray W.R., Olivera B.M., Cruz L.J.;  
 RT "Peptide toxins from venomous Conus snails.";  
 RL Annu. Rev. Biochem. 57:665-700 (1988).  
 CC -!- FUNCTION: Targets vasopressin-oxytocin related receptors.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
 DR PIR; B28495; B28495.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Amidation.  
 FT DISULFID 1 6  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2  
 ||  
 Db 8 RG 9

RESULT 39  
 DNFI LOCFMI STANDARD; PRT; 9 AA.  
 AC P16339;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Locupressin (Diuretic neuropeptide F1/F2).  
 OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;  
 RX MEDLINE=88077077; PubMed=3689410;  
 RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,  
 RA Delaage M., Schooley D.A.;  
 RT "Identification of an arginine vasopressin-like diuretic hormone from  
 RT Locusta migratoria.";  
 RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).  
 CC -!- FUNCTION: DIURETIC HORMONE.  
 CC -!- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.  
 CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR; A29477; A29477.  
 DR InterPro; IPR000981; Neurohyp\_horm.  
 DR Pfam; PF00220; hormone4; 1.  
 DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
 KW Hormone; Neuropeptide; Amidation.  
 FT DISULFID 1 6  
 FT DISULFID 1 6  
 FT DISULFID 1 6  
 FT DISULFID 6 6  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2  
 ||  
 Db 8 RG 9

RESULT 40  
 FAR5 PANRE STANDARD; PRT; 9 AA.  
 ID FAR5 PANRE  
 AC P82661;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE FMRFamide-like neuropeptide PF5 (AMRNALVRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND AMIDATION.  
 RA Moffet C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,  
 RA Maule A.G.;  
 RT "Isolation, characterization and pharmacology of FMRFamide-related  
 RT peptides (FarPs) from free-living nematode, Panagrellus redivivus.";  
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.  
 CC -!- FUNCTION: MYOACTIVE.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9 9  
 SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8  
 ||  
 Db 6 LV 7

RESULT 41  
 FAR9 ASCSU

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ID FAR9 ASCSU STANDARD; PRT; 9 AA.
AC P43172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF9.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
[1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Sretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GP 3
Db 3 GP 4

RESULT 42
FIBB_PAPAN
ID FIBB_PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain (Contains: Fibrinopeptide B) (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9555;
[1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9
SQ SEQUENCE 9 AA; 1076 MW; DDF6409C7287B06 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
[1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Amphibian defense peptide; Vasodilator; Bradykinin.

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SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
||  
Db 7 PF 8

## RESULT 45

LMT3\_LOCM1  
ID LMT3\_LOCM1 STANDARD; PRT; 9 AA.  
AC P41489;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Locustamytropin 3 (LOM-MT-3).  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;  
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,  
de Loof A.;  
RT "Isolation, identification and synthesis of locustamytropin III and  
RT IV, two additional neuropeptides of Locusta migratoria: members of the  
RT locustamytropin peptide family.";  
RL Insect Biochem. Mol. Biol. 22:447-452(1992).  
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTILE ACTIVITY  
(MYOTROPIC ACTIVITY).  
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.  
DR PIR; A61620; A61620.  
DR InterPro; IPR001484; Pyrokinin.  
DR PROSITE; PS00539; PYROKININ; 1.  
KW Neuropeptide; Amidation; Pyrokinin.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1140 MW; D5A81772C9D776C6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4  
||  
Db 4 PF 5

## RESULT 46

OXYT\_BUFRE  
ID OXYT\_BUFRE STANDARD; PRT; 9 AA.  
AC P4295;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Seritocin ([Ser5, Ile8]-oxytocin).  
OS Bufo regularis (Leopard toad).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;  
OC Bufo.  
OX NCBI\_TaxID=8390;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pituitary neurointermediate lobe;  
RX MEDLINE=96059313; PubMed=7591488;  
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;  
RT "A new neurohypophyseal peptide, seritocin ([Ser5, Ile8]-oxytocin),  
RT identified in a dryness-resistant African toad, Bufo regularis.";  
RL Int. J. Pept. Protein Res. 45:482-487(1995).

CC -1- FUNCTION: Devoid of oxytocic activity.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; FALSE\_NEG.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PI 6  
||  
Db 7 PI 8

## RESULT 47

OXYT\_CYPCA  
ID OXYT\_CYPCA STANDARD; PRT; 9 AA.  
AC P23879;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Vasotocin.  
OS Cyprinus carpio (Common carp), and  
OS Petromyzon marinus (Sea lamprey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Cyprinus.  
OX NCBI\_TaxID=7962, 7757;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=C.carpio; TISSUE=Pituitary;  
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;  
RT "Characterization of neurohypophyseal hormones from a fresh water bony  
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea  
RT water bony fish.";  
RL Comp. Biochem. Physiol. 14:245-254(1965).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=P.marinus; TISSUE=Pituitary;  
RX MEDLINE=88225976; PubMed=3371648;  
RA Lane T.F., Sower S.A., Kawauchi H.;  
RT "Arginine vasotocin from the pituitary gland of the lamprey  
RT (Petromyzon marinus): isolation and amino acid sequence.";  
RL Gen. Comp. Endocrinol. 70:152-157(1988).  
CC -1- FUNCTION: ANTIDIURETIC HORMONE.  
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR PIR; B61364; B61364.  
DR PIR; S06375; S06375.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RG 2  
||  
Db 8 RG 9

## RESULT 48

OXYT\_OCTVU

ID OXYT OCTVU STANDARD; PRT; 9 AA.  
AC P80027;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cephalotocin.  
OS Octopus vulgaris (Octopus).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
OX NCBI\_TaxID=6645;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Nerve endings;  
RX MEDLINE=92270139; PubMed=1589145;  
RA Reich G.;  
RT "A new peptide of the oxytocin/vasopressin family isolated from  
nerves of the cephalopod Octopus vulgaris.";  
RL Neurosci. Lett. 134:191-194(1992).  
CC -!- FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA  
CAVA.  
CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.  
DR InterPro; IPR000981; Neurhyp\_horm.  
DR Pfam; PF00220; hormone4; 1.  
DR PROSITE; PS00264; NEUROHYPOPHYS\_HORM; 1.  
KW Hormone; Amidation.  
FT DISULFID 1 6  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 1072 MW; 17FF476EB45409DB CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PI 6  
Db 7 PI 8  
RESULT 49  
PGLR\_DIAAB STANDARD; PRT; 9 AA.  
AC P81179;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Endo-polygalacturonase (PG) (EC 3.2.1.15) (Fragment).  
OS Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phytophaga; Curculionidae; Entiminae; Entimini; Diaprepes.  
OX NCBI\_TaxID=13040;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Larval gut;  
RA Doostdar H., McCollum T.G., Mayer R.T.;  
RT "Purification and characterization of an endo-polygalacturonase from  
the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes  
abbreviatus L.) larvae.";  
RL Comp. Biochem. Physiol. 118B:861-867(1997).  
CC -!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-  
galactosiduronic linkages in pectate and other galacturonans.  
CC -!- INDUCTION: INHIBITED BY CITRUS PGIP.  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
9.4, ITS MW IS: 44.5 KDa.  
CC -!- SIMILARITY: WEAK, TO OTHER POLYGALACTURONASES.  
KW Hydrolase; Glycosidase; Cell wall.  
FT NON\_TER 9  
SQ SEQUENCE 9 AA; 1041 MW; 1F49087042DB41BB CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PI 6  
Db 7 PI 8

Qy 1 RG 2  
Db 8 RG 9  
RESULT 50  
RE42\_LITRU STANDARD; PRT; 9 AA.  
ID RE42\_LITRU  
AC P82075; P82093;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Rubellidin 4.2/4.3.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
RA Tyler M.J., Wallace J.C.;  
RT "The structure of new peptides from the Australian red tree frog  
'Litoria rubella'. The skin peptide profile as a probe for the study  
of evolutionary trends of amphibians.";  
RL Aust. J. Chem. 49:955-963(1996).  
RN [2]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic  
activity.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-  
terminal amidation.  
CC -!- MASS SPECTROMETRY: MW=883; METHOD=FAB.  
KW Amphibian defense peptide; Amidation.  
FT MOD\_RES 9 9  
SQ SEQUENCE 9 AA; 884 MW; 2C2D77205AA72728 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 6 IL 7  
Db 6 IL 7  
RESULT 51  
SAMP MUSCA STANDARD; PRT; 9 AA.  
ID SAMP MUSCA  
AC P19035;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid P-component (SAP) (Fragment).  
OS Mustelus canis (Smooth dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
OC Mustelus.  
OX NCBI\_TaxID=7812;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83160932; PubMed=6403520;  
RA Robey F.A., Tanaka T., Liu T.-Y.;  
RT "Isolation and characterization of two major serum proteins from the

RT dogfish, Mustelus canis, C-reactive protein and amyloid P component.";  
 RL J. Biol. Chem. 258:3889-3894(1983).  
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTAXIN) HAVE A DISCOID  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
 CC IN BASMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 CC PIR; B20569; B20569.  
 DR InterPro; IPR001759; Pentaxin.  
 DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
 FT DOMAIN 1 >9 PENTAXIN.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FP 5  
 DB 2 FP 3  
 RESULT 52  
 ID TKL1 LOCOMI STANDARD; PRT; 9 AA.  
 AC P16223;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Locustatachykinin I (TK-I).  
 OS Locusta migratoria (migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]\_TaxID=7004;  
 RP SEQUENCE  
 RC TISSUE=Brain;  
 RX MEDLINE=90184499; PubMed=2311766;  
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;  
 RT "Locustatachykinin I and II, two novel insect neuropeptides with  
 RT homology to peptides of the vertebrate tachykinin family.";  
 RL FEBS Lett. 261:397-401(1990).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. STIMULATES THE CONTRACTION OF THE  
 CC OVIDUCT AND FOREGUT.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 9  
 FT AMIDATION  
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GP 3  
 DB 1 GP 2  
 RESULT 53  
 ID ULAD\_HUMAN STANDARD; PRT; 9 AA.  
 AC P31929;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6, ITS MW IS: 15 kDa.  
 DR SWISS-2DPAGE; P31929; HUMAN.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LV 8  
 DB 1 LV 2

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE  
 RC TISSUE=Liver;  
 RX MEDLINE=94147969; PubMed=8313870;  
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,  
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;  
 RT "Human liver protein map: update 1993.";  
 RL Electrophoresis 14:1216-1222(1993).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 6, ITS MW IS: 15 kDa.  
 DR SWISS-2DPAGE; P31929; HUMAN.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1129 MW; D02DFB41B6D33322 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 LV 8  
 DB 1 LV 2  
 RESULT 54  
 ID UP3\_HUMAN STANDARD; PRT; 9 AA.  
 AC P30089;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.  
 DR SWISS-2DPAGE; P30089; HUMAN.  
 FT NON\_TER 1  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FP 5  
 DB 4 FP 5  
 RESULT 55  
 ID UP3\_HUMAN STANDARD; PRT; 9 AA.  
 AC P30093;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=93092937; PubMed=1459097;  
 RA Hughes G.J., Frutiger S., Paquet N., Ravier P., Pasquali C.,  
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
 RA Hochstrasser D.F.;  
 RT "Plasma protein map: an update by microsequencing.";  
 RL Electrophoresis 13:707-714(1992).  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.  
 DR SWISS-2DPAGE; P30093; HUMAN.  
 FT NON TER 1 1  
 FT UNSURE 5 5  
 FT NON TER 9 9  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;  
  
 Query Match 25.0%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 7 LV 8  
 Db 2 LV 3  
  
 RESULT 56  
 AH3\_PRUSE STANDARD; PRT; 10 AA.  
 AC P23261;  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DE 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase  
 isozyme II) (AH II) (Fragment).  
 OS Prunus serotina (Black cherry).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.  
 OX NCBI\_TaxID=23207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RA Li C.P., Swain E., Poulton J.E.;  
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";  
 RL Plant Physiol. 100:282-290(1992).  
 CC -!- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-  
 CC glucose.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS  
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON  
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR  
 CC EMBRYONAL TISSUES.  
 CC -!- PTM: GLYCOSYLATED.  
 CC Glycosidase; Hydrolase; Glycoprotein; Multigene family.  
 KW NON TER 10 10  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1033 MW; 3331B8D051E04777 CRC64;  
  
 Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 5 PI 6  
 Db 4 PI 5  
  
 RESULT 57  
 ANGLI\_BOTJA STANDARD; PRT; 10 AA.  
 ID -ANGI\_BOTJA  
 AC Q10581;

DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Angiotensin-like peptide I (Fragment).  
 OS Bothrops jararaca (Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8724;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Plasma;  
 RX MEDLINE=96208932; PubMed=8829801;  
 RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;  
 RT "Isolation and identification of angiotensin-like peptides from the  
 RT plasma of the snake Bothrops jararaca.";  
 RL Comp. Biochem. Physiol. 113B:467-473(1996).  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin.  
 FT NON TER 10 10  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;  
  
 Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 PF 4  
 Db 7 PF 8  
  
 RESULT 58  
 ANGT\_BOVIN STANDARD; PRT; 10 AA.  
 ID -ANGT\_BOVIN  
 AC P01017;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang  
 II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]  
 DE (Fragment).  
 DE AGT OR SERPIN8.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RA Elliott D.F., Peart W.S.;  
 RT "The amino acid sequence in a hypertensin.";  
 RL Biochem. J. 65:246-254(1957).  
 CC -!- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN  
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN  
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE  
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT  
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL  
 CC BALANCE OF BODY FLUIDS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Synthesized by the liver and secreted in the  
 CC plasma.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR PIR; A90345; A90345.  
 DR PUB; 3ER5; 15-JUL-92.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Vasoconstrictor; Plasma; Serpin; 3D-structure.  
 FT PEPTIDE 1 10 ANGIOTENSIN I.  
 FT PEPTIDE 1 8 ANGIOTENSIN II.  
 FT PEPTIDE 2 8 ANGIOTENSIN III.  
 FT NON TER 10 10

SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761F2DB42 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PF 4  
DB 7 PF 8  
RESULT 59  
ANGT\_CHICK  
ID ANGT\_CHICK STANDARD; PRT; 10 AA.  
AC P01018;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Angiotensinogen [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)] (Fragment).  
DE AGT OR SERPINAS.  
GN Gallus gallus (Chicken), and  
OS Coturnix coturnix japonica (Japanese quail).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031, 93934;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=Chicken;  
RX MEDLINE=74127845; PubMed=4361802;  
RA Nakayama T., Nakajima T., Sokabe H.;  
RT "Comparative studies on angiotensins. 3. Structure of fowl angiotensin and its identification by DNS-method.";  
RL Chem. Pharm. Bull. 21:2085-2087(1973).  
RN [2]  
RP SEQUENCE.  
RC SPECIES=C.c.japonica;  
RX MEDLINE=90284684; PubMed=2191893;  
RA Takei Y., Hasegawa Y.;  
RT "Vasopressor and depressor effects of native angiotensins and inhibition of these effects in the Japanese quail.";  
RL Gen. Comp. Endocrinol. 79:12-22(1990).  
CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL BALANCE OF BODY FLUIDS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.  
CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
DR PIR; A60624; A60624.  
DR PIR; A90917; A90917.  
DR InterPro; IPR000215; Serpin.  
DR PROSITE; PS00284; SERPIN; PARTIAL.  
KW Vasoconstrictor; Plasma; Serpin.  
FT PEPTIDE 1 10 ANGIOTENSIN I.  
FT PEPTIDE 1 8 ANGIOTENSIN II.  
FT PEPTIDE 2 8 ANGIOTENSIN III.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1232 MW; CEEFDD761F2DB42 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 PF 4  
DB 7 PF 8

RESULT 60  
BPP VIPAS  
ID BPP VIPAS STANDARD; PRT; 10 AA.  
AC P31351;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).  
OS Vipera aspis (Aspic viper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Viperinae; Vipera.  
OX NCBI\_TaxID=8706;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=90382616; PubMed=2169439;  
RA Komori Y., Sugihara H.;  
RT "Characterization of a new inhibitor for angiotensin converting enzyme from the venom of Vipera aspis aspis.";  
RL Int. J. Biochem. 22:767-771(1990).  
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.  
CC It acts as an indirect hypotensive agent.  
CC PIR; A60377; XASNPC.  
KW Hypotensive agent; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1  
SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GP 3  
DB 5 GP 6  
RESULT 61  
COXO\_RAT  
ID COXO\_RAT STANDARD; PRT; 10 AA.  
AC P80432;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cytochrome c oxidase polypeptide VIIC, mitochondrial (EC 1.9.3.1) (VIIC) (Fragment).  
DE COX7C OR COX7C1.  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=Wistar; TISSUE=Heart, and Liver;  
RX MEDLINE=95324529; PubMed=7601105;  
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.";  
RL Eur. J. Biochem. 230:235-241(1995).  
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.  
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.  
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.  
DR PIR; S65388; S65388.  
KW Oxidoreductase; Mitochondrion.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B08 CRC64;

Query Match	25.0%; Score 2; DB 1; Length 10;	Best Local Similarity 100.0%; Pred. No. 1e+04;	Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RT	with organophosphate resistance in the greenbug, <i>Schizaphis graminum</i> (Homoptera: Aphididae);		
RL	Arch. Insect Biochem. Physiol. 36:229-240(1997).		
CC	-1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.		
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.		
CC	-1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	InterPro; IPR002018; CarboxylesteraseB		
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; PARTIAL.		
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; PARTIAL.		
KW	Hydrolase; Serine esterase.		
FT	NON TER 10		
SQ	SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;		
QY	5 PI 6		
DB	2 PI 3		
RESULT 64			
FA6_PANRE	STANDARD; PRT; 10 AA.		
ID	PANRE		
AC	P82660;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	PMFamide-like neurotoxin PF6 (NGAPQFVRF-amide).		
OS	Panagrellus redivivus.		
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;		
OC	Panagrolaimoidea; Panagrolaimidae; Panagrellus.		
OX	NCBI_TaxID=6233;		
RN	[1]		
RP	SEQUENCE, FUNCTION, AND AMIDATION.		
RA	Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,		
RA	Maule A.G.;		
RT	"Isolation, characterization and pharmacology of PMFamide-related peptides (PaRPs) from free-living nematode, <i>Panagrellus redivivus</i> ."		
RL	Submitted (JUL-2000) to the SWISS-PROT data bank.		
CC	-1- FUNCTION: MYOACTIVE.		
CC	-1- SIMILARITY: BELONGS TO THE FARP (PMFAMIDE RELATED PEPTIDE) FAMILY.		
KW	Neuropeptide; Amidation.		
FT	MOD RES 10 10		
SQ	SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;		
QY	3 PF 4		
DB	6 PF 7		
Query Match	25.0%; Score 2; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred. No. 1e+04;		
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	3 PF 4		
DB	6 PF 7		
RESULT 65			
NS1_MYCTU	STANDARD; PRT; 10 AA.		
ID	NS1_MYCTU		
AC	P81135;		
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	30 kDa non-secretory protein 1 (fragment).		
OS	Mycobacterium tuberculosis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.		
OX	NCBI_TaxID=1773;		
RN	[1]		
RP	SEQUENCE.		
RC	STRAIN=H37RV;		
Query Match	25.0%; Score 2; DB 1; Length 10;		
Best Local Similarity	100.0%; Pred. No. 1e+04;		
Matches	2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	2 GP 3		
DB	6 GP 7		
RESULT 62			
COXO_THUOB	STANDARD; PRT; 10 AA.		
ID	COXO_THUOB		
AC	P80982;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Cytochrome c oxidase polypeptide VIIC (EC 1.9.3.1) (Fragment).		
OS	Thunus obesus (Bigeye tuna).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;		
OC	Scombridae; Thunnus.		
OX	NCBI_TaxID=8241;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Heart, and Liver;		
RX	MEDLINE=97454291; PubMed=9310366;		
RA	Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,		
RA	Kadenbach B.;		
RT	"The subunit structure of cytochrome-c oxidase from tuna heart and liver."		
RL	Eur. J. Biochem. 248:99-103(1997).		
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.		
CC	-1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome c + 2 H(2)O.		
CC	-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.		
CC	-1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.		
DR	PIR; S77990		

RA Prasad H.K., Annapurna P.S.;  
 RL Submitted (DEC-1997) to the SWISS-PROT data bank.  
 CC -!- CAUTION: We are unable to find this protein in the translation of  
 CC the genome of strain H37Rv.  
 CC  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1042 MW; 8767F86AB2C73771 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8

DB 5 LV 6

## RESULT 66

PVK\_LOCMI  
 ID PVK\_LOCMI STANDARD; PRT; 10 AA.

AC P83382;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Periviscerokinin (Lom-PVK-1).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 ON NCBI\_TaxID=7004;  
 RN [1]

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Abdominal perisymphathetic organs;

RX MEDLINE=21896327; PubMed=11897380;

RA Predel R., Gaede G.;

RT "Identification of the abundant neuropeptide from abdominal

RT perisymphathetic organs of locusts.";

RL Peptides 23:621-627(2002).

CC -!- FUNCTION: Myotropic peptide; increases the frequency of

CC contraction of the heart and stimulates amplitude and tonus of the

CC foregut.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MASS SPECTROMETRY: MW=1104.5; METHOD=WALDI.

DR GO; GO:0005576; C:extracellular; IDA.

DR GO; GO:0005184; F:neuropeptide hormone activity; IDA.

DR GO; GO:0007218; P:neuropeptide signaling pathway; IDA.

KW Neuropeptide; Amidation.

FT MOD\_RES 10 10

SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5

DB 7 FP 8

## RESULT 67

Q2OB\_COMTE

ID Q2OB\_COMTE STANDARD; PRT; 10 AA.

AC P80465;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Quinolone 2-oxidoreductase, beta chain [EC 1.3.99.17] (Fragment).

OS Comamonas testosteroni (Pseudomonas testosteroni).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Comamonadaceae; Comamonas.

ON NCBI\_TaxID=285;

RN [1]

RP SEQUENCE.

## RC STRAIN=63;

RX MEDLINE=96035889; PubMed=7556204;

RA Schach S., Tshisuka B., Fetzner S., Lingens F.;

RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-

RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in

RL Quinolone and 3-methylquinoline degradation.";

RL Eur. J. Biochem. 232:536-544 (1995).

CC -!- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-

CC 1,2-DIHYDROQUINOLINE.

CC -!- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoquinolin-

CC 1(2H)-one + reduced acceptor.

CC -!- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.

CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline; first

CC step.

CC -!- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND

CC TWO GAMMA CHAINS (PROBABLE).

KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1241 MW; C2E2C25DD9CDC769 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5

DB 3 FP 4

## RESULT 68

RCA\_PINPS

ID RCA\_PINPS STANDARD; PRT; 10 AA.

AC P81084;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable ribulose biphosphate carboxylase/oxygenase activase (RuBisCO

DE activase) (RA) (Water stress responsive protein 4) (Fragment).

OS Pinus pinaster (Maritime pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

ON NCBI\_TaxID=71647;

OX [1]

RP SEQUENCE.

RC TISSUE=Needle;

RX MEDLINE=98418576; PubMed=9747804;

RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;

RT "Water-deficit-responsive proteins in maritime pine.";

RL Plant Mol. Biol. 38:587-596(1998).

RN [2]

RP SEQUENCE.

RC TISSUE=Needle;

RX MEDLINE=99274088; PubMed=10344291;

RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,

RA Frigerio J.-M., Plomion C.;

RT "Separation and characterization of needle and xylem maritime pine

RT proteins.";

RL Electrophoresis 20:1098-1108(1999).

CC -!- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE  
 CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT  
 CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A  
 CC CARBAMATE STRUCTURE (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).

CC -!- INDUCTION: By water stress.

CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.

KW Chloroplast; ATP-binding.

FT NON\_TER 1 1

FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1e+04;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8  
DB 6 LV 7

RESULT 69  
RRPL PHODV STANDARD; PRT; 10 AA.  
AC P35946;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)  
DE (L protein) (fragment).  
GN L.  
OS Phocine distemper virus (PDV).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;  
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.  
OX NCBI\_TaxID=11240;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=U1ster/88;  
RX MEDLINE=92268877; PubMed=1588321;  
RA Curran M.D., O'Loan D., Kennedy S., Rima B.K.;  
RT "Molecular characterization of phocine distemper virus: gene order  
and sequence of the gene encoding the attachment (H) protein.";  
RL J. Gen. Virol. 73:1189-1194(1992).  
CC -!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY  
FUNCTION IN RNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)  
SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAs. RNA EDITING OF THE P  
GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.  
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +  
{RNA} (N).  
CC -!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: D10371; BAA01208.1;  
KW Transferase; RNA-directed RNA polymerase.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1105 MW; 9C2B7FD452D5A2D5 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7  
DB 9 IL 10

RESULT 70  
SLAP\_BACTG STANDARD; PRT; 10 AA.  
AC P49325;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE S-layer protein (Surface layer protein) (Fragment).  
OS Bacillus thuringiensis (subsp. galleriae).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29338;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=NRRL 4045;  
RX MEDLINE=90078111; PubMed=2592346;

RA Luckevich M.D., Beveridge T.J.;  
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";  
RL J. Bacteriol. 171:6656-6667(1989).  
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CELL WALL WITH OBLIQUE (P2) SYMMETRY.  
DR PIR: A60476; A60476.  
KW Cell wall; S-layer.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FP 5  
DB 5 FP 6

RESULT 71  
TRP8 LEUMA STANDARD; PRT; 10 AA.  
AC P81740;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tachykinin-related peptide 8 (LemTRP 8).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Brain;  
RX MEDLINE=97269266; PubMed=9114447;  
RA Muren J.E., Naessel D.R.;  
RT "Seven tachykinin-related peptides isolated from the brain of the  
Madeira cockroach; evidence for tissue-specific expression of  
isoforms.";  
RL Peptides 18:7-15(1997).  
CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY  
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: BRAIN.  
CC -!- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.  
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
KW Tachykinin; Neuropeptide; Amidation.  
FT MOD RES 10 10  
SQ SEQUENCE 10 AA; 1076 MW; 9E410371E9C87685 CRC64;  
Query Match 25.0%; Score 2; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GP 3  
DB 1 GP 2

RESULT 72  
UPA5 HUMAN STANDARD; PRT; 10 AA.  
AC P30091;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.



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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714 (1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -!- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC ZN-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER 1 1
FT VARIANT 9 9 G -> Y.
FT /FTID=VAR_000002.
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C732C32776 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 7 LV 8

RESULT 73
UXA2_CHLTR STANDARD; PRT; 10 AA.
AC P38003;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G.,
RA Fallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.65, ITS MW IS: 26.5 kDa.
DR Siena-2DPAGE; P38003; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1019 MW; 49C2B5C6CAB862C7 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LV 8
DB 3 LV 4

RESULT 74
XYNB_DICB4 STANDARD; PRT; 10 AA.
AC P80717;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B) (Fragment).

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OS Dictyoglomus sp. (strain B4A).
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=69007;
RN [1]
RP SEQUENCE.
RA Adameen A.K., Jacobsen S., Ahring B.K.;
RL Submitted (OCT-1996) to the SWISS-PROT data bank.
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
CC linkages in xylans.
CC -!- PATHWAY: Xylan degradation.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY F (FAMILY 10 OF GLYCOSYL
CC HYDROLASES).
DR InterPro; IPR001000; Glyco_hydro_10.
DR PROSITE; PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
KW Xylan degradation; Hydrolase; Glycosidase.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; 4554322AA72041A3 CRC64;

Query Match 25.0%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 IL 7
DB 5 IL 6

RESULT 75
ANGT_CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80024575; PubMed=488254;
RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Edean R.;
RT "Amino acid composition and sequence of crinia-angiotensin, an
RT angiotensin II-like endopeptide from the skin of the Australian
RT frog Crinia georgiana.";
RL Experimentia 35:1132-1133 (1979)
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR; S07207; S07207.
KW Vasoconstrictor.
SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 25.0%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PF 4
DB 10 PF 11

Search completed: November 25, 2003, 19:28:25
Job time : 2.90864 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 15.0233 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFPILV 8

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database:

SPTREMBL 23:\*\*

- 1: sp\_archaea:
- 2: sp\_bacteria:
- 3: sp\_fungi:
- 4: sp\_human:
- 5: sp\_invertebrate:
- 6: sp\_mammal:
- 7: sp\_mhc:
- 8: sp\_organelle:
- 9: sp\_phase:
- 10: sp\_plant:
- 11: sp\_rodent:
- 12: sp\_virus:
- 13: sp\_vertebrate:
- 14: sp\_unclassified:
- 15: sp\_virus:
- 16: sp\_bacteriaph:
- 17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	37.5	9	Q9TWD6	Q9TWD6 leptinotars
2	3	37.5	10	Q90Y93	Q90Y93 gallus gall
3	3	37.5	11	P82700	P82700 leucophaea
4	3	37.5	11	Q9TRR7	Q9TRR7 oryctolagus
5	3	37.5	11	Q9QVC5	Q9QVC5 rattus norv
6	3	37.5	12	Q8MJ00	Q8MJ00 saguinus fu
7	3	37.5	12	Q8MJP8	Q8MJP8 callimico g
8	3	37.5	12	Q8MJP7	Q8MJP7 callithrix
9	3	37.5	12	Q8MJP9	Q8MJP9 leontopithe
10	3	37.5	12	Q8MJP6	Q8MJP6 cebuella py
11	3	37.5	12	Q8MJJ3	Q8MJJ3 saimiri sci
12	3	37.5	12	Q8MJ01	Q8MJ01 ateleus fusc
13	3	37.5	12	Q8MJJ2	Q8MJJ2 cebus apell
14	3	37.5	12	Q8MJJ4	Q8MJJ4 actus azara
15	3	37.5	12	Q8KJU3	Q8KJU3 mus musculu
16	3	37.5	13	Q53693	Q53693 streptomyce

17	3	37.5	13	2	034622	034622 borrelia bu
18	3	37.5	13	2	031365	031365 borrelia ga
19	3	37.5	13	2	031364	031364 borrelia ga
20	3	37.5	13	3	093824	093824 candida tro
21	3	37.5	14	2	052220	052220 salmonella
22	3	37.5	14	4	Q16045	Q16045 homo sapien
23	3	37.5	14	13	P82832	P82832 rana luteiv
24	3	37.5	15	2	Q9R5D5	Q9R5D5 chromatium
25	3	37.5	15	4	Q8TCS7	Q8TCS7 homo sapien
26	3	37.5	15	6	Q8WQ02	Q8WQ02 sus scrofa
27	3	37.5	15	6	Q9TRN2	Q9TRN2 sus scrofa
28	3	37.5	15	6	Q9TRN5	Q9TRN5 sus scrofa
29	3	37.5	15	6	Q9TRN4	Q9TRN4 sus scrofa
30	3	37.5	15	8	Q9T2K8	Q9T2K8 spinacia ol
31	3	37.5	15	8	Q35921	Q35921 salmo salar
32	3	37.5	15	10	Q9S929	Q9S929 glycine max
33	3	37.5	15	11	Q9Z1I4	Q9Z1I4 mus musculu
34	3	37.5	15	13	Q9PS10	Q9PS10 gallus gall
35	3	37.5	16	4	Q9UCL0	Q9UCL0 homo sapien
36	3	37.5	16	4	Q9UCK9	Q9UCK9 homo sapien
37	3	37.5	16	5	Q9TZR1	Q9TZR1 halotis fu
38	3	37.5	16	6	Q28324	Q28324 capra hircu
39	3	37.5	16	8	Q8MC25	Q8MC25 sonneratia
40	3	37.5	16	8	Q8MC39	Q8MC39 ammannia ba
41	3	37.5	16	8	Q8LVB1	Q8LVB1 punica gran
42	3	37.5	16	8	Q8MC53	Q8MC53 woodfordia
43	3	37.5	16	8	Q8MC17	Q8MC17 ludwigia hy
44	3	37.5	16	8	Q8LVB2	Q8LVB2 lythrum sal
45	3	37.5	16	8	Q8LVB0	Q8LVB0 trapa maxim
46	3	37.5	16	8	Q8ME12	Q8ME12 saxifraga s
47	3	37.5	16	8	Q8MC45	Q8MC45 decodon ver
48	3	37.5	16	8	Q8MC21	Q8MC21 combreum w
49	3	37.5	16	8	Q8MC51	Q8MC51 cuphea lanc
50	3	37.5	16	8	Q8MC33	Q8MC33 rotala indi
51	3	37.5	16	8	Q8MC19	Q8MC19 quisqualis
52	3	37.5	16	8	Q8MC49	Q8MC49 pemphis aci
53	3	37.5	16	8	Q8MC27	Q8MC27 lagerstroem
54	3	37.5	16	8	Q8MET0	Q8MET0 cercidiphyll
55	3	37.5	16	8	Q8MC23	Q8MC23 sonneratia
56	3	37.5	16	8	Q8MC41	Q8MC41 nesaea lued
57	3	37.5	16	8	Q8MC15	Q8MC15 fuchsia hyb
58	3	37.5	16	8	Q8MC43	Q8MC43 sonneratia
59	3	37.5	16	8	Q8MC47	Q8MC47 peplis port
60	3	37.5	16	8	Q8MC37	Q8MC37 lawsonia in
61	3	37.5	16	8	Q8MC29	Q8MC29 duabanga gr
62	3	37.5	16	8	Q8MC31	Q8MC31 lagerstroem
63	3	37.5	16	8	Q8MS8	Q8MS8 daphniphyll
64	3	37.5	16	8	Q8MC35	Q8MC35 heimia myrt
65	3	37.5	17	4	Q92727	Q92727 homo sapien
66	3	37.5	17	4	Q96RT3	Q96RT3 homo sapien
67	3	37.5	17	6	Q8MIC8	Q8MIC8 orycteropus
68	3	37.5	17	6	Q8MIC1	Q8MIC1 physeter ca
69	3	37.5	17	6	Q8MID3	Q8MID3 manlis sp. p
70	3	37.5	17	6	Q8MIG3	Q8MIG3 diceros bic
71	3	37.5	17	6	Q9TRH5	Q9TRH5 bos taurus
72	3	37.5	17	6	Q8MIF6	Q8MIF6 equus cabal
73	3	37.5	17	6	Q8MI97	Q8MI97 trichechus
74	3	37.5	17	6	Q8MIG9	Q8MIG9 cynopterus
75	3	37.5	17	6	Q8MIF2	Q8MIF2 elephas max
76	3	37.5	17	8	Q9XON9	Q9XON9 sinapis alb
77	3	37.5	17	12	Q85673	Q85673 reovirus (t
78	3	37.5	17	16	Q8X4A4	Q8X4A4 escherichia
79	3	37.5	18	4	Q9BZM7	Q9BZM7 homo sapien
80	3	37.5	18	13	Q90790	Q90790 gallus gall
81	3	37.5	18	13	Q90XC9	Q90XC9 gallus gall
82	3	37.5	19	2	P74875	P74875 salmonella
83	3	37.5	19	2	Q9RLU4	Q9RLU4 lactococcus
84	3	37.5	19	2	Q51278	Q51278 neisseria m
85	3	37.5	19	4	Q8TCB2	Q8TCB2 homo sapien
86	3	37.5	19	6	Q9TR01	Q9TR01 sus scrofa
87	3	37.5	19	10	Q9S8M8	Q9S8M8 triticum ae
88	3	37.5	19	10	Q9S8Q0	Q9S8Q0 pinus sylve
89	3	37.5	19	11	Q925G8	Q925G8 mus musculu

90 3 37.5 19 12 Q90633 baboon herp  
 91 3 37.5 19 12 Q90630 baboon herp  
 92 3 37.5 19 13 Q9DE21 gallus gall  
 93 3 37.5 19 15 Q905K0 human immun  
 94 3 37.5 19 15 Q905G4 human immun  
 95 3 37.5 19 15 Q905I4 human immun  
 96 3 37.5 19 15 Q90RG5 human immun  
 97 3 37.5 19 15 Q905E4 human immun  
 98 3 37.5 19 15 Q905L2 human immun  
 99 3 37.5 20 2 Q9R4V3 pseudomonas  
 100 3 37.5 20 2 Q53346 pseudomonas

## ALIGNMENTS

## RESULT 1

Q9TWD6 Q9TWD6 PRELIMINARY; PRT; 9 AA.  
 AC Q9TWD6;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)  
 DE LBD-NPF-I-NEUROPEPTIDE F-related peptide.  
 OS Leptinotarsa decemlineata (Colorado potato beetle).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
 OC Chrysomelini; Leptinotarsa.  
 OC NCBI\_TaxID=7539;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96245438; PubMed=8814784;  
 RA Spittels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,  
 RA Van Beeumen J., De Loof A.;  
 RT "Insect neuropeptide F (NPF)-related peptides: isolation from Colorado  
 potato beetle (Leptinotarsa decemlineata) brain."  
 RL Insect Biochem. Mol. Biol. 26:375-382 (1996).  
 SQ SEQUENCE 9 AA; 1066 MW; 7502340736C76864 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3  
 |||  
 Db 2 RGP 4

## RESULT 2

Q90Y93 Q90Y93 PRELIMINARY; PRT; 10 AA.  
 AC Q90Y93;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Growth hormone (Fragment).  
 GN GH.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kansaku N., Nakada A., Yagi E., Okabayashi H., Guemene D.;  
 RT "Genetic variation of chicken growth hormone gene."  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB061722; BAB69037.1; --  
 FT NON\_TER 1 1  
 NON\_TER 10 10  
 FT SEQUENCE 10 AA; 1155 MW; 6841751775A40AAB CRC64;

Query Match 37.5%; Score 3; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3  
 |||  
 Db 8 RGP 10

## RESULT 3

P82700 P82700 PRELIMINARY; PRT; 11 AA.  
 AC P82700;  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE Periviscerokinin-3 (LEM-PVK-3).  
 OS Leucophaea maderae (Madeira cockroach).  
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach).  
 OS Blaberus craniifer,  
 OS Blaptica dubia (Argentinian wood cockroach), and  
 OS Gromphadorina portentosa (Cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OC NCBI\_TaxID=6988, 6990, 6982, 132935, 36953;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.  
 RC TYSSUE=ABDOMINAL PERISYMPATHETIC ORGANS;  
 RX MEDLINE=20307624; PubMed=10849006;  
 RA Friedel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;  
 RT "Identification of novel periviscerokinin from single neurohaemal  
 release sites in insects. MS/MS fragmentation complemented by Edman  
 degradation."  
 RL Eur. J. Biochem. 267:3869-3873 (2000).  
 CC -I- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY  
 (MYOTROPIC ACTIVITY)  
 CC -I- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 11 11  
 FT SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 5.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5  
 |||  
 Db 7 PFP 9

## RESULT 4

Q9TRR7 Q9TRR7 PRELIMINARY; PRT; 11 AA.  
 AC Q9TRR7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Calcyclin-associated protein, CAP50=CA2+/phospholipid-binding protein  
 L-13 fragment (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92250478; PubMed=1533622;  
 RA Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;  
 RT "A calcyclin-associated protein is a newly identified member of the  
 Ca2+/phospholipid-binding proteins, annexin family."  
 RL J. Biol. Chem. 267:8919-8924 (1992).  
 FT NON\_TER 1 1  
 NON\_TER 11 11  
 FT SEQUENCE 11 AA; 1155 MW; 6841751775A40AAB CRC64;

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SQ SEQUENCE 11 AA; 1310 MW; 55580B0F5DDAA9C7 CRC64;

Query Match      37.5%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 P I L 7
Db      |||
        2 P I L 4

RESULT 5
O9QVC5 PRELIMINARY; PRT; 11 AA.
AC Q9QVC5;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMELrel. 14, Last annotation update)
DE DM53 protein (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE
RX MEDLINE=92291078; PubMed=1601872;
RA Subramaniam V.N., bin Mohd Yusoff A.R., Wong S.H., Lim G.B., Chew M.,
RA Hong W.;
RT "Biochemical fractionation and characterization of proteins from
RT Golgi-enriched membranes.";
RL J. Biol. Chem. 267:12016-12021(1992).
FT NON_TER 11
SQ SEQUENCE 11 AA; 1210 MW; 5861C10B9DDAB2C7 CRC64;

Query Match      37.5%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 I L V 8
Db      |||
        1 I L V 3

RESULT 6
Q8MJQ0 PRELIMINARY; PRT; 12 AA.
AC Q8MJQ0;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Saginuis fuscicollis (Brown-headed tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9487;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368142; AAN01092.1; -.
KW Kinase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match      37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 G P F 4
Db      |||
        10 G P F 12

RESULT 8
Q8MJP7 PRELIMINARY; PRT; 12 AA.
AC Q8MJP7;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368145; AAN01095.1; -.
KW Kinase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match      37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 G P F 4
Db      |||
        10 G P F 12

RESULT 9
Q8MJP9 PRELIMINARY; PRT; 12 AA.
AC Q8MJP9;

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Db      10 G P F 12

RESULT 7
Q8MJP8 PRELIMINARY; PRT; 12 AA.
AC Q8MJP8;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Callimico goeldii (Goeldi's marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callimico.
OX NCBI_TaxID=9495;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368144; AAN01094.1; -.
KW Kinase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match      37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 G P F 4
Db      |||
        10 G P F 12

RESULT 8
Q8MJP7 PRELIMINARY; PRT; 12 AA.
AC Q8MJP7;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMELrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368145; AAN01095.1; -.
KW Kinase.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match      37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 G P F 4
Db      |||
        10 G P F 12

RESULT 9
Q8MJP9 PRELIMINARY; PRT; 12 AA.
AC Q8MJP9;

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Leontopithecus rosalia (Golden lion tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Leontopithecus.
OX NCBI_TaxID=30588;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368143; AAN01093.1; -.
KW Kinase.
FT NON_TER 1 12
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
Db 10 GPF 12

RESULT 10
Q8MJF6
ID Q8MJF6 PRELIMINARY; PRT; 12 AA.
AC Q8MJF6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (fragment).
GN STK-1.
OS Cebuella pygmaea (Pygmy marmoset) (Callithrix pygmaea).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
OX NCBI_TaxID=9493;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368146; AAN01096.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; 5FBA39254AB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
Db 10 GPF 12

RESULT 11
Q8MJE3
ID Q8MJE3 PRELIMINARY; PRT; 12 AA.
AC Q8MJE3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Saimiri sciureus (Common squirrel monkey).
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368144; AAN01091.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
Db 10 GPF 12

RESULT 12
Q8MJQ1
ID Q8MJQ1 PRELIMINARY; PRT; 12 AA.
AC Q8MJQ1;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OS Ateles fusciceps (Brown-headed spider monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateles.
OX NCBI_TaxID=9508;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368141; AAN01091.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
Db 10 GPF 12

RESULT 13
Q8MJE2
ID Q8MJE2 PRELIMINARY; PRT; 12 AA.
AC Q8MJE2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stem cell tyrosine kinase 1 (Fragment).
GN STK-1.
OC Cebus apella (Brown-capped capuchin).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebus.
OX NCBI_TaxID=9515;
RN [1]
RP SEQUENCE FROM N.A.
RA Singer S.S., Schmitz J., Schwieck C., Zischler H.;
RT "Molecular cladiatic markers in New World monkey phylogeny.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF368141; AAN01091.1; -.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
Db 10 GPF 12
```

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF489262; AAN01127.1; --  
 KW Kinase.  
 FT NON\_TER 1  
 12 12  
 SQ SEQUENCE 12 AA; 1290 MW; 5FBA3924FAB44727 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4  
 ||||  
 Db 10 GPF 12

## RESULT 14

Q8MJEA PRELIMINARY; PRT; 12 AA.  
 AC Q8MJEA;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Stem cell tyrosine kinase 1 (Fragment).  
 GN STK-1.  
 OS Aotus azarai (Aotus azarai).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Actinae; Aotus.  
 OX NCBI\_TaxID=30591;  
 [1]  
 RN RP SEQUENCE FROM N.A.  
 RA Singer S.S., Schmitz J., Schwiegk C., Zischler H.;  
 RT "Molecular cladtastic markers in New World monkey phylogeny."  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF489260; AAN01125.1; --  
 KW Kinase.  
 FT NON\_TER 1  
 12 12  
 SQ SEQUENCE 12 AA; 1314 MW; EBBA3924FAB44721 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4  
 ||||  
 Db 10 GPF 12

## RESULT 15

Q8K3U3 PRELIMINARY; PRT; 12 AA.  
 AC Q8K3U3;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Lectin yml (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RA Welch J.S., Escoubet-Lozach L., Sykes D.B., Glass C.K.;  
 RT "TH2 cytokines and allergic challenge induce yml expression in  
 RT macrophages by a STAT6-dependent mechanism."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF533510; AAN04032.1; --  
 FT NON\_TER 12  
 12 12  
 SQ SEQUENCE 12 AA; 1301 MW; 1373DC4258B2C720 CRC64;

Query Match 37.5%; Score 3; DB 11; Length 12;

Best Local Similarity 100.0%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
 ||||  
 Db 5 ILV 7

## RESULT 16

Q53693 PRELIMINARY; PRT; 13 AA.  
 ID Q53693;  
 AC Q53693;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE Leader peptide.  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=33903;  
 [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=CU-18;  
 RX MEDLINE=96105213; PubMed=8529876;  
 RA De Rossi E., Leva R., Gusberti L., Manachini P.L., Riccardi G.;  
 RT "Cloning, sequencing and expression of the ilvNC gene cluster from  
 RT Streptomyces avermitilis."  
 RL Gene 166:127-132(1995).  
 DR EMBL; L39268; AAA93097.1; --  
 SQ SEQUENCE 13 AA; 1499 MW; 5E080E40PD4E32C7 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
 ||||  
 Db 5 ILV 7

## RESULT 17

O34622 PRELIMINARY; PRT; 13 AA.  
 ID O34622;  
 AC O34622;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
 DE GUAA (Fragment).  
 GN GUAA.  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 [1]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=CT39, DNI27CL9-2, and 25015;  
 RX MEDLINE=97426044; PubMed=9282748;  
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,  
 RA Rosa P.;  
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of  
 RT plasmid structure and targeted inactivation of the ospC gene."  
 RL Mol. Microbiol. 25:361-374(1997).  
 [2]  
 RN RP SEQUENCE FROM N.A.  
 RC STRAIN=DN127CL9-2, and 25015;  
 RX MEDLINE=95154673; PubMed=7851744;  
 RA Stevenson B., Barthold S.W.;  
 RT "Expression and sequence of outer surface protein C among North  
 RT American isolates of Borrelia burgdorferi."  
 RL FEMS Microbiol. Lett. 124:367-372(1994).  
 DR EMBL; U93694; AAC45522.1; --  
 DR EMBL; U04280; AAC45543.1; --  
 DR EMBL; U04282; AAC45541.1; --  
 FT NON\_TER 13  
 13 13

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SQ SEQUENCE 13 AA; 1407 MW; 08FAB3930E0BC720 CRC64;
Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db |||
6 ILV 8

RESULT 18
O31365 PRELIMINARY; PRT; 13 AA.
ID O31365;
AC O31365;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GuAA (Fragment).
GN GUAA.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP90;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "the Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93701; AAC45536.1; -.
FT NON_TER 13
FT SEQUENCE 13 AA; 1382 MW; 08EFB4180E0BC720 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db |||
6 ILV 8

RESULT 19
O31364 PRELIMINARY; PRT; 13 AA.
ID O31364;
AC O31364;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GuAA (Fragment).
GN GUAA.
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G25;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "the Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL; U93700; AAC45534.1; -.
FT NON_TER 13
FT SEQUENCE 13 AA; 1449 MW; 08FAB9B05E0BC720 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ SEQUENCE 13 AA; 1407 MW; 08FAB3930E0BC720 CRC64;
Query Match 37.5%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db |||
6 ILV 8

RESULT 20
O93824 PRELIMINARY; PRT; 13 AA.
ID O93824;
AC O93824;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE UDP-galactose-4-epimerase (Fragment).
GN GAL10.
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PK233;
RA Kanai T., Ueda M., Tanaka A.;
RT "Candida tropicalis promoter region of GAL1 and GAL10 gene.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB019434; BAA34351.1; -.
FT NON_TER 1
FT NON_TER 13
FT SEQUENCE 13 AA; 1312 MW; 0B559D6AE18BC720 CRC64;

Query Match 37.5%; Score 3; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db |||
6 ILV 8

RESULT 21
O52220 PRELIMINARY; PRT; 14 AA.
ID O52220;
AC O52220;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE YecG (Fragment).
GN YECG.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Toguchi A., Harshey R.M.;
RT "Flagellar master operon (fliH and fliC) from Salmonella typhimurium
RT LT2 (includes partial upstream yecG sequence and downstream mocha
RT promoter sequence).";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029300; AAB96642.1; -.
FT NON_TER 14
FT SEQUENCE 14 AA; 1561 MW; 42679A87F94DFBC7 CRC64;

Query Match 37.5%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db |||
6 ILV 8

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RESULT 22  
Q16045  
ID Q16045 PRELIMINARY; PRT; 14 AA.  
AC Q16045  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE D3 dopamine receptor (Fragment).  
GN D3R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=93326145; PubMed=7916609;  
RA Nagai Y., Ueno S., Saeki Y., Soga F., Yanagihara T.;  
RT "Expression of the D3 dopamine receptor gene and a novel variant  
RT transcript generated by alternative splicing in human peripheral blood  
RT lymphocytes";  
RL Biochem. Biophys. Res. Commun. 194:368-374(1993).  
DR EMBL; S63845; AAB27543.2; -.  
KW Receptor.  
FT NON\_TER  
SQ SEQUENCE 14 AA; 1586 MW; EA310BEFE94CF1B1 CRC64;  
Query Match 37.5%; Score 3; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGP 3  
DB 4 RGP 6  
RESULT 23  
P82832  
ID P82832 PRELIMINARY; PRT; 14 AA.  
AC P82832;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Temporin-ILC.  
OS Rana luteiventris.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
OX NCBI\_TaxID=58176;  
RN [1]  
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
RC TISSUE=SKIN;  
RX MEDLINE=20117700; PubMed=10651828;  
RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,  
RA Conlon J.M.;  
RT "Peptides with antimicrobial activity from four different families  
RT isolated from the skins of the North American frogs Rana luteiventris,  
RT Rana berlandieri and Rana pipiens.";  
RL Sur. J. Biochem. 267:894-900(2000).  
CC -!- FUNCTION: ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE BACTERIUM  
CC S.AUREUS. WEAK ACTIVITY AGAINST GRAM-NEGATIVE BACTERIUM E.COLI AND  
CC THE YEAST C.ALBICANS.  
CC -!- MASS SPECTROMETRY: MW=1603.1; METHOD=ELECTROSPRAY.  
CC -!- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN  
CC FAMILY.  
KW Antibiotic; Amidation; Fungicide.  
FT MOD\_RES 14 14  
SQ SEQUENCE 14 AA; 1604 MW; 0B540E1B7FCA8924 CRC64;  
Query Match 37.5%; Score 3; DB 13; Length 14;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 PIL 7

Db 3 PIL 5  
RESULT 24  
Q9R5D5  
ID Q9R5D5 PRELIMINARY; PRT; 15 AA.  
AC Q9R5D5;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE POLY(3-HYDROXYBUTYRIC acid) granule-associated 40 kDa protein  
DE (Fragment).  
OS Chromatium vinosum.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales;  
OC Chromatiaceae; Allochromatium.  
OX NCBI\_TaxID=1049;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93146381; PubMed=1490603;  
RA Liebergesell M., Schmidt B., Steinbuechel A.;  
RT "Isolation and identification of granule-associated proteins relevant  
RT for poly(3-hydroxyalkanoic acid) biosynthesis in Chromatium vinosum  
RT D.";  
RL FEMS Microbiol. Lett. 78:227-232(1992).  
SQ SEQUENCE 15 AA; 1834 MW; 215B7FCF65BB8E CRC64;  
Query Match 37.5%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 FPI 6  
DB 2 FPI 4  
RESULT 25  
Q8TCS7  
ID Q8TCS7 PRELIMINARY; PRT; 15 AA.  
AC Q8TCS7;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Complement component C7 (Fragment).  
GN C7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Gonzalez S., Martinez Borra J., Lopez Larrea C.;  
RT "Cloning and characterization of human complement component C7  
RT promoter";  
RL Genes Immun. 0:0-0(2002).  
DR EMBL; Y11720; CAA72407.1; -.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1666 MW; 10984ADCA7B43F19 CRC64;  
Query Match 37.5%; Score 3; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 6 ILV 8  
DB 8 ILV 10  
RESULT 26  
Q8WNQ2  
ID Q8WNQ2 PRELIMINARY; PRT; 15 AA.  
AC Q8WNQ2;



DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
 DE Niemann-Pick type C1 protein (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gevry N.Y., Murphy B.D.;  
 RT "Porcine Niemann-Pick type C1 gene, promoter region."  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF329087; AL37473.1; -.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1572 MW; D96760FBED64A840 CRC64;  
  
 Query Match 37.5%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RGP 3  
 Db ||||  
 4 RGP 6  
  
 RESULT 27  
 Q9TRN2 ID Q9TRN2 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRN2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE LOW MR zona pellucida binding protein (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92378826; PubMed=1510840;  
 RA Parry R.V., Barker P.J., Jones R.;  
 RT "Characterization of low Mr zona pellucida binding proteins from boar  
 spermatozoa and seminal plasma."  
 RL Mol. Reprod. Dev. 33:108-115(1992).  
 SQ SEQUENCE 15 AA; 1572 MW; 7FEC9786771A722E CRC64;  
  
 Query Match 37.5%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RGP 3  
 Db ||||  
 4 RGP 6  
  
 RESULT 28  
 Q9TRN5 ID Q9TRN5 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRN5;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE LOW MR zona pellucida binding protein (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92378826; PubMed=1510840;  
 RA Parry R.V., Barker P.J., Jones R.;  
 RT "Characterization of low Mr zona pellucida binding proteins from boar

RT spermatozoa and seminal plasma.";  
 RL Mol. Reprod. Dev. 33:108-115(1992).  
 SQ SEQUENCE 15 AA; 1604 MW; 7FAA10EE0ECA722E CRC64;  
  
 Query Match 37.5%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RGP 3  
 Db ||||  
 4 RGP 6  
  
 RESULT 29  
 Q9TRN4 ID Q9TRN4 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRN4;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE LOW MR zona pellucida binding protein (Fragment).  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92378826; PubMed=1510840;  
 RA Parry R.V., Barker P.J., Jones R.;  
 RT "Characterization of low Mr zona pellucida binding proteins from boar  
 spermatozoa and seminal plasma."  
 RL Mol. Reprod. Dev. 33:108-115(1992).  
 SQ SEQUENCE 15 AA; 1768 MW; 7FA2379E1461610E CRC64;  
  
 Query Match 37.5%; Score 3; DB 6; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 RGP 3  
 Db ||||  
 4 RGP 6  
  
 RESULT 30  
 Q9TRK8 ID Q9TRK8 PRELIMINARY; PRT; 15 AA.  
 AC Q9TRK8;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE LHCII kinase, 64 kDa kinase (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92183823; PubMed=1544419;  
 RA Gal A., Herrmann R.G., Lottspeich F., Ohad I.;  
 RT "Phosphorylation of cytochrome b6 by the LHC II kinase associated with  
 the cytochrome complex."  
 RL FEBS Lett. 298:33-35(1992).  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1556 MW; 6E00A4F917DDF33E CRC64;  
  
 Query Match 37.5%; Score 3; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 5 PIL 7



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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=93099171; PubMed=1463770;
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
RT an individual patient of AA-amyloidosis.";
RL Biochim. Biophys. Acta 1180:195-200(1992).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
KW Acute phase; HDL.
SQ SEQUENCE 16 AA; 1585 MW; 1CAB41E77C839CC1 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 1 RGP 3

RESULT 36
Q9UCK9 PRELIMINARY; PRT; 16 AA.
AC Q9UCK9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Serum amyloid A isotype 2 alpha protein (Serum amyloid A protein)
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=93099171; PubMed=1463770;
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
RT an individual patient of AA-amyloidosis.";
RL Biochim. Biophys. Acta 1180:195-200(1992).
CC -!- FUNCTION: MAJOR ACUTE PHASE REACTANT. APOLIPOPROTEIN OF THE HDL
CC COMPLEX (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: PLASMA, SYNTHESIZED BY THE LIVER (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SAA FAMILY.
DR InterPro: IPR000096; Serum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
KW Acute phase; HDL.
SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8CC1 CRC64;

Query Match 37.5%; Score 3; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 1 RGP 3

RESULT 37
Q9TZR1 PRELIMINARY; PRT; 16 AA.
AC Q9TZR1;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fertilization protein (Fragment).
OS Haliotis fulgens (Green abalone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Vetigastropoda; Haliotoidea; Haliotidae; Haliotis.
OX NCBI_TaxID=6456;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98393704; PubMed=9724763;
RA Metz E.C., Robles-Sikisaka R., Vacquier V.D.;
RT "Nonsynonymous substitution in abalone sperm fertilization genes
RT exceeds substitution in introns and mitochondrial DNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:10676-10681(1998).
DR EMBL; AF076837; AAC33936.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1788 MW; 0CAECAB163DA5154 CRC64;

Query Match 37.5%; Score 3; DB 5; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 3 RGP 5

RESULT 38
Q28324 PRELIMINARY; PRT; 16 AA.
ID Q28324;
AC Q28324;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-x-globin (Fragment).
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80227766; PubMed=6248519;
RA Haynes J.R., Rosteck P.R.Jr., Schon E.A., Gallagher P.M., Burks D.J.,
RA Smith K., Lingrel J.B.;
RT "The isolation of the beta-a-, beta-c-, and gamma-globin genes and a
RT presumptive embryonic globin gene from a goat dna recombinant
RT library.";
RL J. Biol. Chem. 255:6355-6367(1980).
DR EMBL; K00659; AAA30919.1; -.
FT NON_TER 1
FT NON_TER 16
FT NON_TER 16
SQ SEQUENCE 16 AA; 1784 MW; D027A9E223320213 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 5 ILV 7

RESULT 39
Q8MC25 PRELIMINARY; PRT; 16 AA.
ID Q8MC25;
AC Q8MC25;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE PsaA (Fragment).

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GN PSAA.
OS Sonneratia apetala.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S165;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035740; AAL14161.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 40
Q8MC39 PRELIMINARY; PRT; 16 AA.
AC Q8MC39;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE PSAA (Fragment).
GN PSAA.
OS Ammannia baccifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Ammannia.
OX NCBI_TaxID=16202;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A610;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035733; AAL14147.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 41
Q8LVE1 PRELIMINARY; PRT; 16 AA.
AC Q8LVE1;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

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DE PSAA (Fragment).
GN PSAA.
OS Punica granatum (Pomegranate).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Punica.
OX NCBI_TaxID=22663;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P728, and P745;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035724; AAL14129.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 42
Q8MC53 PRELIMINARY; PRT; 16 AA.
AC Q8MC53;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE PSAA (Fragment).
GN PSAA.
OS Woodfordia fruticosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Woodfordia.
OX NCBI_TaxID=141189;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W493;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225 (2002).
DR EMBL; AY035722; AAL14125.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 12 ILV 14

RESULT 43
Q8MC17 PRELIMINARY; PRT; 16 AA.
AC Q8MC17;
DT 01-OCT-2002 (TReMBLrel. 22, Created)

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DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE PsaA (Fragment).
GN PSAA.
OS Ludwigia hyssopifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Ludwigia.
OX NCBI_TaxID=155013;
RN [1]_TaxID=155013;
RP SEQUENCE FROM N.A.
RC STRAIN=L787;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035745; AAL14171.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 44
Q8LVE2
ID Q8LVE2 PRELIMINARY; PRT; 16 AA.
AC Q8LVE2;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE PsaA (Fragment).
GN PSAA.
OS Lythrum salicaria (Purple loosestrife).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Lythrum.
OX NCBI_TaxID=13129;
RN [1]_TaxID=13129;
RP SEQUENCE FROM N.A.
RC STRAIN=L758, and 758F;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035727; AAL14135.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 45
Q8LVE0
ID Q8LVE0 PRELIMINARY; PRT; 16 AA.

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AC Q8LVE0;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE PsaA (Fragment).
GN PSAA.
OS Trapa maximowiczii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Trapa.
OX NCBI_TaxID=162053;
RN [1]_TaxID=162053;
RP SEQUENCE FROM N.A.
RC STRAIN=r744, and T010;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035729; AAL14139.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 46
Q8MET2
ID Q8MET2 PRELIMINARY; PRT; 16 AA.
AC Q8MET2;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DE PSI P700 apoprotein A1 (Fragment).
GN PSAA.
OS Saxifraga stolonifera.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Saxifragales; Saxifragaceae; Saxifraga.
OX NCBI_TaxID=182070;
RN [1]_TaxID=182070;
RP SEQUENCE FROM N.A.
RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;
RT "Phylogeny of the Altingiaceae based on cpDNA matK, psbA and rDNA
RT ITS sequences.";
RL Plant Syst. Evol. 230:13-24(2001).
DR EMBL; AF377995; AAM45512.1; -.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 47
Q8MC45
ID Q8MC45 PRELIMINARY; PRT; 16 AA.

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AC Q8MC45;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE psaa (Fragment).
GN psaa
OS Decodon verticillatus (Swamp loosestrife).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Decodon.
OX NCBI_TaxID=162018;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D212;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035728; AAL14137.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 48
Q8MC21
ID Q8MC21 PRELIMINARY; PRT; 16 AA.
AC Q8MC21;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE psaa (Fragment).
GN psaa
OS Combretum wallichii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Combretaceae; Combretum.
OX NCBI_TaxID=131243;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C505;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035743; AAL14167.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 49
Q8MC51
ID Q8MC51 PRELIMINARY; PRT; 16 AA.
AC Q8MC51;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE psaa (Fragment).
GN psaa
OS Cuphea lanceolata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Cuphea.
OX NCBI_TaxID=3930;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C490;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035723; AAL14127.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 50
Q8MC33
ID Q8MC33 PRELIMINARY; PRT; 16 AA.
AC Q8MC33;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DE psaa (Fragment).
GN psaa
OS Rotala indica.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Rotala.
OX NCBI_TaxID=162024;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R492;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035736; AAL14153.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 51
Q8MC51

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Q8MC19 Q8MC19 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC19;  
 AC Q8MC19;  
 DT 01-OCT-2002 (T8EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last annotation update)  
 DE P8AA (Fragment).  
 GN P8AA.  
 OS Quisqualis indica (Rangoon creeper).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Myrtales; Combretaceae; Quisqualis.  
 OX NCBI\_TaxID=3956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Q379;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";   
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035744; AAL14169.1; -.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db 12 ILV 14

RESULT 52  
 Q8MC49 Q8MC49 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC49;  
 AC Q8MC49;  
 DT 01-OCT-2002 (T8EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last annotation update)  
 DE P8AA (Fragment).  
 GN P8AA.  
 OS Pemphis acidula.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Myrtales; Lythraceae; Pemphis.  
 OX NCBI\_TaxID=126635;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=P630;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";   
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035725; AAL14131.1; -.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db 12 ILV 14

RESULT 53  
 Q8MC27 Q8MC27 PRELIMINARY; PRT; 16 AA.  
 ID Q8MC27;  
 AC Q8MC27;  
 DT 01-OCT-2002 (T8EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last annotation update)  
 DE P8AA (Fragment).  
 GN P8AA.  
 OS Lagerstroemia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Myrtales; Lythraceae; Lagerstroemia.  
 OX NCBI\_TaxID=162025;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=L688;  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 RT on Chloroplast rbcL Gene, psaA-ycf3 Spacer, and Nuclear rDNA Internal  
 RT Transcribed Spacer (ITS) Sequences.";   
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035739; AAL14159.1; -.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db 12 ILV 14

RESULT 54  
 Q8MET0 Q8MET0 PRELIMINARY; PRT; 16 AA.  
 ID Q8MET0;  
 AC Q8MET0;  
 DT 01-OCT-2002 (T8EMBLrel. 22, Created)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (T8EMBLrel. 22, Last annotation update)  
 DE P8A P700 apoprotein A1 (Fragment).  
 GN P8AA.  
 OS Cercidiphyllum japonicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Saxifragales; Cercidiphyllaceae; Cercidiphyllum.  
 OX NCBI\_TaxID=13413;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, psbA and rDNA  
 RT ITS sequences.";   
 RL Plant Syst. Evol. 230:13-24(2001).  
 DR EMBL; AF377996; AAM45514.1; -.  
 KW Chloroplast.  
 FT NON\_TER 16 16  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db 12 ILV 14

RESULT 55

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Q8MC23
ID Q8MC23 PRELIMINARY; PRT; 16 AA.
AC Q8MC23;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia alba.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122812;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S482;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AV035741; AAL14163.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 56
Q8MC41
ID Q8MC41 PRELIMINARY; PRT; 16 AA.
AC Q8MC41;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Nesaea luederitzi.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Nesaea.
OX NCBI_TaxID=162020;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N213;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AV035732; AAL14145.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 57
Q8MC15
ID Q8MC15 PRELIMINARY; PRT; 16 AA.
AC Q8MC15;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Fuchsia hybrid cultivar.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Onagraceae; Fuchsia.
OX NCBI_TaxID=133545;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F016;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AV035746; AAL14173.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

RESULT 58
Q8MC43
ID Q8MC43 PRELIMINARY; PRT; 16 AA.
AC Q8MC43;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Sonneratia caseolaris.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Myrtales; Lythraceae; Sonneratia.
OX NCBI_TaxID=122814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S435;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AV035731; AAL14143.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 12 ILV 14

```



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RESULT 59
Q8MC47
ID Q8MC47 PRELIMINARY; PRT; 16 AA.
AC Q8MC47;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Peplis portula.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Myrtales; Lythraceae; Peplis.
OX NCBI_TaxID=162016;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P220;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035726; AAL14133.1; -.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 12 ILV 14

RESULT 60
Q8MC37
ID Q8MC37 PRELIMINARY; PRT; 16 AA.
AC Q8MC37;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Lawsonia inermis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Myrtales; Lythraceae; Lawsonia.
OX NCBI_TaxID=141191;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L494;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035734; AAL14149.1; -.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 12 ILV 14

RESULT 61
Q8MC29
ID Q8MC29 PRELIMINARY; PRT; 16 AA.
AC Q8MC29;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Duabanga grandiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Myrtales; Lythraceae; Duabanga.
OX NCBI_TaxID=122808;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D441;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035738; AAL14157.1; -.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 12 ILV 14

RESULT 62
Q8MC31
ID Q8MC31 PRELIMINARY; PRT; 16 AA.
AC Q8MC31;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE PsaA (Fragment).
GN PSAA.
OS Lagerstroemia speciosa.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Myrtales; Lythraceae; Lagerstroemia.
OX NCBI_TaxID=122810;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L477;
RA Huang Y., Shi S.;
RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based
RT on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal
RT Transcribed Spacer (ITS) Sequences.";
RL Int. J. Plant Sci. 163:215-225(2002).
DR EMBL; AY035737; AAL14155.1; -.
KW Chloroplast.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;

Query Match 37.5%; Score 3; DB 8; Length 16;
Best Local Similarity 100.0%; Pred. No. 7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 12 ILV 14

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Db 12 ILV 14

## RESULT 63

Q8MES8 PRELIMINARY; PRT; 16 AA.  
 ID AC Q8MES8  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE PSI P700 apoprotein A1 (Fragment).  
 GN PSAA.  
 OS Daphniphyllum calycinum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Saxifragales; Daphniphyllaceae; Daphniphyllum.  
 OX NCBI\_TaxID=182071;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shi S., Huang Y., Zhong Y., Du Y., Zhang Q., Chang H., Boufford D.E.;  
 RT "Phylogeny of the Altingiaceae based on cpDNA matK, psA-IGS and nrDNA  
 ITS sequences."  
 RL Plant Syst. Evol. 230:13-24(2001).  
 DR EMBL; AF377997; AAM45516.1; -.  
 KW Chloroplast. 16 16  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 12 ILV 14

## RESULT 64

Q8MC35 PRELIMINARY; PRT; 16 AA.  
 ID AC Q8MC35  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Psaa (Fragment).  
 GN PSAA.  
 OS Heimia myrtifolia.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Myrtales; Lythraceae; Heimia.  
 OX NCBI\_TaxID=135798;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Huang Y., Shi S.;  
 RT "Phylogenetics of Lythraceae sensu lato: A Preliminary Analysis Based  
 on Chloroplast rbcL Gene, psaa-ycf3 Spacer, and Nuclear rDNA Internal  
 Transcribed Spacer (ITS) Sequences."  
 RL Int. J. Plant Sci. 163:215-225(2002).  
 DR EMBL; AY035735; ANU14151.1; -.  
 KW Chloroplast. 16 16  
 FT NON\_TER  
 SQ SEQUENCE 16 AA; 1895 MW; 517FE691B89355B9 CRC64;  
 Query Match 37.5%; Score 3; DB 8; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 12 ILV 14

## RESULT 65

Q92727 PRELIMINARY; PRT; 17 AA.  
 ID AC Q92727; P78498;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-NOV-1998 (TrEMBLrel. 09, Last annotation update)  
 DE Retinoblastoma susceptibility protein (RB1) (Fragment).  
 GN RB1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=92319557; PubMed=1352398;  
 RA Hogg A., Onadim Z., Baird P.N., Cowell J.K.;  
 RT "Detection of heterozygous mutations in the RB1 gene in retinoblastoma  
 patients using single-strand conformation polymorphism analysis and  
 RT polymerase chain reaction sequencing."  
 RL Oncogene 7:1445-1451(1992).  
 RN [2]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RX MEDLINE=95187159; PubMed=7881418;  
 RA Lohmann D.R., Brandt B., Hopping W., Passarge E., Horsthemke B.;  
 RT "Spectrum of small length germline mutations in the RB1 gene."  
 RL Hum. Mol. Genet. 3:2187-2193(1994).  
 DR EMBL; L41911; AAB59483.1; -.  
 DR EMBL; L49233; AAA82562.1; -.  
 FT NON\_TER 1 1  
 FT VARIANT 12 12 F->S.  
 SQ SEQUENCE 17 AA; 1907 MW; 1BSF711F14D24F18 CRC64;  
 Query Match 37.5%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8

Db 1 ILV 3

## RESULT 66

Q96RT3 PRELIMINARY; PRT; 17 AA.  
 ID AC Q96RT3  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Tuberous sclerosis 1 (Fragment).  
 GN TSC1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Fang L., Wu Z.Y., Wang N., MuRong S.X., Lin M.T., Chao D.R.,  
 RA Fang Z.M.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF274229; AAK60416.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1971 MW; 611013A3BB6826F5 CRC64;  
 Query Match 37.5%; Score 3; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3

Db 1 ILV 3

```
Db 1 RGP 3

RESULT 67
Q8MIC8 PRELIMINARY; PRT; 17 AA.
AC Q8MIC8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Prion protein (Fragment).
GN PRMP.
OS Orycteropus afer (Aardvark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Tubulidentata; Orycteropodidae; Orycteropus.
OX NCBI_TaxID=9818;
RN [1]
RP SEQUENCE FROM N.A.
RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
RT "Sequence gaps join mice and men.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ438206; CAD27291.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1869 MW; 40B52A0CCEFA40D8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 10 ILV 12

RESULT 68
Q8MIC1 PRELIMINARY; PRT; 17 AA.
AC Q8MIC1;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Prion protein (Fragment).
GN PRMP.
OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Physetridae; Physeter.
OX NCBI_TaxID=9755;
RN [1]
RP SEQUENCE FROM N.A.
RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
RT "Sequence gaps join mice and men.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ438193; CAD27278.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1942 MW; B1AB5496B11C40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 10 ILV 12

RESULT 69
Q8MID3 PRELIMINARY; PRT; 17 AA.
AC Q8MID3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Prion protein (Fragment).
GN PRMP.
OS Prion protein (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Pholidota; Manidae; Manis.
OX NCBI_TaxID=49127;
RN [1]
RP SEQUENCE FROM N.A.
RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
RT "Sequence gaps join mice and men.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ438196; CAD27281.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1859 MW; 5CC03E10121C40D8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 10 ILV 12

RESULT 70
Q8MIG3 PRELIMINARY; PRT; 17 AA.
AC Q8MIG3;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Prion protein (Fragment).
GN PRMP.
OS Dicerus bicornis (Black rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.
OX NCBI_TaxID=9805;
RN [1]
RP SEQUENCE FROM N.A.
RA Poux C., van Rheede T., Madsen O., de Jong W.W.;
RT "Sequence gaps join mice and men.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ438195; CAD27280.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1885 MW; B1A03E10121C5FF8 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
Db 10 ILV 12

RESULT 71
Q9TRH5 PRELIMINARY; PRT; 17 AA.
AC Q9TRH5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Alpha-SI-casein homolog (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93231344; PubMed=1299613;
RA Neuteboom B., Giuffrida M.G., Conti A.;
RT "Isolation of a new ligand-carrying casein fragment from bovine
```

RT mammary gland microsomes.";  
 RL FEBS Lett. 305:189-191(1992).  
 SQ SEQUENCE 17 AA; 1950 MW; 8890EF0685A0537F CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PFP 5  
 Db ||||  
 4 PFP 6

RESULT 72  
 Q8MIF6 PRELIMINARY; PRT; 17 AA.  
 AC Q8MIF6  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Prion protein (Fragment).  
 GN PRMP.  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 ON NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;  
 RT "Sequence gaps join mice and men."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ438194; CAD27279.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1857 MW; B1A03E10121C40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db ||||  
 10 ILV 12

RESULT 73  
 Q8M197 PRELIMINARY; PRT; 17 AA.  
 AC Q8M197  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Prion protein (Fragment).  
 GN PRMP.  
 OS Trichechus manatus (Caribbean manatee) (West Indian manatee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Sirenia; Trichechidae; Trichechus.  
 ON NCBI\_TaxID=9778;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;  
 RT "Sequence gaps join mice and men."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ438205; CAD27290.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1837 MW; B1A52A0CECF40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db ||||  
 10 ILV 12

RESULT 74

Q8MIG9 PRELIMINARY; PRT; 17 AA.  
 AC Q8MIG9  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Prion protein (Fragment).  
 GN PRMP.  
 OS Cynopterus sphinx (Indian short-nosed fruit bat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;  
 OC Pteropodidae; Cynopterus.  
 ON NCBI\_TaxID=9400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;  
 RT "Sequence gaps join mice and men."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ438197; CAD27282.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1857 MW; B1A03E101FAA40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db ||||  
 10 ILV 12

RESULT 75

Q8MIF2 PRELIMINARY; PRT; 17 AA.  
 AC Q8MIF2  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Prion protein (Fragment).  
 GN PRMP.  
 OS Elephas maximus (Indian elephant).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Proboscidea; Elephantaidea; Elephas.  
 ON NCBI\_TaxID=9783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Poux C., van Rheede T., Madsen O., de Jong W.W.;  
 RT "Sequence gaps join mice and men."  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ438204; CAD27289.1; -.  
 FT NON TER 17  
 SQ SEQUENCE 17 AA; 1857 MW; B1A52A0CFDAB40C5 CRC64;

Query Match 37.5%; Score 3; DB 6; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 7.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 ILV 8  
 Db ||||  
 10 ILV 12

Search completed: November 25, 2003, 19:34:10  
 Job time : 16.0233 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 20.4186 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGFPPILV 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

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- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	100.0	8	22 AAB72274	Colostrinin derive
2	8	100.0	8	22 AAB72527	Colostrinin peptid
3	8	100.0	8	22 AAB72559	Colostrinin peptid
4	8	100.0	8	22 AAB59339	Ewe colostrinin pe
5	8	100.0	8	23 AAE20256	Colostrinin consti
6	8	100.0	8	23 AAM51063	Colostrinin consti
7	8	100.0	8	23 AAO14605	Neural cell regula
8	6	75.0	6	20 AAY30980	Non-crosslinked pr
9	6	75.0	6	21 AAB18488	Peptide substrate

10	6	75.0	15	15 AAB58340	Hypotensive polype
11	6	75.0	15	15 AAB58341	Hypotensive polype
12	5	62.5	13	13 AAR28573	DCase inhibitor p
13	5	62.5	7	15 AAR45831	Aureobasidin type
14	5	62.5	8	15 AAR58333	Hypotensive polype
15	5	62.5	16	24 ABR83258	G protein-coupled
16	5	62.5	18	21 AAB27612	Human secreted pro
17	5	62.5	18	21 AAB27613	Human secreted pro
18	4	50.0	5	18 AAW54333	Bradykinin analogo
19	4	50.0	5	19 AAW57933	Polypyrrol inhibi
20	4	50.0	5	22 AAB86116	Serine proteinase
21	4	50.0	5	22 AAB86117	Internal sequence
22	4	50.0	6	16 AAR77192	Amino acid sequenc
23	4	50.0	7	19 AAW56422	Bacteriophage Type
24	4	50.0	7	22 AAS09134	Aureobasidin type
25	4	50.0	8	15 AAR45825	Cw6 consensus pept
26	4	50.0	9	17 AAR89371	Active site sequen
27	4	50.0	9	19 AAW80249	Human C35 peptid
28	4	50.0	9	22 ABB14561	DPI tryptic digest
29	4	50.0	9	22 AAU28830	Depression-Associ
30	4	50.0	9	22 AAU26478	p53 epitope B7 sup
31	4	50.0	9	22 AAG89664	p53 epitope B7 sup
32	4	50.0	9	22 AAG89665	Tumour associated
33	4	50.0	9	22 AAB76157	Tumour associated
34	4	50.0	9	22 AAB76158	Human leukocyte an
35	4	50.0	9	23 AAG96732	Human ADPI tryptic
36	4	50.0	9	23 AAG67743	Human cancer-relat
37	4	50.0	9	24 ABR20445	Human cancer-relat
38	4	50.0	9	24 ABR20847	Human cancer-relat
39	4	50.0	9	24 ABR21656	Human cancer-relat
40	4	50.0	9	24 ABR21837	Human cancer-relat
41	4	50.0	9	24 ABR22240	Human cancer-relat
42	4	50.0	9	24 ABR22262	Human cancer-relat
43	4	50.0	9	24 ABR23247	Human cancer-relat
44	4	50.0	9	24 ABR23645	Human cancer-relat
45	4	50.0	10	17 AAV17845	Backbone cyclised
46	4	50.0	10	17 AAV17846	Backbone cyclised
47	4	50.0	10	17 AAV17847	Backbone cyclised
48	4	50.0	10	18 AAX36625	Thrombopoietin rec
49	4	50.0	10	18 AAW09474	Thrombopoietin rec
50	4	50.0	10	21 AAB17007	TPO-mimetic peptid
51	4	50.0	10	22 AAU25844	Human thrombopoiet
52	4	50.0	10	22 AAG7037	Saccharomyces cere
53	4	50.0	10	22 AAG7037	TPO mimetic peptid
54	4	50.0	10	23 ABR72893	Staphylococcus aur
55	4	50.0	10	24 ABR47211	Staphylococcus aur
56	4	50.0	10	24 ABR47287	Staphylococcus aur
57	4	50.0	10	24 ABR20396	Human cancer-relat
58	4	50.0	10	24 ABR21693	Human cancer-relat
59	4	50.0	10	24 ABR21964	Human cancer-relat
60	4	50.0	10	24 ABR23102	Human cancer-relat
61	4	50.0	11	18 AAW13931	CDR-3 fragment of
62	4	50.0	11	23 AAG68633	Desmocollin 1 pept
63	4	50.0	11	23 AAG68635	Desmocollin 1 pept
64	4	50.0	12	18 AAW36886	HTLV-II protease c
65	4	50.0	12	21 AAB12848	STAR3 binding pept
66	4	50.0	13	18 AAW36330	Antimicrobial phot
67	4	50.0	13	22 AAG73433	Human gene 27-enco
68	4	50.0	13	23 AAG64297	Human albumin fusi
69	4	50.0	14	19 AAW81795	D. viviparus DV17
70	4	50.0	15	17 AAW49166	Human leukocyte an
71	4	50.0	15	18 AAW38927	Peptide resembling
72	4	50.0	15	23 ABB98785	Human ribosomal pr
73	4	50.0	15	23 AAU77172	Transcriptional co
74	4	50.0	15	24 ABR41125	LRP6 specific poly
75	4	50.0	15	24 ABR34952	Human cancer-relat
76	4	50.0	15	24 ABR34957	Human cancer-relat
77	4	50.0	15	24 ABR35179	Human cancer-relat
78	4	50.0	15	24 ABR35572	Human cancer-relat
79	4	50.0	15	24 ABR35614	Human cancer-relat
80	4	50.0	15	24 ABR35687	Human cancer-relat
81	4	50.0	15	24 ABR35776	Human cancer-relat
82	4	50.0	15	24 ABR35777	Human cancer-relat

83 4 50.0 15 24 ABR35800 Human cancer-relat  
84 4 50.0 15 24 ABR35873 Human cancer-relat  
85 4 50.0 15 24 ABR35928 Human cancer-relat  
86 4 50.0 15 24 ABR35933 Human cancer-relat  
87 4 50.0 15 24 ABR36130 Human cancer-relat  
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89 4 50.0 15 24 ABR36513 Human cancer-relat  
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97 4 50.0 15 24 ABR37021 Human cancer-relat  
98 4 50.0 15 24 ABR37420 Human cancer-relat  
99 4 50.0 15 24 ABR37463 Human cancer-relat  
100 4 50.0 15 24 ABR37534 Human cancer-relat

## ALIGNMENTS

## RESULT 1

AAB72274  
ID AAB72274 standard; peptide; 8 AA.

XX AC AAB72274;

XX DT 14-MAY-2001 (first entry)

XX DE Colostrinin derived cytokine inducing peptide SEQ ID 29.

XX KW Colostrinin; immune response; cytokine; blood cell proliferation;  
XX KW central nervous system disorder; neurological disorder; mental disorder;  
XX KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
XX KW neurosis; infection.

XX OS Synthetic.

XX PN WO200111937-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22818.

XX PR 17-AUG-1999; 99US-0149311.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGE-) REGEN THERAPEUTICS PLC.

XX PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
XX WPI; 2001-202804/20.

XX DR Inducing a cytokine and modulating an immune response, useful for  
XX PT treating central nervous system diseases and bacterial and viral  
XX PT infections, comprises administering colostrinin as an immunological  
XX PT regulator -

XX PS Claim 1; Page 34; 50pp; English.

XX CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
XX CC a proline rich polypeptide aggregate contained in colostrum. The  
XX CC peptides have immune response-modulatory activity, and are capable of  
XX CC inducing cytokines. Colostrinin and its derived peptides are useful for  
XX CC inducing cytokine production, for modulating an immunological response  
XX CC and for inducing blood cell proliferation. The peptides are useful in the  
XX CC treatment of disorders of the central nervous system, neurological  
XX CC disorders, mental disorders, dementia, neurodegenerative diseases,  
XX CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
XX CC disorders of the immune system, bacterial and viral infections and  
XX CC acquired immunological deficiencies.

XX SQ Sequence 8 AA;  
Query Match 100.0%; Score 8; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGPPFPLV 8  
DB 1 RGPPFPLV 8

## RESULT 2

AAB72527  
ID AAB72527 standard; Peptide; 8 AA.

XX AC AAB72527;

XX DT 09-MAY-2001 (first entry)

XX DE Colostrinin peptide #28.

XX KW Dermatological; oxidative stress regulator; colostrinin.

XX OS Unidentified.

XX PN WO200112650-A2.

XX PD 22-FEB-2001.

XX PF 17-AUG-2000; 2000WO-US22665.

XX PR 17-AUG-1999; 99US-0149310.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Stanton GJ, Hughes TK, Boldogh I;  
XX WPI; 2001-218342/22.

XX PT Modulating oxidative stress level in a cell, involves contacting the  
XX PT cell with an oxidative stress regulator selected from colostrinin, its  
XX PT constituent peptide, analog or their combinations -

XX PS Claim 6; Page 26; 48pp; English.

XX CC The present invention relates to a method for modulating the oxidative  
XX CC stress level in a cell or a patient, comprising contacting the cell with,  
XX CC or administering to the patient, an oxidative stress regulator selected  
XX CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
XX CC to change the level of an oxidising species in the cell. The method can  
XX CC be used to treat oxidative damage to skin, by decreasing or preventing an  
XX CC increase in the level of damage to a biomolecule of the patient.

XX SQ Sequence 8 AA;  
Query Match 100.0%; Score 8; DB 22; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPPFPLV 8  
DB 1 RGPPFPLV 8

## RESULT 3

AAB72559  
ID AAB72559 standard; Peptide; 8 AA.

XX AC AAB72559;

XX DT 09-MAY-2001 (first entry)

XX



CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidizing species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX  
 SQ Sequence 8 AA;  
 Query Match 100.0%; Score 8; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGPFPILV 8  
 |||||  
 Db 1 RGPFPILV 8

RESULT 6  
 AAM51063  
 ID AAM51063 standard; Peptide; 8 AA.

XX AC AAM51063;  
 XX DT 30-MAY-2002 (first entry)  
 XX DE Colostrinin constituent peptide (casein amino acids 214-222).  
 XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;  
 XX KW blood cell regulator; cytokine inducer; beta-casein; human.  
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT Modified-site 8 /note= "optional C-terminal amidation"  
 XX PN WC200213849-A1.  
 XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having a beta-casein homologue precursor, and corresponds to  
 CC casein amino acids 214-222. Methods are claimed for: inducing a  
 CC cytokine in a cell by contact with an immunological regulator,  
 CC where the cell is present in a cell culture, a tissue, an organ  
 CC or an organism, and the cell is mammalian, including human;  
 CC modulating an immune response in a cell by contact with the

CC immunological regulator under conditions effective to induce a  
 CC cytokine; modulating an immune response in a patient by administering  
 CC an immunological regulator under conditions effective to induce a  
 CC cytokine, where the immunological regulator is administered topically  
 CC or as part of a dietary supplement, and where the immune response is  
 CC specific or non specific, an interferon response or an antibody  
 CC response; modulating blood cell proliferation by contacting blood  
 CC cells with a blood cell regulator, where the blood cells are present  
 CC in a cell culture or an organism, are mammalian or human, and where  
 CC the blood cells are increased in number or differentiated; and a  
 CC method for modulating blood cell proliferation in a patent. A  
 CC claimed cytokine-inducing composition comprises a pharmaceutical  
 CC carrier and an active agent such as the present peptide.

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RGPFPILV 8  
 |||||  
 Db 1 RGPFPILV 8

RESULT 7  
 AAO14605  
 ID AAO14605 standard; peptide; 8 AA.

XX AC AAO14605;  
 XX DT 27-MAY-2002 (first entry)  
 XX DE Neural cell regulatory colostrinin peptide 28.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;  
 XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;  
 XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
 FT Modified-site 8 /note= "Optional C-terminal amide"

XX PN WC200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX PS Claim 7; Page 22; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in



CC the method of the invention.

XX Sequence 8 AA;

Query Match 100.0%; Score 8; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPILV 8  
|||||

Db 1 RGPFPILV 8

RESULT 8

AAAY30980  
ID AAY30980 standard; peptide; 6 AA.

XX AC AAY30980;

XX AC AAY30980;

DT 21-OCT-1999 (first entry)

XX Non-crosslinked protein particle peptide 29.

XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;  
XX albumin; haemoglobin; nanometer; micrometer; clearance.

OS Synthetic.

XX US5945033-A.

XX 31-AUG-1999.

XX 12-NOV-1996; 96US-0747137.  
XX 14-MAR-1994; 94US-0212546.  
XX 15-JAN-1991; 91US-0641720.  
XX 13-OCT-1992; 92US-0959560.  
XX 01-JUN-1993; 93US-0069831.  
XX 12-NOV-1996; 96US-0747137.

XX (HEMO-) HEMOSPHERE INC.

XX Yen RCK;

XX WPI; 1999-508153/42.

XX Non-crosslinked protein particles for therapeutic and diagnostic use  
XX Example 22; Column 61-62; 65pp; English.  
XX This invention describes a novel aqueous suspension of monodisperse  
XX particles on non-crosslinked, non-denatured albumin (50-5000 nm) which  
XX is stable against dissolving upon dilution with an alcohol-free aqueous  
XX medium. The method involves (a) forming an aqueous solution containing  
XX albumin and hemoglobin and (b) treating the aqueous solution with an  
XX alcohol to cause the solution to become turbid. The particles are useful  
XX as agents for in vivo administration, either of their own administration  
XX or as a vehicle for other therapeutic or diagnostic agents. The method  
XX permits the formation of albumin and hemoglobin particles in the  
XX nanometer and micrometer size range, in a form closer to their natural  
XX form than the forms of the prior art. The particles therefore constitute  
XX a more closely controlled agent for in vivo administration, with greater  
XX ease of clearance from the body after their period of usefulness.  
XX AAY30952-Y31135 represent peptides used in the method of the invention.

XX Sequence 6 AA;

Query Match 75.0%; Score 6; DB 20; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPPI 6  
|||||

Db 1 RGPFPPI 6

RESULT 10

AAR58340  
ID AAR58340 standard; peptide; 17 AA.

XX AC AAR58340;

XX AAR58340;

Db 1 RGPFPPI 6

RESULT 9

AAB18488  
ID AAB18488 standard; peptide; 6 AA.

XX AC AAB18488;

XX 15-JAN-2001 (first entry)

XX Peptide substrate used to test prolyl-tripeptidyl peptidase activity.  
XX Prolyl tripeptidyl-peptidase; amidolytic activity; periodontal disease;  
XX gingivitis; periodontitis.

OS Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "hydrogen attached"

XX WO200052147-A2.

XX 08-SEP-2000.

XX 03-MAR-2000; 2000WO-US05551.

XX 05-MAR-1999; 99US-0123148.

XX (UYGE-) UNIV GEORGIA RES FOUND INC.

XX (TRAV/) TRAVIS J.

XX (FOTE/) FOTEMPA J.

XX (BANB/) BANBULA A.

XX Travis J, Fotempa J, Banbula A;

XX WPI; 2000-594181/56.

XX Prolyl tripeptidyl-peptidase, active analog, fragment or variant useful  
XX for identifying its inhibitor which is useful for protecting an animal  
XX from a periodontal disease such as gingivitis and periodontitis -  
XX Claim 3; Page 37; 58pp; English.  
XX The present sequence represents a substrate which was used to test  
XX the activity of prolyl tripeptidyl-peptidases PTP-A and DPP IV. The  
XX prolyl tripeptidyl-peptidase has an amidolytic activity, and cleaves  
XX a peptide bond in a target polypeptide having at least 4 amino acids.  
XX This bond is between a proline and an amino acid attached to the  
XX alpha-carboxyl group end of the proline. The polypeptide is useful for  
XX identifying inhibitors. These inhibitors are then useful for reducing  
XX the growth of bacterium or for protecting an animal from a periodontal  
XX disease such as gingivitis and periodontitis caused by Porphyromonas  
XX gingivalis.

XX Sequence 6 AA;

Query Match 75.0%; Score 6; DB 21; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPPI 6  
|||||

Db 1 RGPFPPI 6

RESULT 10

AAR58340  
ID AAR58340 standard; peptide; 17 AA.

XX AC AAR58340;

XX AAR58340;

DT 22-SEP-1994 (first entry)  
 XX Hypotensive polypeptide.  
 DE  
 XX  
 KW Hypotensive; antioxiative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 OS Lactobacillus helveticus.  
 XX JP06041191-A.  
 PN  
 PD 15-FEB-1994.  
 XX  
 PF 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 PA (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 XX  
 DR WPI; 1994-089332/11.  
 XX  
 PT New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxiative and calcium absorption promoting  
 PT activity  
 PS Claim 1-2; Page 10; 10pp; Japanese.  
 XX  
 CC Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxiative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX  
 XX Sequence 17 AA;  
 Query Match 75.0%; Score 6; DB 15; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGPFPPI 6  
 DB 10 RGPFPPI 15  
 |||||  
 RESULT 11  
 AAR58341  
 ID AAR58341 standard; peptide; 19 AA.  
 AC  
 XX  
 XX AAR58341;  
 DT 22-SEP-1994 (first entry)  
 DE  
 XX Hypotensive polypeptide.  
 KW Hypotensive; antioxiative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 XX Lactobacillus helveticus.  
 OS JP06041191-A.  
 PN  
 PD 15-FEB-1994.  
 XX  
 PF 03-MAR-1993; 93JP-0043047.  
 XX  
 PR 04-MAR-1992; 92JP-0047340.  
 XX  
 PA (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 XX  
 DR WPI; 1994-089332/11.  
 XX  
 PT New polypeptide - used in physiologically active agents having  
 PT e.g. hypotensive antioxiative and calcium absorption promoting

PT activity  
 XX Claim 1-2; Page 10; 10pp; Japanese.  
 PS  
 XX Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxiative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX  
 XX Sequence 19 AA;  
 Query Match 75.0%; Score 6; DB 15; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.1;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGPFPPI 6  
 DB 12 RGPFPPI 17  
 |||||  
 RESULT 12  
 AAR28573  
 ID AAR28573 standard; peptide; 5 AA.  
 XX  
 AC AAR28573;  
 XX  
 DT 22-MAR-1993 (first entry)  
 XX  
 DE DCPase inhibitor peptide.  
 XX  
 KW Dipeptidyl carboxypeptidase; DCPase; inhibitor; vasodepression;  
 KW internal blood pressure.  
 XX  
 OS Bacillus sp.  
 XX JP04288098-A.  
 PN  
 XX 13-OCT-1992.  
 PD  
 PF 14-MAR-1991; 91JP-0074581.  
 XX  
 PR 14-MAR-1991; 91JP-0074581.  
 XX  
 PA (EZAK ) EZAKI GLICO CO.  
 XX  
 DR WPI; 1992-387722/47.  
 XX  
 PT New peptide obtd. from Bacillus sp. strain - inhibits di:peptidyl  
 PT carboxy:peptidase and so are blood pressure regulators  
 XX  
 PS Disclosure; Page 2; 3pp; Japanese.  
 XX  
 CC This peptide is a preferred example of the generic sequence given in  
 CC AAR28574. Peptides covered by this formula are dipeptidyl  
 CC carboxypeptidase (DCPase) inhibitors. They inhibit vasodepressor  
 CC activity and keep internal blood pressures normal. These peptides  
 CC may be administered orally, eg. daily in food, without side effects.  
 XX  
 XX Sequence 5 AA;  
 Query Match 62.5%; Score 5; DB 13; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPFPI 6  
 DB 1 GPFPI 5  
 |||||  
 RESULT 13  
 AAR45831  
 ID AAR45831 standard; Protein; 7 AA.

XX AAR45831;  
 XX 25-MAR-2003 (updated)  
 DT 20-JUL-1994 (first entry)  
 XX Aureobasidin type cyclic peptide (cpd. 29).  
 DE Aureobasidin; alpha-hydroxy acid; N-methyl-alpha-amino acid;  
 KW antifungal; synthesis; cyclic.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Modified-site 1 /label= MeVal  
 FT /note= "MeVal has a D-Hmp (2(R)-hydroxy-  
 FT 3(R)-methylpentanoate) substituent  
 FT which is bound to residue 8 to  
 FT form the cyclic peptide"  
 FT Modified-site 3 /label= OTHER  
 FT /note= "MePhe"  
 FT Modified-site 5 /label= aile  
 FT /note= "aile has a D-Hmb (2(R)-hydroxy-  
 FT 3-methylbutanoate) substituent  
 FT which is bound to residue 6"  
 FT Modified-site 7 /label= OTHER  
 FT /note= "betaHOMEVal"  
 FT Misc-difference 2..5  
 FT /note= "two intramolecular hydrogen bonds between  
 FT residues 2 and 5"  
 FT Misc-difference 6..1  
 FT /note= "one intramolecular hydrogen bond between  
 FT residues 6 and the D-Hmp substituent of  
 FT residue 1"  
 XX EP581429-A2.  
 XX 02-FEB-1994.  
 XX 10-JUN-1993; 93EP-0304515.  
 XX 19-JUN-1992; 92JP-0184661.  
 PR 16-OCT-1992; 92JP-0303177.  
 XX (TAKI ) TAKARA SHUZO CO LTD.  
 XX Inami K, Kato I, Kurome T, Shiba T, Takesako K;  
 XX WPI; 1994-036663/05.  
 XX Synthesis of cyclic peptide(s) of aureobasidin type - and new  
 FT cyclic peptide(s) with antifungal activity  
 XX Disclosure; Page 9; 74pp; English.  
 XX Cyclic aureobasidin type peptides (e.g. of generic formula given  
 CC in AAR45804) may be synthesised by cyclizing an O-protected or  
 CC unprotected linear peptide (e.g. of generic formula given in  
 CC AAR45803) or a reactive deriv. of it.  
 CC Representative cyclic peptides obtained by this method are given  
 CC in AAR45806-35. Peptides given AAR45820 and AAR45284-26 are new cpds.  
 CC and can be prep'd. by a fermentation method. Peptides given in  
 CC AAR45828-35 are new cpds. which are prep'd. by the new method.  
 CC The cpd. given AAR45834 showed higher activity against Candida  
 CC albicans T11M 0171 than the cpd. given in AAR45805.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 7 AA;

Query Match 62.5%; Score 5; DB 15; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FPILV 8  
 DB 3 FPILV 7  
 RESULT 14  
 AAR58333  
 ID AAR58333 standard; peptide; 8 AA.  
 XX AAR58333;  
 AC AAR58333;  
 DT 22-SRP-1994 (first entry)  
 DE Hypotensive polypeptide.  
 XX Hypotensive; antioxidative; calcium absorption; salt; food;  
 KW pharmaceuticals; physiologically active agents.  
 XX Lactobacillus helveticus.  
 OS JP06041191-A.  
 DN 15-FEB-1994.  
 PD 03-MAR-1993; 93JP-0043047.  
 PF 04-MAR-1992; 92JP-0047340.  
 PR (CALV ) CALPIS SHOKUHIN KOGYO KK.  
 XX WPI; 1994-089332/11.  
 DR New polypeptide - used in physiologically active agents having  
 FT e.g. hypotensive antioxidative and calcium absorption promoting  
 FT activity  
 XX Claim 1-2; Page 9; 10pp; Japanese.  
 XX Sequences (AAR58319-341) are used in conjunction with  
 CC physiologically active agents showing a property such as  
 CC hypotensive activity, calcium absorption promoting activity and  
 CC antioxidative activity. The peptides are non-toxic and can be  
 CC used in physiologically active agents.  
 XX Sequence 8 AA;  
 SQ Query Match 62.5%; Score 5; DB 15; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGFPP 5  
 DB 4 RGFPP 8  
 RESULT 15  
 ABR83258  
 ID ABR83258 standard; Peptide; 16 AA.  
 XX ABR83258;  
 AC ABR83258;  
 DT 04-MAR-2003 (first entry)  
 DE G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1931.  
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 XX Homo sapiens.  
 XX WO200261087-A2.  
 XX  
 XX PD 08-AUG-2002.  
 XX PF 19-DEC-2001; 2001WO-US50107.  
 XX PR 19-DEC-2000; 2000US-257144P.  
 XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX PI Burner GC, Roush CL, Brown JP;  
 XX DR WPI; 2003-046718/04.  
 XX  
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases -  
 XX  
 XX Claim 1; Fig 2; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.  
 XX  
 XX SQ Sequence 16 AA;  
 Query Match 62.5%; Score 5; DB 24; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PFPIL 7  
 Db 1 PFPIL 5  
 RESULT 16  
 AAB27612  
 ID AAB27612 standard; Peptide; 18 AA.  
 XX  
 XX AC AAB27612;

XX 02-FEB-2001 (first entry)  
 XX Human secreted protein BLAST search protein SEQ ID NO: 113.  
 DE  
 XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
 KW vulnery; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX  
 XX Homo sapiens.  
 XX WO200055175-A1.  
 XX PD 21-SEP-2000.  
 XX PF 09-MAR-2000; 2000WO-US06049.  
 XX PR 12-MAR-1999; 99US-0124144.  
 XX PR 11-JUN-1999; 99US-0138574.  
 XX PR 03-DEC-1999; 99US-0168667.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Ruben SM, Komatsoulis G;  
 XX DR WPI; 2000-638175/61.  
 XX  
 XX Isolated nucleic acid molecule encoding a human secreted protein is  
 PT used in preventing, treating or ameliorating a medical condition -  
 PT  
 XX Disclosure; Page 399; 428pp; English.  
 XX  
 CC The invention relates to the isolation of genes AAC58990-C59039 encoding  
 CC the human secreted proteins AAB27560-B27609. This sequence represents a  
 CC peptide fragment homologous to the protein encoded by the gene given  
 CC in the descriptor line. The sequence is a search result from a BLASTX  
 CC homology search. The genes and proteins are useful for preventing,  
 CC ameliorating or treating medical conditions, e.g. by protein or gene  
 CC therapy. The genes are isolated from a range of human tissues disclosed  
 CC in the specification. The nucleic acids, proteins, antibodies and  
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:  
 CC (a) cancer, e.g. breast and ovarian cancer, and other cancers of the  
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,  
 CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,  
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,  
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid  
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such  
 CC as myocardial ischaemia; (d) wound healing; (e) neurological diseases  
 CC e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such  
 CC as viral, bacterial, fungal and parasitic infections.  
 XX  
 XX SQ Sequence 18 AA;  
 Query Match 62.5%; Score 5; DB 21; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGPPP 5  
 Db 11 RGPPP 15  
 RESULT 17  
 AAB27613  
 ID AAB27613 standard; Peptide; 18 AA.  
 XX  
 XX AC AAB27613;  
 XX  
 XX DT 02-FEB-2001 (first entry)  
 XX  
 XX DE Human secreted protein BLAST search protein SEQ ID NO: 114.

XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
 KW antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiact; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.  
 XX Homo sapiens.  
 XX WO200055175-A1.  
 XX 21-SEP-2000.  
 XX 09-MAR-2000; 2000WO-US06049.  
 XX 12-MAR-1999; 99US-0124144.  
 XX 11-JUN-1999; 99US-0138574.  
 XX 03-DEC-1999; 99US-0168667.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 XX Rosen CA, Ruben SM, Komatsoulis G;  
 XX WPI; 2000-638175/61.  
 XX Isolated nucleic acid molecule encoding a human secreted protein is  
 XX used in preventing, treating or ameliorating a medical condition -  
 XX Disclosure; Page 399; 428pp; English.  
 XX The invention relates to the isolation of genes AAC58990-C59039 encoding  
 CC the human secreted proteins AAB27560-B27609. This sequence represents a  
 CC fragment of the protein encoded by the gene given in the descriptor  
 CC line. The sequence is used as a query sequence for doing BLASTX searches  
 CC to determine homologous sequence to the protein. The genes and proteins  
 CC are useful for preventing, ameliorating or treating medical conditions,  
 CC e.g. by protein or gene therapy. The genes are isolated from a range of  
 CC human tissues disclosed in the specification. The nucleic acids,  
 CC proteins, antibodies and (ant)agonists are useful in the diagnosis,  
 CC treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer,  
 CC and other cancers of the adrenal gland, bone, bone marrow, breast,  
 CC gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders  
 CC e.g. Addison's disease, allergies, autoimmune haemolytic anaemia,  
 CC autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple  
 CC sclerosis, rheumatoid arthritis and ulcerative colitis; (c)  
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound  
 CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and  
 CC (f) infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections.  
 XX Sequence 18 AA;  
 XX  
 XX Query Match 62.5%; Score 5; DB 21; Length 18;  
 XX Best Local Similarity 100.0%; Pred. No. 29;  
 XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 1 RGPFP 5  
 XX Db 11 RGPFP 15  
 XX  
 XX RESULT 18  
 XX AAW54333  
 XX ID AAW54333 standard; peptide; 5 AA.  
 XX AC AAW54333;  
 XX 30-JUL-1998 (first entry)  
 XX Bradykinin analogous peptide 16.  
 XX Inhibition; thrombin-induced platelet; prevention; platelet aggregation;  
 KW ADP-induced activation.

XX Synthetic.  
 XX OS WO9641640-A1.  
 XX PN 27-DEC-1996.  
 XX PD 07-JUN-1996; 96WO-US09940.  
 XX PF 09-JUN-1995; 95US-0000096.  
 XX PR (UNMI ) UNIV MICHIGAN.  
 XX PA Hasan AAK, Schmaier AH;  
 XX WPI; 1997-065304/06.  
 XX Inhibition of platelet activation and aggregation - by admin. of new  
 XX or known bradykinin analogues  
 XX Disclosure; Page 42; 73pp; English.  
 XX Administration of a peptide or multimer related to bradykinin or other  
 CC disclosed peptides and multimers can be used for the inhibition of  
 CC thrombin-induced platelets or other cells. They can also be used for  
 CC preventing platelet aggregation, or inhibiting ADP-induced activation.  
 CC This is useful to prevent arterial occlusions arising from coronary  
 CC thrombosis and stroke.  
 XX Sequence 5 AA;  
 XX  
 XX Query Match 50.0%; Score 4; DB 18; Length 5;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX Qy 2 GPPF 5  
 XX Db 1 GPPF 4  
 XX  
 XX RESULT 19  
 XX AAW65793  
 XX ID AAW65793 standard; peptide; 5 AA.  
 XX AC AAW65793;  
 XX 19-OCT-1998 (first entry)  
 XX Polypyrrol inhibitor of cyclophilin.  
 XX polypyrrol; cyclophilin; inhibitor; neurotrophic compound; PPI;  
 KW ptiptydyl-prolyl isomerase; rotamase; immunophilin protein; degeneration;  
 KW neuronal damage.  
 XX Synthetic.  
 XX OS WO9825950-A1.  
 XX PN 18-JUN-1998.  
 XX PD 08-DEC-1997; 97WO-US23102.  
 XX PF 09-DEC-1996; 96US-0761902.  
 XX PR (GUIL-) GUILFORD PHARM INC.  
 XX PA Hamilton GS, Steiner JP, Wei L;  
 XX WPI; 1998-348444/30.  
 XX Effecting neuronal activity in mammals - by administering tetra-  
 PT and penta- peptide inhibitors of cyclophilin and rotamase enzyme,  
 KW useful in treatment of neuronal damage or degeneration disorders

XX Claim 11; Page 40; 70pp; English.

CC The invention relates to a method of effecting a neuronal activity. It comprises administering a neurotrophic compound with an affinity for a cyclophilin type immunophilin. The immunophilin shows peptidyl-prolyl isomerase (rotamase) activity. The neurotrophic compound achieves the stimulation of damaged neurons, promotion of neuronal regeneration or prevention of neurodegeneration, and treatment of neurological disorder. The neurotrophic compounds are potent peptidyl-proline isomerase (rotamase) inhibitors. They are of use in disorders which include peripheral neuropathy caused by physical injury or disease state, i.e. physical injury to the brain or spinal cord, stroke, or neurological disorder leading to neurodegeneration, notably Alzheimer's and Parkinson's diseases, or amyotrophic lateral sclerosis. The neurotrophic compounds avoid the side effects of immunosuppressant drugs, including nephrotoxicity, impaired glomerular filtration, interstitial fibrosis, involuntary tremors, headaches, and hypertension. They are also free from the difficulties in delivery and bioavailability of large molecular weight proteins. The present sequence represents a specifically claimed neurotrophic compound.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 4; DB 19; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6  
|||||  
Db 2 PPPI 5

RESULT 20

AAB86116

ID AAB86116 standard; peptide; 5 AA.

XX AC AAB86116;

XX 17-JUL-2001 (first entry)

XX Serine proteinase inhibiting pentapeptide.

XX Serine proteinase inhibitor; topical; prophylactic; cosmetic; dry skin treatment; desmosome-degrading proteinase inhibitor; desmosome; skin-flaking; desquamation.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT /note= "Gly residue modified by N-CBZ (N-benzoyloxycarbonyl)"

XX DE19950020-A1.

XX 19-APR-2001.

XX 16-OCT-1999; 99DE-1050020.

XX 16-OCT-1999; 99DE-1050020.

XX (HENK ) HENKEL KGAA.

XX Saettler A, Weiss A, Schlottmann K, Foerster T;

XX WPI; 2001-336587/36.

XX Use of compositions containing inhibitors of desmosome degradation to prevent skin-flaking during prophylactic or cosmetic treatment of dry skin -

PS Claim 6; Page 3; 14pp; German.

XX This sequence represents a novel pentapeptide capable of inhibiting serine proteinases. The product of the invention can be used in the topical prophylactic or cosmetic treatment of dry skin of a composition which contains a skin-compatible carrier and an inhibitor for desmosome-degrading proteinases. The product can also be used in skin treatments to prevent breakdown of desmosome structures, the compositions being used as alcohol solutions, gels, emulsions, e.g. in shampoos. A wide range of inhibitors prevent skin-flaking (desquamation) caused by (preferably serine) proteinases and help to retain the keratinocytes.

XX SQ Sequence 5 AA;

Query Match 50.0%; Score 4; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5  
|||||  
Db 1 GPFP 4

RESULT 21

AAB86117

ID AAB86117 standard; peptide; 5 AA.

XX AC AAB86117;

XX 17-JUL-2001 (first entry)

XX Serine proteinase inhibiting pentapeptide.

XX Serine proteinase inhibitor.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /label= OTHER

FT /note= "Gly residue modified by N-CBZ (N-benzoyloxycarbonyl)"

XX DE19950019-A1.

XX 19-APR-2001.

XX 16-OCT-1999; 99DE-1050019.

XX 16-OCT-1999; 99DE-1050019.

XX (HENK ) HENKEL KGAA.

XX Saettler A, Weiss A, Schlottmann K, Foerster T;

XX WPI; 2001-336586/36.

XX Surfactant-containing detergents or cleaning agents for cleaning the skin or hard surfaces contain inhibitors against proteinase-caused skin flaking -

XX Claim 2; Page 3; 18pp; German.

XX This invention describes a novel serine proteinase inhibitor which can be used in surfactant-containing detergents or cleaning agents also contain inhibitors against proteinase-caused desmosome degradation, where the inhibitors being such that at 0.0005% concentration they show an at least 5% prevention effect. Claimed uses are: (i) topical prophylactic or cosmetic treatment of dry skin, especially in cleaning of the skin with prevention of, or reduction in, dry skin formation; or (ii) manual cleaning of hard surfaces with similar prevention or reduction on the hands. A wide range of inhibitors prevent skin-flaking (desquamation) caused by (preferably serine) proteinases and help to retain the

CC keratinocytes whether being used to wash the skin or being used manually  
 CC to clean hard surfaces.

SQ Sequence 5 AA;

Query Match 50.0%; Score 4; DB 22; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5  
 DB 1 GPPF 4

RESULT 22

AAAR77192  
 ID AAR77192 standard; Protein; 6 AA.

XX AC AAR77192;

XX 25-MAR-2003 (updated)  
 DT 24-NOV-1995 (first entry)

XX Internal sequence of cytochrome P-450OX.

XX Cytochrome; P-450ox; monooxygenase.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6  
 FT /note= "X represents unspecified AA"

XX WO9516041-A1.

XX 15-JUN-1995.

XX 28-NOV-1994; 94WO-EP03938.

XX 08-DEC-1993; 93EP-0810860.

XX (CIBA ) CIBA GEIGY AG.

PA (UYRO-) UNIV ROYAL VETERINARY & AGRIC.

XX Halkier BA, Koch BM, Lindberg MLLER B, Sibbesen O;

PI Lindberg MOLLER B;

XX WPI; 1995-224324/29.

XX DNA encoding cytochrome P-450 mono:oxygenase(s) - for modifying  
 PT biosynthetic production of cyanogenic glycoside(s) and  
 PT glucosinolate(s) in crop plant (s) for increased pest resistance  
 PT or improved nutritive value

XX Example; Page 27; 73pp; English.

XX Cytochrome P-450OX resembles the cytochrome P-450 reported to  
 CC convert oximes to nitriles in rat liver microsomes. The mol. wt.  
 CC of P-450OX as determined by SDS-PAGE is 51 kD. AA sequences are  
 CC obtd. by Edman degradation. The internal polypeptides are obtd.  
 CC by trypsin digestion of the purified protein and subsequence sepn.  
 CC of peptides using reverse phase HPLC. The N-terminal sequence is  
 CC given in AAR77188. A cytochrome with a mol. wt. of 51 kD and this  
 CC N-terminal sequence is claimed. Internal peptides are given in  
 CC AAR77189-R77192.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 6 AA;

Query Match 50.0%; Score 4; DB 16; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPFI 6  
 DB 3 PPFI 6

RESULT 23

AAW56422  
 ID AAW56422 standard; peptide; 7 AA.

XX AC AAW56422;

XX 31-JUL-1998 (first entry)

XX Amino acid sequence of a tasty peptide.

XX Tasty peptide; flavour; food; modification; enhance; food taste.

XX Unidentified.

XX EP832972-A2.

XX 01-APR-1998.

XX 17-SEP-1997; 97EP-0116132.

XX 23-SEP-1996; 96EP-0115211.

XX (GIVA ) GIVAUDAN-ROURE INT SA.

XX Lerch K, Muheim A, Silke N;

XX WPI; 1998-195226/18.

XX New tasty peptide(s) in homogeneous form - useful for, e.g.  
 PT preparing foods and masking food taste

XX Claim 3; Page 3; 27pp; English.

XX The present sequence represents a tasty peptide. Tasty peptides  
 CC contribute, in combination with volatile compounds, to the overall  
 CC impression of a flavour. The specification describes the production of  
 CC several tasty peptides in homogeneous form, isolated DNA sequences  
 CC encoding them and organisms transformed with these sequences. The tasty  
 CC peptides may be used in preparing food to modify, enhance or mask  
 CC different food tastes.

SQ Sequence 7 AA;

Query Match 50.0%; Score 4; DB 19; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4  
 DB 1 RGPF 4

RESULT 24

AAE09134  
 ID AAE09134 standard; peptide; 7 AA.

XX AC AAE09134;

XX 15-NOV-2001 (first entry)

XX Bacteriophage Type VI peptide, used in the invention.

XX Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;  
 KW polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;  
 KW Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;  
 KW demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;  
 KW hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;  
 KW inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;

KW Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;  
KW Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;  
KW polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;  
KW sarcoidosis; rheumatic fever; anti-phospholipid syndrome; farmer's lung;  
KW Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;  
KW pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;  
KW Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;  
KW erythroblastosis foetalis; cystitis; IGA nephropathy; Hodgkin's lymphoma;  
KW renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;  
KW thrombotic; neuroprotective; cytostatic; nephrotropic; antiallergic;  
KW dengue; antiulcer; vasotropic; antipyretic; hepatotropic.  
XX Bacteriophage.  
OS  
XX  
XX WO200158481-A2.  
XX  
XX 16-AUG-2001.  
XX  
XX 09-FEB-2001; 2001WO-US04191.  
XX  
XX 09-FEB-2000; 2000US-0500904.  
XX  
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
XX  
XX Harley JB, James JA, Kaufman KM;  
XX WPI; 2001-522437/57.  
XX  
XX Novel vaccine for alleviating or preventing autoimmune disorders  
PT induced Epstein-Barr virus (EBV) infection e.g. systemic lupus  
PT erythematous, juvenile onset diabetes mellitus, comprises EBV virus or  
PT its component  
XX  
XX Example 10; Page 56; 114pp; English.  
XX  
XX The present invention relates to a vaccine for alleviating or preventing  
CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),  
CC comprising EBV or its component in a carrier. The vaccine is useful for  
CC preventing or alleviating autoimmune disorders induced by EBV, e.g.  
CC systemic lupus erythematosus (SLE). Sjogren's syndrome, juvenile onset  
CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,  
CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple  
CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's  
CC disease, adrenalitis, primary biliary cirrhosis, Graves' disease,  
CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,  
CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating  
CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,  
CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune  
CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,  
CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia  
CC areata, autoimmune cystitis, pemphigoid, scleroderma, progressive  
CC systemic sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal  
CC dysmotility, sclerodactyly and telangiectasia), adult onset diabetes  
CC mellitus (Type II diabetes), male or female autoimmune infertility,  
CC ankylosing spondylitis, ulcerative colitis, Crohn's disease, mixed  
CC connective tissue disease, polyarteritis nodosa, systemic necrotising  
CC vasculitis, glomerulonephritis, atopic dermatitis, atopic rhinitis,  
CC Goodpasture's syndrome, Chagas' disease, sarcoidosis, rheumatic fever,  
CC asthma, recurrent abortion, anti-phospholipid syndrome, farmer's lung,  
CC erythema multiforme, postcardotomy syndrome, Cushing's syndrome,  
CC autoimmune chronic active hepatitis, bird-fancier's lung, allergic  
CC encephalomyelitis, toxic necrodermal lysis, alopecia, Alport's syndrome,  
CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,  
CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic  
CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,  
CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,  
CC Sampter's syndrome (triaditis, nasal polyps, eosinophilia) and Behcet's  
CC disease, Caplan's syndrome, encephalomyositis, erythema elevatum et  
CC tintinum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA  
CC nephropathy, Felty's syndrome, fascitis with eosinophilia, filariasis,  
CC chronic cystitis, heterochromic cystitis, Fuch's cyclitis, Hodgkin's and  
CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schonlein purpura, post  
CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or

CC relapsing polychondritis. The present sequence is Bacteriophage Type VI  
CC peptide used in the invention.  
XX  
SQ Sequence 7 AA;  
Query Match 50.0%; Score 4; DB 22; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 PPIL 7  
Db 4 PPIL 7  
RESULT 25  
AAR45825  
ID AAR45825 standard; Protein; 8 AA.  
XX  
AC AAR45825;  
XX  
DT 25-MAR-2003 (updated)  
DT 20-JUL-1994 (first entry)  
XX  
DE Aureobasidin type cyclic peptide (cpd. 23).  
XX  
XX Aureobasidin; alpha-hydroxy acid; N-methyl-alpha-amino acid;  
KW antifungal; synthesis; cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1 /label= MeVal  
FT /note= "MeVal has a D-Hmp (2(R)-hydroxy-  
FT 3(R)-methylpentanoate) substituent  
FT which is bound to residue 8 to  
FT form the cyclic peptide"  
FT  
FT Modified-site 3 /label= OTHER  
FT /note= "Mephe"  
FT  
FT Modified-site 5 /label= alle  
FT  
FT Modified-site 6 /label= OTHER  
FT /note= "MeLeu"  
FT  
FT Modified-site 8 /label= OTHER  
FT /note= "betaHOMeVal"  
FT  
FT Misc-difference 2..5 /note= "two intramolecular hydrogen bonds between  
FT residues 2 and 5"  
FT  
FT Misc-difference 7..1 /note= "one intramolecular hydrogen bond between  
FT residues 7 and the D-Hmp substituent of  
FT residue 1"  
XX  
XX EP581429-A2.  
XX  
XX 02-FEB-1994.  
XX  
XX 10-JUN-1993; 93EP-0304515.  
XX  
XX 19-JUN-1992; 92JP-0184661.  
XX 16-OCT-1992; 92JP-0303177.  
XX  
XX (TAKI ) TAKARA SHUZO CO LTD.  
XX  
XX Inami K, Kato I, Kurome T, Shiba T, Takesako K;  
XX WPI; 1994-036663/05.  
XX  
XX Synthesis of cyclic peptide(s) of aureobasidin type - and new  
XX cyclic peptide(s) with antifungal activity



XX PS Disclosure; Page 9; 74pp; English.

XX CC Cyclic aureobasidin type peptides (e.g. of generic formula given in AAR45804) may be synthesised by cyclizing an O-protected or unprotected linear peptide (e.g. of generic formula given in AAR45803) or a reactive deriv. of it.

XX CC Representative cyclic peptides obtained by this method are given in AAR45806-35. Peptides given AAR45820 and AAR45284-26 are new cpds. and can be prepd. by a fermentation method. Peptides given in AAR45828-35 are new cpds. which are prepd. by the new method.

XX CC The cpd. given AAR45834 showed higher activity against Candida albicans TIMM 0171 than the cpd. given in AAR45805.

XX CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA;

Query Match 50.0%; Score 4; DB 15; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7  
Db 3 FPIL 6

RESULT 26  
AAR89371  
ID AAR89371 standard; peptide; 9 AA.  
AC AAR89371;  
DT 18-SEP-1996 (first entry)  
TX Cw6 consensus peptide derived immunogenic peptide #3.  
DE Immunogenic peptide; supermotif; HLA molecule; CTL response;  
KW therapeutic; diagnostic; cancer; viral infection; hepatitis B;  
KW hepatitis C.  
XX Synthetic.  
XX WO9603140-A1.  
XX 08-FEB-1996.  
XX 21-JUL-1995; 95WO-US09234.  
XX 30-MAY-1995; 95US-0452843.  
XX 21-JUL-1994; 94US-0278634.  
XX 23-NOV-1994; 94US-0344824.  
XX (CYTE-) CYTEL CORP.  
XX Sette A, Sidney J;  
XX WPI; 1996-116784/12.  
XX Compsn. comprising immunogenic peptide with supermotif allowing more than one HLA mol. to bind - used to induce CTL response in patient and for in vivo and ex vivo therapeutic and diagnostic applications

XX PS Claim 2; Page 26; 32pp; English.

XX CC The sequences given in AAR89362-82 are immunogenic peptides which were use in the composition of the invention. The composition comprises an immunogenic peptide of 9-10 residues with a supermotif which allows binding of more than one HLA molecule. It pref. comprises two conserved residues, a first at the 2nd position from the N-terminal is Pro, and a 2nd at the C-terminal is Met. These peptides are used to induce a CTL response in a patient. They are also useful in compositions for in vivo and ex vivo therapeutic and diagnostic applications, e.g the treatment of cancer and viral

CC infections, e.g. hepatitis B and C.

XX SQ Sequence 9 AA;

Query Match 50.0%; Score 4; DB 17; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PPPI 6  
Db 2 PPPI 5

RESULT 27  
AAW80249  
ID AAW80249 standard; Peptide; 9 AA.  
XX AAW80249;  
AC AAW80249;  
DT 06-JAN-1999 (first entry)  
TX Active site sequence of the beta-lactamase gene in mutant #7.  
DE plasmid pBR322; tetracycline resistance gene; TetR; mutant;  
KW Escherichia coli; active site; beta-lactamase gene.  
XX Synthetic.  
XX US5824469-A.  
XX 20-OCT-1998.  
XX 30-SEP-1994; 94US-0316415.  
XX 19-JUN-1989; 89US-0368674.  
XX 17-JUL-1986; 86US-0887070.  
XX 12-MAY-1992; 92US-0881607.  
XX 11-AUG-1993; 93US-0105108.  
XX 30-SEP-1994; 94US-0316415.  
XX (UNIW ) UNIV WASHINGTON.  
XX Horwitz MS, Loeb IA;  
XX WPI; 1998-582545/49.  
XX N-PSDB; AAV66448.  
XX Identification of biologically active DNA sequences - by transforming cells with random oligo-nucleotide(s)

XX PS Example 8; Fig 6; 24pp; English.

XX CC AAW80243-49 represent new carbenicillin resistant mutants identified from a screening of tetracycline resistant mutants. The sequences are mutant active site sequences of the beta-lactamase gene, derived from plasmid pBR322. The carbenicillin resistant sequences were produced to exemplify the invention. The specification describes a method for obtaining an oligonucleotide that confers a predetermined biological function, such as regulation of expression or a biological activity of a polypeptide, on a cell. The method comprises cloning a heterogeneous pool of oligonucleotides into an expression vector, where the clones oligonucleotides are transcribed or act as regulatory sequences, introducing a random sample of the cloned oligonucleotides into a population of cells that do not exhibit the predetermined biological function, selecting a subpopulation of cells exhibiting the predetermined biological function, and isolating an oligonucleotide that confers this function from the selected subpopulation of cells. The process is used, for example, for identifying new forms of the Escherichia coli tetracycline resistance gene promoter and the active site of the beta-lactamase gene.

XX SQ Sequence 9 AA;

```

Query Match      50.0%; Score 4; DB 19; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
   ||||
Db 2 FPIL 5

RESULT 28
ABB14561
ID ABB14561 standard; Peptide; 9 AA.
XX
AC ABB14561;
XX
DT 22-JAN-2002 (first entry)
XX
DE Human C35 peptide epitope #2065.
XX
KW Human; C35; cytostatic; gene therapy; vaccine; tumour antigen;
KW breast cancer; bladder cancer; tumour immunotherapy; epitope;
KW major histocompatibility complex binding peptide; MHC.
XX
OS Homo sapiens.
XX
FN WO200174859-A2.
XX
PD 11-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US10855.
XX
PR 04-APR-2000; 2000US-194463P.
XX
PA (UVRP ) UNIV ROCHESTER.
XX
PI Zauderer M, Evans EE, Borrello MA;
XX
DR WPI; 2001-626383/72.
XX
PT Novel C35 polypeptides and C35 genes useful in immunogenic compositions
PT and vaccines, for inducing antibody and cell-mediated immunity against
PT target cells, such as tumor cells that express C35 gene -
XX
PS Disclosure; Page 171; 331pp; English.
XX
CC The present invention relates to human C35 (see AAG78997). C35 is a novel
CC tumour antigen that is overexpressed in human breast and bladder
CC carcinoma. C35 is thought to be a promising candidate for tumour
CC immunotherapy, in immunogenic compositions and vaccines, to induce
CC antibody and cell-mediated immunity against target cells such as tumour
CC cells that express C35 genes. The present sequence is a C35 peptide
CC epitope. This peptide is predicted to be a major histocompatibility
CC complex (MHC) binding peptide.
XX
SQ Sequence 9 AA;

Query Match      50.0%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
   ||||
Db 1 GPFP 4

RESULT 29
AAU28830
ID AAU28830 standard; Peptide; 9 AA.
XX
AC AAU28830;
XX
DT 03-JAN-2002 (first entry)
XX

```

```

DE DPI tryptic digest peptide #427.
XX
KW Human; depression associated protein isoform; tryptic digest peptide;
KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;
KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;
KW maniac-depressive illness; schizoaffective disorder.
XX
OS Homo sapiens.
XX
FN WO200162787-A1.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-GB00786.
XX
PR 24-FEB-2000; 2000GB-0004412.
PR 08-DEC-2000; 2000GB-0030050.
PR 12-DEC-2000; 2000US-0254830.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAAC, Parekh RB, Rohlff C, Terrett JA, Tyson KL;
XX
DR WPI; 2001-570626/64.
XX
PT Novel nucleic acid encoding a protein associated with bipolar affective
PT disorder, which is used for diagnosis, prophylaxis and therapy of
PT neuropsychiatric disorders, such as bipolar affective disorder -
XX
PS Disclosure; Page 39; 153pp; English.
XX
CC The present invention relates to the identification of depression
CC associated protein isoforms (DPIs), particularly the tryptic digest
CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)
CC described are decreased in the cerebrospinal fluid (CSF) of BAD
CC (bipolar affective disorder) subjects, whilst other DPIs
CC (AAU28626-AAU28887) are increased in BAD subjects. Also described
CC are peptide sequences identified from DPI-45 and DPI-213 and the
CC nucleic acid sequence they are encoded by. The sequences of the
CC invention are useful for clinical screening, diagnosis, prognosis,
CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also
CC known as bipolar mood disorder, BP), maniac-depressive illnesses,
CC attention deficit disorders, schizoaffective disorders, and unipolar
CC affective disorders. The present sequence represents one of the DPI
CC tryptic digest peptides of the present invention.
XX
SQ Sequence 9 AA;

Query Match      50.0%; Score 4; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
   ||||
Db 2 PPPI 5

RESULT 30
AAU26478
ID AAU26478 standard; Peptide; 9 AA.
XX
AC AAU26478;
XX
DT 18-DEC-2001 (first entry)
XX
DE Depression-Associated Protein isoform DPI-255 #2.
XX
KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;
KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;
KW CSF; antidepressant; antimanic; nootropic; tranquiliser; neuroleptic;
KW attention deficient disorder; schizoaffective disorder;
KW unipolar affective disorder.
XX

```

OS Homo sapiens.  
 PN WO200163294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 XX 23-FEB-2001; 2001WO-GB00791.  
 PF  
 XX 24-FEB-2000; 2000GB-0004412.  
 PR  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA  
 XX Herath HWAC, Parekh RB, Rohlf C;  
 PI  
 XX WPI; 2001-582081/65.  
 DR  
 XX Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX  
 XX Claim 8; Page 39; 163pp; English.  
 PS  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPIs are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PFPI 6  
 DB 2 PFPI 5  
 RESULT 31  
 AAG89664  
 ID AAG89664 standard; Peptide; 9 AA.  
 AC  
 AC AAG89664;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE p53 epitope B7 supermotif peptide #29.  
 XX  
 XX Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;  
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
 KW vaccine; epitope; cytostatic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200141788-A1.  
 PN  
 XX 14-JUN-2001.  
 PD

XX 11-DEC-2000; 2000WO-US33629.  
 PF  
 XX 10-DEC-1999; 99US-0458297.  
 PR  
 XX (EPIM-) EPIMMUNE INC.  
 PA  
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogh E;  
 XX  
 XX WPI; 2001-381493/40.  
 DR  
 XX Epitope-based vaccines comprising p53 epitope having a specified  
 PT sequences, useful for treating and preventing cancer, the epitopic  
 PT peptides is useful as diagnostic agents and for evaluating immune  
 PT response -  
 XX  
 PS Claim 1; Page 123; 138pp; English.  
 XX  
 CC The present invention describes isolated p53 epitopes (I). Also  
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)  
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (II), a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53, and a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (I) and (II)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
 CC present in whole antigens can be avoided with the use of the vaccine  
 CC composition of (I). The ability to combine selected epitopes and  
 CC further, to modify the composition of the epitopes enhances the  
 CC immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigens, which might have their own  
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
 CC represent amino acid sequences used in the exemplification of the  
 CC present invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 4; DB 22; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FPIL 7  
 DB 1 FPIL 4  
 RESULT 32  
 AAG89665  
 ID AAG89665 standard; Peptide; 9 AA.  
 XX  
 AC AAG89665;  
 XX  
 DT 11-SEP-2001 (first entry)  
 XX  
 DE p53 epitope B7 supermotif peptide #30.  
 XX  
 XX Human; p53; tumour suppressor; human leukocyte antigen; HLA; CTL;  
 KW cytotoxic T lymphocyte; T cell; immune response; tumour; cancer;  
 KW vaccine; epitope; cytostatic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200141788-A1.  
 PN  
 XX 14-JUN-2001.  
 PD  
 XX 11-DEC-2000; 2000WO-US33629.  
 PF

XX 10-DEC-1999; 99US-0458297.  
 XX (EPIM-) EPIMUNE INC.  
 XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 XX Keogh E;  
 XX WPI; 2001-381493/40.  
 XX  
 XX Epitope-based vaccines comprising p53 epitope having a specified  
 PT sequences, useful for treating and preventing cancer, the epitopic  
 PT peptides is useful as diagnostic agents and for evaluating immune  
 PT response -  
 XX  
 XX Claim 1; Page 123; 138pp; English.  
 XX  
 XX The present invention describes isolated prepared P53 epitopes (I). Also  
 CC described are: (1) a cytotoxic T lymphocyte (CTL) that is cultured  
 CC in vivo and binds to a complex of (I); (2) a peptide (II) comprising (I)  
 CC and a second epitope and has less than 50 contiguous amino acids; (3) a  
 CC vaccine composition comprising (II), a unit dose of a peptide with less  
 CC than 50 contiguous amino acids with 100% identity to the native peptide  
 CC sequence of p53; and (4) a pharmaceutical excipient; (4) an isolated nucleic  
 CC acid encoding (I); and (5) an isolated nucleic acid encoding (II). (I)  
 CC has cytostatic activity and can be used in vaccines. The vaccine  
 CC composition is useful for treating or preventing cancer. (I) and (II)  
 CC are useful as diagnostic agents and for evaluating immune responses.  
 CC Unlike conventional epitopes, immunosuppressive epitopes that may be  
 CC present in whole antigens can be avoided with the use of the vaccine  
 CC composition of (I). The ability to combine selected epitopes and  
 CC further, to modify the composition of the epitopes enhances the  
 CC immunogenicity. The possible pathological side effects caused by  
 CC infectious agents or whole protein antigens, which might have their own  
 CC intrinsic biological activity, are eliminated. AAG89363 to AAG89747  
 CC represent amino acid sequences used in the exemplification of the  
 CC present invention.  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 50.0%; Score 4; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05; Indels 0; Gaps 0;  
 XX Matches 4; Conservative 0; Mismatches 0;  
 QY 4 FPIL 7  
 Db 1 FPIL 4  
 XX  
 XX RESULT 33  
 XX AAB76157  
 XX ID AAB76157 standard; Peptide; 9 AA.  
 XX AC AAB76157;  
 XX DT 10-APR-2001 (first entry)  
 XX DE Tumour associated antigen p53 immunogenic peptide.  
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
 KW viricide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
 KW human immunodeficiency virus; protozoacide; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
 KW condyloma acuminatum.  
 XX Homo sapiens.  
 XX OS  
 XX WO200100225-A1.  
 XX PN  
 XX PD  
 XX 04-JAN-2001.  
 XX 28-JUN-2000; 2000WO-US17842.

PD 04-JAN-2001.  
 XX 28-JUN-2000; 2000WO-US17842.  
 XX 29-JUN-1999; 99US-0141422.  
 XX (EPIM-) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S;  
 XX WPI; 2001-112389/12.  
 XX  
 XX Composition comprising human leukocyte antigen binding peptide which  
 PT comprises isolated, prepared epitope useful for treating viral  
 PT infections such as acquired immunodeficiency syndrome, and cancer -  
 XX  
 XX Claim 1; Page 48; 58pp; English.  
 XX  
 XX The present invention describes a composition (I) which comprises at  
 CC least one human leukocyte antigen (HLA) binding peptide comprising an  
 CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid  
 CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,  
 CC viricide, hepatotropic, antiinflammatory, anti-HIV (human  
 CC immunodeficiency virus) and protozoacide activities, which can be used  
 CC in vaccine production and is an inducer of cytotoxic T-cell response.  
 CC (I) is useful for inducing a cytotoxic T cell response against a  
 CC preselected antigen in a patient expressing a specific major  
 CC histocompatibility complex (MHC) class I allele, by contacting cytotoxic  
 CC T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to  
 CC treat and/or prevent viral infection and cancer such as prostate cancer,  
 CC hepatitis B, hepatitis C, human papilloma virus (HPV) infection,  
 CC cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal  
 CC carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma  
 CC acuminatum.  
 XX Sequence 9 AA;  
 XX  
 XX Query Match 50.0%; Score 4; DB 22; Length 9;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FPIL 7  
 Db 1 FPIL 4  
 XX  
 XX RESULT 34  
 XX AAB76158  
 XX ID AAB76158 standard; Peptide; 9 AA.  
 XX AC AAB76158;  
 XX DT 10-APR-2001 (first entry)  
 XX DE Tumour associated antigen p53 immunogenic peptide.  
 XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;  
 KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;  
 KW HLA binding peptide; immune response; glycoprotein; cytostatic;  
 KW viricide; hepatotropic; antiinflammatory; anti-HIV; vaccine;  
 KW human immunodeficiency virus; protozoacide; viral infection; cancer;  
 KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;  
 KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;  
 KW renal carcinoma; cervical carcinoma; lymphoma; malaria;  
 KW condyloma acuminatum.  
 XX Homo sapiens.  
 XX OS  
 XX WO200100225-A1.  
 XX PN  
 XX PD  
 XX 04-JAN-2001.  
 XX 28-JUN-2000; 2000WO-US17842.

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XX 29-JUN-1999; 99US-0141422.
XX (EPIM-) EPIMMUNE INC.
XX Sette A, Sidney J, Southwood S;
XX WPI; 2001-112389/12.
XX Composition comprising human leukocyte antigen binding peptide which
XX comprises isolated, prepared epitope useful for treating viral
XX infections such as acquired immunodeficiency syndrome, and cancer -
XX Claim 1; Page 48; 58pp; English.
XX The present invention describes a composition (I) which comprises at
XX least one human leukocyte antigen (HLA) binding peptide comprising an
XX isolated, prepared epitope comprising one of 547 8-11 residue amino acid
XX sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
XX virucide, hepatotropic, antiinflammatory, anti-HIV (human
XX immunodeficiency virus) and protozoacide activities, which can be used
XX in vaccine production and is an inducer of cytotoxic T cell response.
XX (I) is useful for inducing a cytotoxic T cell response against a
XX preselected antigen in a patient expressing a specific major
XX histocompatibility complex (MHC) class I allele, by contacting cytotoxic
XX T cells (CTLs) from the patient with (I). (I) is useful as a vaccine to
XX treat and/or prevent viral infection and cancer such as prostate cancer,
XX hepatitis B, hepatitis C, human papilloma virus (HPV) infection,
XX cytomegalovirus (CMV), acquired immunodeficiency syndrome (AIDS), renal
XX carcinoma, cervical carcinoma, lymphoma, malaria, and condyloma
XX acuminatum.
XX Sequence 9 AA;
XX Query Match 50.0%; Score 4; DB 22; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 FPIL 7
Db 1 FPIL 4
XX
XX Sequence 9 AA;
XX Query Match 50.0%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RGPF 4
Db 6 RGPF 9
XX
XX RESULT 36
XX ABG67743
XX ID ABG67743 standard; Peptide; 9 AA.
XX XX
XX AC ABG67743;
XX XX
XX DT 07-OCT-2002 (first entry)
XX XX
XX DE Human ADPI tryptic digest peptide #452.
XX XX
XX KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;
XX KW Alzheimer's disease-associated feature; neuroprotective;
XX KW Alzheimer's disease-associated protein isoform; nootropic;
XX KW ADPI tryptic digest peptide.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200246767-A2.
XX XX
XX PD 15-AUG-2002.
XX XX
XX PF 18-DEC-2001; 2001WO-US49744.
XX XX
XX PR 18-DEC-2000; 2000US-256409P.
XX PR 18-DEC-2000; 2000US-256410P.
XX PR 10-OCT-2001; 2001US-0974366.
XX XX
XX PA (HILD/) HILDEBRAND W H.
XX (PRIL/) PRILLIMAN K R.

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Hildebrand WH, Prilliman KR;  
WPI; 2002-698563/75.  
Producing soluble human leukocyte antigen (HLA) in cell pharm useful for studies of peptide loading for characterizing human immune responses involves using HLA allelic cDNA or genomic DNA as starting material -  
Disclosure; Page 172; 300pp; English.  
The invention describes a method of producing soluble human leukocyte antigen (HLA) molecules (sHLA) in cell pharm involving amplifying HLA allelic DNA by PCR using a locus specific primer to produce truncated a PCR product (PI), inserting PI into mammalian expression vector; electroporating the plasmid into a host cell; inoculating the cell pharm with the host cell such that cell pharm produces sHLA. A multimeric HLA complex (I) is useful for testing functionality of peptide ligands bound by at least two soluble HLA molecules. (I) can be tested for its ability to serve as ligands for cytotoxic T lymphocytes (CTLs) and induce immune responses in humans. (I) is useful for studying T cell responses to pathological conditions such as viral infections and cancer, and for modulating the human immune system to induce tolerance in autoimmune diseases. The individual secreted major histocompatibility complex (MHC) molecules produced are useful for studies of peptide loading (i.e., in vaccine development) and to the development of diagnostics. With the secreted MHC molecules, naturally loaded peptides can be eluted from the MHC molecule and characterised. The secreted MHC molecules allow the assessment of structural and functional impact of HLA class I polymorphism. The molecules are also useful to generate ligands and hence ligand maps from the peptide pools extracted from series of distinct yet related class I HLA-B\*55 allotypes; compare the different ligand maps to identify potentially shared elements; and characterise the elements identified to positively or negatively validate the occurrence of overlapping ligands. The truncated version of (MHC) can be produced in mammalian or insect/bacterial cells such that milligram or greater quantities of an individual class I or class II molecule can be obtained. This sequence represents a HLA (human leukocyte antigen) epitope.

Query Match 50.0%; Score 4; DB 23; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGPF 4  
Db 6 RGPF 9

RESULT 36  
ABG67743  
ID ABG67743 standard; Peptide; 9 AA.  
XX  
AC ABG67743;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE Human ADPI tryptic digest peptide #452.  
XX  
KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;  
KW Alzheimer's disease-associated feature; neuroprotective;  
KW Alzheimer's disease-associated protein isoform; nootropic;  
KW ADPI tryptic digest peptide.  
XX  
OS Homo sapiens.  
XX  
PN WO200246767-A2.  
XX  
PD 13-JUN-2002.  
XX  
PF 29-NOV-2001; 2001WO-GB05289.

```

XX PR 08-DEC-2000; 2000US-254431P.
XX PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.
XX PI Herath HMC, Parekh RB, Rohlf C;
XX DR WPI; 2002-508575/54.
XX PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
XX PT comprises detecting Alzheimer's disease-associated features or
XX PT Alzheimer's disease-associated protein isoforms in brain tissue
XX PT from the subject -
XX PS Claim 7; Page 63; 427pp; English.
XX CC The present invention relates to methods and compositions for the
XX CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in
XX CC a subject. The method comprises analysing a sample of brain tissue
XX CC from a subject by 2D electrophoresis to generate a 2D array of
XX CC Alzheimer's disease-associated features (ADFs), whose relative
XX CC abundance correlates with the presence, absence, stage or severity of
XX CC AD and comparing the abundance of each feature with the abundance of
XX CC that chosen feature in brain tissue from persons free from AD. The
XX CC invention also describes Alzheimer's disease-associated protein
XX CC isoforms (ADPIs) detectable in brain tissue. The methods and
XX CC compositions of the invention are useful for the screening, diagnosis
XX CC or prognosis of AD in a subject, for determining the stage or severity
XX CC of AD in a subject, for identifying a subject at risk of developing AD,
XX CC or for monitoring the effect of therapy administered to a subject
XX CC having AD. Antibodies capable of binding to ADPIs are useful for
XX CC treating or preventing AD, and for determining the efficacy of a given
XX CC treatment regime. An agent that modulates the activity of ADPI is
XX CC useful in the manufacture of a medicament for the treatment or
XX CC prevention of AD in a subject. ABG67292-ABG68038 represent human ADPI
XX CC tryptic digest peptides.
XX SQ Sequence 9 AA;
XX Query Match 50.0%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFPI 6
Db |||||
2 PFPI 5

RESULT 37
ABR20445
ID ABR20445 standard; Peptide; 9 AA.
XX AC ABR20445;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #280.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients -
XX PS Claim 13; Page 323; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC inhibiting the expression of the protein, as tools for modulating or
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
XX Query Match 50.0%; Score 4; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
Db |||||
5 GPFP 8

RESULT 38
ABR20847
ID ABR20847 standard; Peptide; 9 AA.
XX AC ABR20847;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #682.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients -

```

PT in cancer patients -  
 XX Claim 13; Page 327; 1021pp; English.  
 PS  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPPF 5  
 Db |||||  
 3 GPPF 6

RESULT 39  
 ABR21656  
 ID ABR21656 standard; Peptide; 9 AA.  
 XX  
 AC ABR21656;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #1491.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 337; 1021pp; English.  
 PS  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 4; DB 24; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPPF 5  
 Db |||||  
 3 GPPF 6

RESULT 40  
 ABR21837  
 ID ABR21837 standard; Peptide; 9 AA.  
 XX  
 AC ABR21837;  
 XX  
 DT 19-MAY-2003 (first entry)  
 XX  
 DE Human cancer-related protein 185P2C9 HLA peptide #1672.  
 XX  
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200283921-A2.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 10-APR-2002; 2002WO-US11654.  
 XX  
 PR 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX  
 PA (AGEN-) AGENSYS INC.  
 XX  
 PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX  
 DR WPI; 2003-075555/07.  
 XX  
 PT New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX  
 PS Claim 13; Page 339; 1021pp; English.  
 PS  
 CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 50.0%; Score 4; DB 24; Length 9;

```

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5
DB 5 GPPF 8

RESULT 41
ABR22240
ID ABR22240 standard; Peptide; 9 AA.
XX
AC ABR22240;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 185P2C9 HLA peptide #2075.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PR 10-APR-2001; 2001US-283112P.
XX
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
PF WI; 2003-075555/07.
XX
DR New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 344; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 9 AA;
Query Match 50.0%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5
DB 3 GPPF 6

RESULT 42
ABR22262
ID ABR22262 standard; Peptide; 9 AA.
XX
AC ABR22262;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 185P2C9 HLA peptide #2097.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US11654.
XX
PR 10-APR-2001; 2001US-282739P.
XX
PR 10-APR-2001; 2001US-283112P.
XX
PR 25-APR-2001; 2001US-286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
PF WI; 2003-075555/07.
XX
DR New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response
PT in cancer patients -
XX
PS Claim 13; Page 344; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention.
XX
SQ Sequence 9 AA;
Query Match 50.0%; Score 4; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5
DB 3 GPPF 6

RESULT 43
ABR23247
ID ABR23247 standard; Peptide; 9 AA.
XX
AC ABR23247;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 185P2C9 HLA peptide #3082.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.

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XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients -
XX PS Claim 13; Page 355; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
XX QY Query Match 50.0%; Score 4; DB 24; Length 9;
XX DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX M Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 GPPP 5
XX DB 5 GPPP 8
XX RESULT 44
XX ID ABR23645
XX AC ABR23645 standard; Peptide; 9 AA.
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 185P2C9 HLA peptide #3480.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US11654.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 10-APR-2001; 2001US-283112P.
XX PR 25-APR-2001; 2001US-286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX DR WPI; 2003-075555/07.
XX PT New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response
XX PT in cancer patients -
XX PS Claim 13; Page 355; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention.
XX SQ Sequence 9 AA;
XX QY Query Match 50.0%; Score 4; DB 24; Length 9;
XX DB Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX M Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 2 GPPP 5
XX DB 5 GPPP 8
XX RESULT 45
XX ID AAY17845
XX AC AAY17845 standard; peptide; 10 AA.
XX DT 13-AUG-1999 (first entry)
XX DE Backbone cyclised peptide analogue #4.
XX KW Backbone cyclised peptide; bridging group; bradykinin; somatostatin;
XX KW acute asthma; septic shock; brain trauma; traumatic injury;
XX KW post-surgical pain; inflammation; cancer; endocrine disorder;
XX KW gastrointestinal disorder.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "Adamantane acetyl"
XX FT Misc-difference 2 /note= "D-form residue"
XX FT Modified-site 4 /note= "Gly is bonded to Asp at position 7 to form a
XX FT FT cyclic region"
XX FT Modified-site 5 /label= 4Hyp
XX FT FT /note= "4-hydroxyproline"
XX FT Modified-site 7 /note= "Asp is bonded to Gly at position 4 to form a
XX FT FT cyclic region"
XX FT Misc-difference 8
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FT FT /label= 4Hyp
FT FT /note= "4-hydroxyproline"
FT FT Modified-site 6
FT FT /note= "Phe is bonded to Gly at position 3 to form a
FT FT cyclic region"
FT FT Misc-difference 8
FT FT /note= "D-form residue"
XX XX
XX WO9533765-A1.
XX PD 14-DEC-1995.
XX XX
XX PF 08-JUN-1995; 95WO-IB00455.
XX XX
XX PR 08-JUN-1994; 94IL-0109943.
XX XX
XX PA (PEPT-) PEPTOR LTD.
XX PA (YISS ) YISSUM RES & DEV CO.
XX XX
XX PI Bitan G, Eren D, Gilon C, Muller D, Seri-Levy A;
XX PI Zeltser I;
XX XX
XX DR WPI; 1996-040184/04.
XX XX
XX PT New backbone-cyclised bradykinin and somatostatin analogues - used
XX PT to treat acute asthma, septic shock, trauma, post-operative pain,
XX PT inflammation, cancer and endocrine and GI disorders.
XX XX
XX PS Claim 19; Page 123; 143pp; English.
XX XX
XX CC The present invention describes new backbone-cyclised peptide analogues
XX CC comprising a peptide sequence that incorporates at least two building
XX CC units, each of which contains one N atom of the peptide group connected
XX CC to a bridging group comprising a disulphide, amide, thioether, thioester,
XX CC inine, ether or alkene bridge, where at least two building units are
XX CC joined together to form a cyclic structure. The analogues are used to
XX CC treat acute asthma, septic shock, brain trauma and other traumatic
XX CC injury, post-surgical pain, inflammation, cancers, and endocrine and
XX CC gastrointestinal disorders. The peptides are conformationally stabilised
XX CC without affecting pharmacologically active amino acids.
XX XX
XX SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db ||||
2 RGPF 5

RESULT 48
AAW36625
ID AAW36625 standard; peptide; 10 AA.
XX AC
XX AC AAW36625;
XX XX
XX DT 11-MAR-1998 (first entry)
XX XX
XX DE Thrombopoietin receptor binding peptide.
XX XX
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX OS Synthetic.
XX OS
XX PN WO9640750-A1.
XX XX
XX PD 19-DEC-1996.
XX XX

Query Match 50.0%; Score 4; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
Db ||||
2 RGPF 5

RESULT 49
AAW09474
ID AAW09474 standard; protein; 10 AA.
XX AC
XX AC AAW09474;
XX XX
XX DT 10-SEP-1997 (first entry)
XX XX
XX DE Thrombopoietin receptor binding peptide.
XX XX
XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS Synthetic.
XX OS
XX PN WO9640189-A1.
XX XX
XX PD 19-DEC-1996.
XX XX
XX PF 05-JUN-1996; 96WO-US08998.
XX XX
XX PR 07-JUN-1995; 95US-0485301.
XX PR 07-JUN-1995; 95US-0472371.
XX PR 07-JUN-1995; 95US-0473604.
XX PR 07-JUN-1995; 95US-0476168.
XX PR 07-JUN-1995; 95US-0478128.
XX PR 07-JUN-1995; 95US-0484090.
XX XX
XX PA (GLAX ) GLAXO GROUP LTD.
XX XX
XX PI Barrett RW, Cwirla SE, Dower WJ, Duffin DJ, Gates CM;
XX PI Johnson SS, Mattheakis LC, Schatz PJ, Wagstrom CR;
XX PI Wrighton NC;
XX XX

```

DR WPI; 1997-051883/05.  
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide  
PT mimetic(s) - useful in treatment of haematological disorders, esp.  
PT thrombocytopenia resulting from chemotherapy, etc.  
XX  
PS Disclosure; Page 26; 106pp; English.  
XX  
CC The present sequence is a peptide which binds to thrombopoietin (TPO)  
CC receptor (TR). The compound can be used for treating patients suffering  
CC from haematological disorders and thrombocytopenia resulting from  
CC chemotherapy, radiation therapy or bone marrow transusions. The  
CC peptide may also be used to maintain the proliferation and growth of  
CC TPO-dependent cell lines and for use in biological research, for  
CC detecting TPO receptors on living cells.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 50.0%; Score 4; DB 18; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGPF 4  
Db |||||  
2 RGPF 5  
RESULT 50  
AAB17007  
ID AAB17007 standard; Peptide; 10 AA.  
XX  
XX AAB17007;  
DT 31-OCT-2000 (first entry)  
XX  
XX TPO-mimetic peptide sequence SEQ ID NO: 63.  
DE  
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;  
KW MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
KW vascular endothelial growth factor; matrix metalloproteinase;  
KW asthma; thrombosis; pharmaceutical.  
XX  
XX Synthetic.  
OS  
XX WO200024782-A2.  
PN  
XX 04-MAY-2000.  
PD  
XX 25-OCT-1999; 99WO-US25044.  
PF  
XX 23-OCT-1998; 98US-0105371.  
PR  
XX 22-OCT-1999; 99US-0428082.  
PR  
XX (AMGE-) AMGEN INC.  
PA  
XX Feige U, Liu C, Cheetham J, Boone TC;  
PI  
XX WPI; 2000-350702/30.  
DR  
XX Novel composition of matter comprising an Fc domain and  
PT pharmacologically active peptides, useful for treating cancer and  
PT autoimmune diseases -  
XX  
XX Claim 19; Page 216; 608pp; English.  
PS  
XX The present invention describes composition of matter (I) comprising an  
CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each  
CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2,  
CC -(L1)c-P1-(L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4

CC where P1, P2, P3, and P4 = are each independently sequences of  
CC pharmacologically active peptides; L1, L2, L3, and L4 = are each  
CC independently linkers; and a, b, c, d, e, and f = are each independently  
CC 0 or 1, provided that at least 1 of a and b is 1. The composition can  
CC have cytostatic, antiasthmatic, thrombolytic and immunosuppressive  
CC activities. DNAs, vectors and host cells from the present invention can  
CC be used for producing pharmaceutical compositions. The compositions are  
CC useful for treating cancer, asthma, thrombosis, or autoimmune diseases.  
CC The use of an Fc domain (rather than a Fab domain) can provide a longer  
CC half-life or incorporate functions such as Fc receptor binding, protein  
CC A binding, complement fixation, and possibly placental transfer. AAA69443  
CC to AAA69526 and AAB16955 to AAB18003 represent nucleotide and amino acid  
CC sequences used in the exemplification of the present invention.  
XX  
XX Sequence 10 AA;  
SQ  
Query Match 50.0%; Score 4; DB 21; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGPF 4  
Db |||||  
2 RGPF 5  
RESULT 51  
AAU25844  
ID AAU25844 standard; Peptide; 10 AA.  
XX  
XX AAU25844;  
AC  
XX 17-DEC-2001 (first entry)  
DT  
XX Human thrombopoietin receptor (TPO-R) activator peptide #30.  
DE  
XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; cytokine;  
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;  
KW bone marrow transplantation; haematological disorder; platelet disorder;  
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;  
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;  
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.  
XX  
XX Homo sapiens.  
OS  
XX US6251864-B1.  
PN  
XX 26-JUN-2001.  
XX  
XX 01-MAR-2000; 2000US-0516704.  
PF  
XX 07-JUN-1995; 95US-0478128.  
PR  
XX 07-JUN-1995; 95US-0485301.  
PR  
XX 07-JUN-1996; 96WO-US09623.  
PR  
XX 15-AUG-1996; 96US-0693027.  
PR  
XX (GLAX) GLAXO GROUP LTD.  
PA  
XX Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PJ;  
PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB;  
PI Podduturi S, Yin Q;  
XX  
XX WPI; 2001-564142/63.  
DR  
XX Activating thrombopoietin receptors in cells, used to treat  
PT thrombocytopenia and haematological disorders, comprises contacting  
PT cells with peptides and peptide mimetics attached to hydrophilic  
PT polymers -  
XX  
XX Disclosure; Column 19; 128pp; English.  
PS  
XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that  
CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods  
CC of activating thrombopoietin receptors in cells comprise contacting the

CC cells with effective amounts of peptides and peptide mimetics attached to  
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such  
 CC as that due to chemotherapy, radiation therapy or bone-marrow  
 CC transplantation and to prevent thrombocytopenia in patients at risk. The  
 CC sequences are used to treat and prevent haematological disorders  
 CC including thrombocytopenia and platelet disorders. They are used in vitro  
 CC as unique tools for understanding the biological role of thrombopoietin  
 CC (TPO) and to develop other compounds that bind to and activate the TPO  
 CC receptor. The peptides can be used to detect TPO receptors on living  
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and  
 CC in purified or natural biological materials. They may also be used for in  
 CC situ staining, fluorescence-activated cell sorting, Western blotting and  
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can  
 CC be used for in vitro expansion of megakaryocytes and their committed  
 CC progenitors alone or in conjunction with additional cytokines.

XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFF 4  
 ||||  
 DB 2 RGPFF 5

RESULT 52

AAU06436  
 ID AAU06436 standard; Peptide; 10 AA.

AC AAU06436;

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #28.

XX Prostate cancer-associated antigen; supermotif; human leukocyte antigen;  
 KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;  
 KW immunogenicity; immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMUNE INC.

PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;  
 PI Keogn E;

DR WPI; 2001-398311/42.

PT Tumour antigen-associated group-based vaccines useful for vaccinating  
 PT against prostate cancer -

XX Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived  
 CC motif or supermotif epitopes. The peptide epitopes are included in  
 CC prostate cancer vaccine compositions due to their ability to bind to  
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.  
 CC Peptides with a high binding affinity are further tested for their  
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte  
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their  
 CC binding affinity to multiple alleles within the HLA superfamily. The  
 CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to  
 CC alter the immune response to suit the target disease. These group-based  
 CC vaccines allow the focus of an immune response to multiple selected  
 CC antigens from the same pathogen. Variability among the immune responses  
 CC of patients can therefore be alleviated by the inclusion of groups from  
 CC multiple antigens in a vaccine.

XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8  
 ||||  
 DB 7 PILV 10

RESULT 53

AAG87057  
 ID AAG87057 standard; Peptide; 10 AA.

XX AAG87057;

DT 11-SEP-2001 (first entry)

DE Saccharomyces cerevisiae peptide, SEQ ID NO: 2006.

XX Saccharomyces cerevisiae; complementary peptide; peptide identification;  
 KW drug discovery; drug design.

OS Saccharomyces cerevisiae.

PN WO200142276-A1.

PD 14-JUN-2001.

PF 13-DEC-2000; 2000WO-GB04773.

PR 13-DEC-1999; 99GB-0029471.

XX (PROT-) PROTEOM LTD.

PI Roberts GW, Heal JR;

DR WPI; 2001-367863/38.

PT Identifying complementary peptides by analysis of protein and  
 PT nucleotide sequence databases, useful in drug design -

XX Example 3; Page 306; 488pp; English.

CC The invention relates to the identification of complementary peptides  
 CC by analysis of protein and nucleotide sequence databases from higher  
 CC eukaryotic genomes, excluding human and plants. The specific  
 CC complementary peptides interact with their relevant target proteins  
 CC encoded in the eukaryote genome. The peptides may be used as reagents  
 CC and drugs for drug discovery and as lead ligands for drug design and  
 CC development. The present sequence is a complementary peptide from  
 CC Saccharomyces cerevisiae.

XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 22; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8  
 ||||  
 DB 2 PILV 5

RESULT 54

ABB72893  
ID ABB72893 standard; Peptide; 10 AA.

XX  
AC ABB72893;  
XX  
DT 05-APR-2002 (first entry)  
XX  
DE TPO mimetic peptide SEQ ID NO:63.  
XX  
KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG;  
KW EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;  
KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;  
KW antianemic; anorectic; antiinfertility; haemostatic; dermatological;  
KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
KW sleep disorder; neurological degenerative disease; anaemia;  
KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
KW Fanconi's syndrome.

OS Homo sapiens.  
OS Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US14310.

XX 03-MAY-2000; 2000US-0563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheatham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.

XX Novel vehicle-peptide molecule or its multimers useful for treating  
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
PT diabetic retinopathy, obesity, sleep disorders and infertility -

XX Claim 39; Page 43; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its  
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
CC antianemic, anorectic, antiinfertility, haemostatic, dermatological and  
CC neuroprotective activities. (I) can be used as a therapeutic or  
CC prophylactic agent as well as for screening purposes. (I) is useful for  
CC diagnosing diseases characterised by dysfunction of their associated  
CC protein of interest, for identifying normal or abnormal proteins of  
CC interest, as a part of diagnostic kit to detect the presence of their  
CC proteins of interest in a biological sample. Additionally, (I) is useful  
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
CC infertility, and neurological degenerative diseases. (I), comprising  
CC EPO-mimetic compounds are useful for treating disorders characterised by  
CC low red blood cell levels such as anaemia. The TPO-mimetic comprising  
CC compounds are useful for treating conditions that involve an existing  
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
CC represent amino acid and nucleic acid sequences used in the  
CC exemplification of the present invention.

XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 23; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RQPF 4  
DB 2 RGPF 5

RESULT 55

ABR47211  
ID ABR47211 standard; Peptide; 10 AA.

XX ABR47211;

DT 10-JUN-2003 (first entry)

DE Staphylococcus aureus CHIPS-related peptide #2400.

XX CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;  
KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;  
KW inflammation; cardiovascular disease; central nervous system disease;  
KW gastrointestinal disease; skin disease; genitourinary disease;  
KW joint disease; respiratory disease; HIV infection; antiinflammatory;  
KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;  
KW gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

XX 23-JAN-2003.

XX 11-JUL-2001; 2001WO-EP08004.

XX 11-JUL-2001; 2001WO-EP08004.

XX (JARI-) JARI PHARM BV.

XX Van Kessel CPM, Gosselaar-de Haas CJC, Kruijtz JAW;

XX Van Strijp JAG;

XX WPI; 2003-247783/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from  
PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in  
PT prophylaxis and treatment of inflammation, cardiovascular, skin and  
PT kidney diseases -

XX Example 1; Page 55; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and  
CC ABR47164-ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS)  
CC from Staphylococcus aureus. The peptide fragments are useful in the  
CC prophylaxis or treatment of diseases or disorders involving the  
CC C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or  
CC neutrophils, monocytes and endothelial cells or involving acute or  
CC chronic inflammation reactions. The diseases or disorders include  
CC cardiovascular diseases, disease of the central nervous system,  
CC gastrointestinal diseases, skin diseases, genitourinary diseases, joint  
CC diseases, respiratory diseases and HIV infection.

XX Sequence 10 AA;

Query Match 50.0%; Score 4; DB 24; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPFI 6  
DB 5 PPFI 8

RESULT 56

ABR47287

ID	Sequence	Score	DB	Length	Indels	Gaps
ABR47287	Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.	50.0%	4	24	0	0
OS	Homo sapiens.	100.0%	4	24	0	0
PN	WO200283921-A2.	Conservative	0	Mismatches	0	Indels
XX	24-OCT-2002.	2 GPPF 5	4 GPPF 7			
XX	10-APR-2002; 2002WO-US11654.					
XX	10-APR-2001; 2001US-282739P.					
XX	10-APR-2001; 2001US-283112P.					
XX	25-APR-2001; 2001US-286630P.					
XX	(AGEN-) AGENSYS INC.					
XX	Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS; Morrison K, Morrison RK, Raitano AB; MPI; 2003-075555/07.					
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients					
XX	Claim 13; Page 321; 1021pp; English.					
XX	The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.					
XX	Sequence 10 AA;					
XX	Query Match 50.0%; Score 4; DB 24; Length 10; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2 GPPF 5					
DB	4 GPPF 7					
XX	RESULT 58					
XX	ABR21693					
XX	ID ABR21693 standard; Peptide; 10 AA.					
XX	AC ABR21693;					
XX	DT 19-MAY-2003 (first entry)					
XX	DE Human cancer-related protein 185P2C9 HLA peptide #1528.					
XX	Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.					
XX	Homo sapiens.					
XX	WO200283921-A2.					
XX	24-OCT-2002.					
XX	10-APR-2002; 2002WO-US11654.					
XX	10-APR-2001; 2001US-282739P.					
XX	10-APR-2001; 2001US-283112P.					
XX	25-APR-2001; 2001US-286630P.					
XX	(AGEN-) AGENSYS INC.					
XX	Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS; Morrison K, Morrison RK, Raitano AB; MPI; 2003-075555/07.					
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients					
XX	Claim 13; Page 321; 1021pp; English.					
XX	The present invention relates to novel human cancer-related genes and proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and proteins are useful for eliciting a humoral or cellular immune response. The genes are useful as probes and primers for the amplification and/or detection of genes, mRNAs or their fragments, as reagents for the diagnosis and/or prognosis of cancer, as coding sequences capable of directing the expression of the protein, as tools for modulating or inhibiting the expression of genes and/or translation of transcripts, and as therapeutic agents. The proteins and peptides are useful as therapeutic, prognostic and diagnostic reagents for cancer. The present sequence is a human leukocyte antigen (HLA) peptide, used in an example from the invention.					
XX	Sequence 10 AA;					
XX	Query Match 50.0%; Score 4; DB 24; Length 10; Best Local Similarity 100.0%; Pred. No. 2.6e+02; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY	2 GPPF 5					
DB	4 GPPF 7					
XX	RESULT 57					
XX	ABR20306					
XX	ID ABR20306 standard; Peptide; 10 AA.					
XX	AC ABR20306;					
XX	DT 19-MAY-2003 (first entry)					
XX	DE Human cancer-related protein 185P2C9 HLA peptide #141.					
XX	Human; cytostatic; vaccine; cancer; immune response; HLA; human leukocyte antigen.					
XX	Homo sapiens.					
XX	WO200283921-A2.					
XX	24-OCT-2002.					
XX	10-APR-2002; 2002WO-US11654.					
XX	10-APR-2001; 2001US-282739P.					
XX	10-APR-2001; 2001US-283112P.					
XX	25-APR-2001; 2001US-286630P.					
XX	(AGEN-) AGENSYS INC.					
XX	Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS; Morrison K, Morrison RK, Raitano AB; MPI; 2003-075555/07.					
XX	New composition comprising a substance that modulates the structure of proteins and polynucleotides, useful for therapeutic, prognostic and diagnostic reagents for eliciting cellular or humoral immune response in cancer patients					

XX 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 337; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX Sequence 10 AA;  
 SQ Query Match 50.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPFP 5  
 Db ||||  
 4 GPFP 7  
 RESULT 59  
 ABR21964  
 ID ABR21964 standard; Peptide; 10 AA.  
 XX ABR21964;  
 AC  
 XX 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 185P2C9 HLA peptide #1799.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 KW Homo sapiens.  
 XX WO200283921-A2.  
 PN 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 337; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX Sequence 10 AA;  
 SQ Query Match 50.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPFP 5  
 Db ||||  
 4 GPFP 7

DR WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 340; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX Sequence 10 AA;  
 SQ Query Match 50.0%; Score 4; DB 24; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GPFP 5  
 Db ||||  
 6 GPFP 9  
 RESULT 60  
 ABR23102  
 ID ABR23102 standard; Peptide; 10 AA.  
 XX ABR23102;  
 AC 19-MAY-2003 (first entry)  
 DT Human cancer-related protein 185P2C9 HLA peptide #2937.  
 DE Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 KW Homo sapiens.  
 XX WO200283921-A2.  
 PN 24-OCT-2002.  
 PD 10-APR-2002; 2002WO-US11654.  
 PF 10-APR-2001; 2001US-282739P.  
 PR 10-APR-2001; 2001US-283112P.  
 PR 25-APR-2001; 2001US-286630P.  
 XX (AGEN-) AGENSYS INC.  
 XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.  
 XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -  
 XX Claim 13; Page 354; 1021pp; English.  
 XX The present invention relates to novel human cancer-related genes and



CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC The genes are useful for eliciting a humoral or cellular immune response.  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.  
 XX  
 XX  
 SQ Sequence 10 AA;

Query Match 50.0%; Score 4; DB 24; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5

Db 4 GPPF 7

RESULT 61

AAW13931

ID AAW13931 standard; Protein; 11 AA.

XX AC AAW13931;

XX DT 15-MAY-1997 (first entry)

XX DE CDR-3 fragment of heavy chain of anti-HB virus antibody #1.

XX KW Antibody; heavy chain; light chain; variable region; human; monoclonal;

XX KW Complementarity determining region; human; adr type hepatitis B virus;

XX KW HB virus; CDR; virus antigen; anti-HB antibody; vaccine.

XX OS Homo sapiens.

XX PN JP09020798-A.

XX PD 21-JAN-1997.

XX PF 11-JUL-1995; 95JP-0174752.

XX PR 11-JUL-1995; 95JP-0174752.

XX PA (ASAH ) ASAH KASEI KOGYO KK.

XX DR WPI; 1997-140911/13.

XX DR N-PSDB; AAT60126.

XX PT Human anti-Hepatitis B antibody - used in a adr type HB virus

XX PT vaccine

XX PS Example 1; Page 10; 20pp; Japanese.

XX CC AAW13929-W13943 represent fragments of the complementarity determining  
 CC regions of the heavy and light chains of the human monoclonal antibodies  
 CC of the invention. The antibody of the invention preferably contains the  
 CC sequence represented by AAW13912 in the complementarity determining  
 CC region-1 (CDR-1) of the heavy chain variable region. The antibody of  
 CC the invention also contains the sequence represented by AAW13913 in the  
 CC CDR-3 of the light chain variable region. The antibody is capable of  
 CC binding to adr type hepatitis B (HB) virus antigen. A human anti-HB  
 CC virus monoclonal antibody preparation which is highly safe and is  
 CC effective to adr type HB virus can be provided, using the monoclonal  
 CC antibody. It can also be used as a vaccine against HB infection.

XX SQ Sequence 11 AA;

Query Match

Best Local Similarity 50.0%; Score 4; DB 18; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7

Db 6 FPIL 9

RESULT 62

ABG68633

ID ABG68633 standard; Peptide; 11 AA.

XX AC ABG68633;

XX DT 07-OCT-2002 (first entry)

XX DE Desmocollin 1 peptide sequence #1.

XX KW Human; secretory leukoprotease inhibitor; SLPI; corneodesmosin; mouse;

XX KW stratum corneum chymotryptic enzyme; envoplaklin; desmoplakin; pig; SCCE;

XX KW desmocollin 1; adhesion protein; protease; protease inhibitor; eczema;

XX KW contact dermatitis; lung atopic asthma; post viral asthma; viral warts;

XX KW bronchial hyper-reactivity; chronic obstructive pulmonary disease;

XX KW Crohn's disease; ulcerative colitis; coeliac disease; peptic ulceration;

XX KW impetigo; meningitis; skin melanoma; squamous cell carcinoma; psoriasis;

XX KW basal cell carcinoma; cutaneous lymphoma; skin cancer; lung malignancy;

XX KW gastrointestinal tract malignancy; acne vulgaris; psoriasis vulgaris;

XX KW antipsoriatic; dermatological; antiinflammatory; antiallergic.

XX OS Unidentified.

XX PN WO200244736-A2.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-GB05303.

XX PR 30-NOV-2000; 2000GB-0029225.

XX PR 07-DEC-2000; 2000GB-0029879.

XX PA (MOLE-) MOLECULAR SKINCARE LTD.

XX PI Tazi-Ahmini R, Bavik C, Ward S, Duff G, Cork M;

XX DR WPI; 2002-557554/59.

XX CC Diagnosing a disease or susceptibility to a disease associated with  
 CC abnormal cell-cell adhesion between epithelial cells, by detecting  
 CC mutation in nucleic acid encoding adhesion protein, protease or  
 CC protease inhibitor -  
 XX Example C4; Page 145; 257pp; English.

XX CC The invention relates to a method for diagnosis of a disease or  
 CC susceptibility to a disease associated with abnormal cell-cell adhesion  
 CC between epithelial cells, comprising detecting a mutation in a nucleic  
 CC acid encoding an adhesion protein, a protease or a protease inhibitor, or  
 CC modulated level of adhesion protein, protease or protease inhibitor, or  
 CC its fragment polypeptide. The method is useful for diagnosing a disease  
 CC such as eczema, contact dermatitis, lung atopic asthma, post viral  
 CC asthma, bronchial hyper-reactivity, chronic obstructive pulmonary  
 CC disease, Crohn's disease, ulcerative colitis, coeliac disease, peptic  
 CC ulceration, impetigo, viral warts, meningitis, skin melanoma, squamous  
 CC cell carcinoma, basal cell carcinoma, cutaneous lymphoma, skin cancer,  
 CC malignancy of the gastrointestinal tract, malignancy of the lung,  
 CC psoriasis, acne vulgaris and psoriasis vulgaris. This sequence represents  
 CC a peptide used in the scope of the invention.

XX SQ Sequence 11 AA;

Query Match

Best Local Similarity 50.0%; Score 4; DB 23; Length 11;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5  
 ||||  
 Db 6 GPPF 9

## RESULT 63

ABG68635  
 ID ABG68635 standard; Peptide; 11 AA.

XX AC  
 XX AC ABG68635;

XX DT 07-OCT-2002 (first entry)

XX DE Desmocollin 1 peptide sequence #2.

XX KW Human; secretory leukoprotease inhibitor; SLPI; corneodesmosin; mouse;  
 KW stratum corneum chymotryptic enzyme; envoplaklin; desmoplakin; pig; SCCE;  
 KW desmocollin 1; adhesion protein; protease; protease inhibitor; eczema;  
 KW contact dermatitis; lung atopic asthma; post viral asthma; viral warts;  
 KW bronchial hyper-reactivity; chronic obstructive pulmonary disease;  
 KW Crohn's disease; ulcerative colitis; coeliac disease; peptic ulceration;  
 KW impetigo; meningitis; skin melanoma; squamous cell carcinoma; psoriasis;  
 KW basal cell carcinoma; cutaneous lymphoma; skin cancer; lung malignancy;  
 KW gastrointestinal tract malignancy; acne vulgaris; psoriasis vulgaris;  
 KW antipsoriatic; dermatological; antiinflammatory; antiallergic.

XX OS Unidentified.

XX PN WO200244736-A2.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-GB05303.

XX PR 30-NOV-2000; 2000GB-0029225.

XX PR 07-DEC-2000; 2000GB-0029879.

XX PA (MOLE-) MOLECULAR SKINCARE LTD.

XX PI Tazi-Ahmini R, Bavik C, Ward S, Duff G, Cork M;

XX PF; 2002-557554/59.

XX PT Diagnosing a disease or susceptibility to a disease associated with  
 PT abnormal cell-cell adhesion between epithelial cells, by detecting  
 PT mutation in nucleic acid encoding adhesion protein, protease or  
 PT protease inhibitor

XX PS Example E5; Page 193; 257pp; English.

XX CC The invention relates to a method for diagnosis of a disease or  
 CC susceptibility to a disease associated with abnormal cell-cell adhesion  
 CC between epithelial cells, comprising detecting a mutation in a nucleic  
 CC acid encoding an adhesion protein, a protease or a protease inhibitor, or  
 CC modulated level of adhesion protein, protease or protease inhibitor, or  
 CC its fragment polypeptide. The method is useful for diagnosing a disease  
 CC such as eczema, contact dermatitis, lung atopic asthma, post viral  
 CC asthma, bronchial hyper-reactivity, chronic obstructive pulmonary  
 CC disease, Crohn's disease, ulcerative colitis, coeliac disease, peptic  
 CC ulceration, impetigo, viral warts, meningitis, skin melanoma, squamous  
 CC cell carcinoma, basal cell carcinoma, cutaneous lymphoma, skin cancer,  
 CC malignancy of the gastrointestinal tract, malignancy of the lung,  
 CC psoriasis, acne vulgaris and psoriasis vulgaris. This sequence represents  
 CC a peptide used in the scope of the invention.

XX SQ Sequence 11 AA;

Query Match 50.0%; Score 4; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPF 5  
 ||||

Db 6 GPPF 9

## RESULT 64

AAW36886  
 ID AAW36886 standard; Peptide; 12 AA.

XX AC AAW36886;

XX DT 11-MAY-1998 (first entry)

XX DE HTLV-II protease cleavage recognition site.

XX KW Ricin; toxin; antiviral; virucide; retrovirus; protease; HTLV-I;  
 KW cancer; infection; therapy; linker.

XX OS Synthetic.

XX PN WO9741233-A1.

XX PD 06-NOV-1997.

XX PF 29-APR-1997; 97WO-CA00288.

XX PR 30-APR-1996; 96US-0016509.

XX PA (CANG-) CANGENE CORP.

XX PI Borgford T;

XX DR WPI; 1997-549735/50.

XX PT DNAs encoding ricin like toxins A and B - are linked via linker  
 PT containing cleavage site for retroviral protease, used to inhibit or  
 PT destroy mammalian cells infected with retrovirus

XX PS Claim 5; Page 41; 105pp; English.

XX CC This claimed peptide is a cleavage recognition site for a HTLV-I  
 CC protease. It is utilised as a linker between the A and B chains  
 CC of a ricin-like protein in a novel recombinant protein. A nucleic  
 CC acid (see A497919) encoding such a construct is obtained by PCR  
 CC mutagenesis of the wild-type ricin linker sequence. The invention  
 CC provides novel recombinant proteins which incorporate the A and B  
 CC chains of a ricin-like toxin (preferably the A and B chains of  
 CC ricin) linked by a heterologous linker sequence containing a  
 CC cleavage recognition site for a retroviral protease such as HIV  
 CC protease (see AAW36880-82), HTLV-I (see AAW36883-43) or HTLV-II (see  
 CC AAW36885-65). The recombinant proteins selectively inhibit or  
 CC destroy mammalian cells infected with a retrovirus such as cancer  
 CC cells associated with HTLV or cells associated with HIV. The  
 CC recombinant proteins are non-toxic until the ricin A chain is  
 CC liberated from the B chain by a retroviral protease, and thus can  
 CC be used to specifically target infected cells without the need  
 CC for a cell binding component.

XX SQ Sequence 12 AA;

Query Match 50.0%; Score 4; DB 18; Length 12;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7  
 ||||

Db 6 FPIL 9

## RESULT 65

AAAB12848  
 ID AAB12848 standard; peptide; 12 AA.

XX AC AAB12848;

XX XX

DT 06-DEC-2000 (first entry)  
 XX STAT3 binding peptide #1.  
 DE  
 KW STAT; signal transducer and activator of transcription; human; cancer;  
 KW cell signalling; cytokine; growth factor; oncogenesis; tumour;  
 KW apoptosis; cytostatic; tumourigenesis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 3  
 FT /label= Ser, Pro  
 XX  
 XX WO200044774-A2.  
 XX  
 XX 03-AUG-2000.  
 XX  
 XX 27-JAN-2000; 2000WO-US01845.  
 XX  
 XX 27-JAN-1999; 99US-0117600.  
 XX  
 XX (UYSF-) UNIV SOUTH FLORIDA.  
 XX  
 XX Jove R, Dalton W, Sebt S, Yu H, Heller R, Jaroszeski M;  
 XX WPI; 2000-505964/45.  
 XX  
 XX Administering antagonists of STAT (signal transducer and activator of  
 XX transcription) signaling in cells for the treatment of cancers -  
 XX  
 XX Example 13; Page 54; 92pp; English.  
 XX  
 XX The present invention describes methods for inhibiting the growth of  
 XX (I), inducing apoptosis in (II), inhibiting tumourigenesis in (III),  
 XX inhibiting neoplastic transformation in (IV) cancer cells and for  
 XX enhancing the effectiveness of chemo- (IV) and radiotherapies (VI) for  
 XX the treatment of cancer. The methods comprise administering an antagonist  
 XX of STAT (signal transducer and activator of transcription) signalling.  
 XX The methods may be used for inhibiting the growth of cancer cells (I),  
 XX inducing apoptosis in cancer cells (II), inhibiting tumourigenesis  
 XX in cancer cells (III), inhibiting neoplastic transformation in cancer  
 XX cells (IV) and for enhancing the effectiveness of chemo- (IV) and  
 XX radiotherapies (VI) for the treatment of cancer. The present sequence  
 XX represents a STAT3 binding peptide, which is used in an example from the  
 XX present invention.  
 XX  
 XX Sequence 12 AA;  
 SQ  
 Query Match 50.0%; Score 4; DB 21; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PILV 8  
 Db |||||  
 4 PILV 7  
 RESULT 66  
 AAW36390  
 ID AAW36390 standard; peptide; 13 AA.  
 XX  
 AC AAW36390;  
 XX  
 DT 13-FEB-1998 (first entry)  
 XX  
 XX Antimicrobial protegrin peptide (190).  
 XX  
 XX Antimicrobial protegrin; broad spectrum; gram-positive; bacterium;  
 KW gram-negative; bacteria; yeast; fungus; fungi; protozoa; virus;  
 KW retrovirus; HIV; human immunodeficiency virus; preservation;  
 KW disinfection; prophylaxis; treatment; infection; disease;  
 KW Conjunctivitis; keratitis; corneal ulcer; stomach ulcer; STD;

KW Helicobacter pylori; sexually transmitted disease; oral mucositis;  
 KW gram-negative sepsis; endocarditis; pneumonia; biocidal; biostatic;  
 KW respiratory infection; urinary tract infection; MRSA; protozoan;  
 KW vancomycin resistant Enterococcus; pathogen; multi-drug resistance;  
 KW penicillin resistant Streptococcus pneumoniae; pig; porcine;  
 KW methicillin resistant Staphylococcus aureus; systemic candidiasis.  
 XX  
 OS Synthetic.  
 OS Sus scrofa.  
 XX  
 XX WO9718826-A1.  
 XX  
 XX 29-MAY-1997.  
 XX  
 XX 22-NOV-1996; 96WO-US18544.  
 XX  
 XX 21-NOV-1996; 96US-0752852.  
 XX  
 XX 22-NOV-1995; 95US-0562346.  
 XX  
 XX 17-MAY-1996; 96US-0649811.  
 XX  
 XX 01-AUG-1996; 96US-0690921.  
 XX  
 XX (INTR-) INTRABIOTICS PHARM INC.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Chang CC, Chen J, Gu CL, Lehrer RI, Steinberg DA;  
 XX WPI; 1997-297871/27.  
 XX  
 XX New antimicrobial protegrin peptide(s) - having activity against  
 XX bacteria, yeast, fungi, protozoa and certain strains of viruses  
 XX (e.g. HIV)  
 XX  
 XX Claim 23; Page 109; 130pp; English.  
 XX  
 XX The present sequence is an antimicrobial protegrin peptide, which  
 XX has a broad spectrum of activity against microbial targets,  
 XX including gram-positive and gram-negative bacteria, yeast, fungi,  
 XX protozoa and certain strains of viruses and retroviruses, e.g. HIV.  
 XX It can be used to preserve or disinfect a variety of materials,  
 XX including medical equipment, foodstuffs, cosmetics, contact lens  
 XX solutions, medicaments or other nutrient containing materials. It  
 XX can also be used for the prophylaxis or treatment of microbial  
 XX infections or diseases in plants and animals, e.g. conjunctivitis,  
 XX keratitis, corneal ulcers, stomach ulcers associated with  
 XX Helicobacter pylori, sexually transmitted diseases, gram-negative  
 XX sepsis, endocarditis, pneumonia and other respiratory infections,  
 XX urinary tract infections, systemic candidiasis and oral mucositis.  
 XX It is biostatic or biocidal against clinically relevant pathogens  
 XX exhibiting multi-drug resistance, e.g. vancomycin resistant  
 XX Enterococcus faecium or faecalis, penicillin resistant  
 XX Streptococcus pneumoniae and methicillin resistant Staphylococcus  
 XX aureus (MRSA). It is given at a dosage of 0.1 to 5, preferably 0.5  
 XX to 1 mg/kg/day, by injection.  
 XX  
 XX Sequence 13 AA;  
 SQ  
 Query Match 50.0%; Score 4; DB 18; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RGPF 4  
 Db |||||  
 6 RGPF 9  
 RESULT 67  
 AAG73433  
 ID AAG73433 standard; peptide; 13 AA.  
 XX  
 XX AAG73433;  
 XX  
 XX 10-AUG-2001 (first entry)  
 XX

DE Human gene 27-encoded secreted protein HUAJ58, SEQ ID NO:206.  
 XX Human; secreted protein; proliferative disorder; cancer;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder; tumour;  
 KW endocrine disorder; infection; wound healing; vulnery;  
 KW cell culture; chemotaxis; food additive;  
 KW binding partner identification.  
 XX Homo sapiens.  
 OS  
 XX  
 FN WO200134628-A1.  
 XX  
 PD 17-MAY-2001.  
 XX  
 XX 08-NOV-2000; 2000WO-US30653.  
 PF  
 XX 12-NOV-1999; 9SUS-0164735.  
 PR  
 XX 27-JUL-2000; 2000US-0221193.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Ruben SM, Komatsoulis GA, Birse CE, Ni J, Moore PA;  
 PI  
 XX WPI; 2001-329066/34.  
 DR N-PSDB; AAH32611.  
 XX  
 XX Nucleic acids encoding 35 human secreted polypeptides, useful for  
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's  
 PT disease and diabetic retinopathy -  
 XX  
 PS Claim 11; Page 553; 604pp; English.  
 XX  
 XX AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted  
 CC protein genes, and AAG73346-AAG73448 represent the proteins they encode.  
 CC AAG73449-AAG73519 represent human secreted protein fragments. The genes  
 CC and their corresponding secreted proteins are useful for preventing,  
 CC treating or ameliorating medical conditions, e.g., by protein or gene  
 CC therapy. Pathological conditions can be diagnosed by determining the  
 CC amount of the new protein in a sample or by determining the presence of  
 CC mutations in the new genes. Specific uses are described for each of the  
 CC 52 genes, based on the tissues in which they are most highly expressed,  
 CC and include developing products for the diagnosis or treatment of  
 CC proliferative disorders, cancer, tumours, foetal and developmental  
 CC abnormalities, haematopoietic disorders, diseases of the immune system,  
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,  
 CC allergies, neurological disorders (e.g., Alzheimer's disease,  
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,  
 CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,  
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,  
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine  
 CC disorders, and infections. The proteins can also be used to aid wound  
 CC healing and epithelial cell proliferation, to prevent skin aging due to  
 CC sunburn, to maintain organs before transplantation, for supporting cell  
 CC culture of primary tissues, to regenerate tissues, to identify their  
 CC cognate ligands or binding partners, and in chemotaxis, and can be used  
 CC as a food additive or preservative to modify storage properties.  
 CC Antibodies specific for a protein of the invention can be used in  
 CC alleviating symptoms associated with the disorders mentioned above, and  
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked  
 CC immunosorbent assay (ELISA). The present sequence represents a human  
 CC secreted protein of the invention.  
 XX  
 SQ Sequence 13 AA;

Query Match 50.0%; Score 4; DB 22; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 PILV 8  
 Db 8 PILV 11  
 RESULT 68  
 ABG64297  
 ID ABG64297 standard; Protein; 13 AA.  
 XX  
 AC ABG64297;  
 XX  
 DT 27-AUG-2002 (first entry)  
 XX  
 DE Human albumin fusion protein #972.  
 XX  
 KW Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytosstatic; antiinfertility; antiinflammatory; antiulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO200177137-A1.  
 XX  
 PD 18-OCT-2001.  
 XX  
 XX 12-APR-2001; 2001WO-US11988.  
 PF  
 XX 12-APR-2000; 2000US-229358P.  
 PR  
 XX 25-APR-2000; 2000US-199384P.  
 PR  
 XX 21-DEC-2000; 2000US-256931P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Haseltine WA;  
 PI  
 XX WPI; 2002-010886/01.  
 DR  
 XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein -  
 XX  
 PS Claim 1; Page 1119; 2102pp; English.  
 XX  
 CC The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA), also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or  
 CC disorder that may be modulated by therapeutic protein X. The albumin  
 CC extends the shelf-life of protein X and may increase its biological  
 CC in vitro/in vivo activity. The protein is useful for treating and  
 CC diagnosing disorders such as cancer, reproductive disorders, digestive  
 CC disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders  
 CC (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders  
 CC (e.g. diabetes), haematopoietic disorders, neural disorders  
 CC (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease,  
 CC encephalomyelitis, meningitis, schizophrenia), and connective disorders  
 CC (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin  
 CC fusion proteins of the invention.  
 XX  
 SQ Sequence 13 AA;

Query Match 50.0%; Score 4; DB 23; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 PILV 8  
 Db 8 PILV 11

```

RESULT 69
AAW81795
ID AAW81795 standard; peptide; 14 AA.
XX
XX AAW81795;
AC
XX
XX
DT 29-JAN-1999 (first entry)
XX
XX D. viviparus DV17 antigen Lys C proteolytic peptide fragment #7.
XX
XX DV17; antigen; lungworm; immunogenic protein; ELISA; antibody; cattle;
KW enzyme linked immunosorbent assay; vaccine; dictyocauliasis.
XX
XX Dictyocaulus viviparus.
OS
XX
XX DE19715586-A1.
PN
XX
XX 22-OCT-1998.
PD
XX
XX 15-APR-1997; 97DE-1015586.
PF
XX
XX 15-APR-1997; 97DE-1015586.
PR
XX
XX (FARH) HOECHST AG.
PA
XX
XX Hofmann J, Pauli A, Schmid K;
PI
XX
XX WPI; 1998-558238/48.
DR
XX
XX N-PSDB; AAV64653.
DR
XX
XX New Dictyocaulus viviparus lungworm protein (DV17) - used in ELISA
PT assay for DV17-specific antibodies and in vaccines against
PT dictyocauliasis in cattle
XX
XX Claim 2; Page 9; 15pp; German.
PS
XX
XX This sequence represents a fragment of an immunogenic protein (DV17)
CC isolated from adult Dictyocaulus viviparus lungworms and generated by
CC Lys C proteolysis. The protein is used in an ELISA assay for
CC DV17-specific antibodies and fragments of the protein can be used in
CC vaccines against dictyocauliasis in cattle.
XX
XX
SQ Sequence 14 AA;
Query Match 50.0%; Score 4; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
DB 2 FPIL 5

RESULT 70
AAW49166
ID AAW49166 standard; peptide; 15 AA.
XX
XX AAW49166;
AC
XX
XX
DT 05-JUN-1998 (first entry)
XX
XX Human leucocyte antigen DQ4 binding peptide #57.
XX
XX Human leucocyte antigen; HLA-DQ4; combinatorial library;
KW Human leucocyte antigen; HLA-DQ4; combinatorial library;
XX autoimmune disease; Chronic articular rheumatism.
XX
XX Synthetic.
OS
XX
XX JP08151396-A.
PN
XX
XX 11-JUN-1996.
PD

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XX
PF 28-NOV-1994; 94JP-0292657.
XX
XX 28-NOV-1994; 94JP-0292657.
XX
XX (TEIJ) TEIJIN LTD.
PA
XX
XX WPI; 1996-329479/33.
DR
XX
XX HLA-binding oligopeptide and an immuno:regulator contg it - used in
PT the treatment of auto:immune disease
XX
XX Claim 3; Page 15; 61pp; Japanese.
PS
XX
XX This peptide is an example of a peptide which binds to a human leucocyte
CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
CC combinatorial library comprising the sequence AAV05953, by screening
CC with an HLA-DQ4 molecule. The peptide is used for the treatment of
CC autoimmune disease, or especially for treatment of viral diseases.
XX
XX
SQ Sequence 15 AA;
Query Match 50.0%; Score 4; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 9 RGPF 12

RESULT 71
AAW38927
ID AAW38927 standard; peptide; 15 AA.
XX
XX AAW38927;
AC
XX
XX 27-MAR-1998 (first entry)
DT
XX
XX Peptide resembling an SH3 domain binding peptide SEQ ID NO:324.
DE
XX
XX Cortactin; SH3 domain; binding peptide; Src homology region 3;
KW tyrosine kinase; immune response; lymphokine; interleukin 1; Nck;
KW Abi; PLCgamma; p53bp2; Crk; Yes; Grb2.
XX
XX Synthetic.
OS
XX
XX WO9730074-A1.
PN
XX
XX 21-AUG-1997.
PD
XX
XX 14-FEB-1997; 97WO-US02298.
PF
XX
XX 16-FEB-1996; 96US-0602999.
PR
XX
XX (CYTO-) CYTOGEN CORP.
PA (UYNC-) UNIV NORTH CAROLINA.
XX
XX
XX Der CJ, Fowlkes DM, Kay BK, Quilliam LA, Rider JE;
PI Sparks AB, Thorn JM;
XX
XX WPI; 1997-424972/39.
DR
XX
XX Src homology region 3 binding peptide - used to activate Src
PT tyrosine kinase(s) and to stimulate immune response by increasing
PT production of certain lymphokine(s), e.g. interleukin-1
XX
XX Claim 22; Page 90; 131pp; English.
PS
XX
XX The present sequence represents a peptide which resembles a Src homology
CC region 3 (SH3) binding peptide. SH3 binding peptides are selected from:
CC (a) peptides which bind the SH3 domain of Cortactin; (b) peptides which
CC bind the middle SH3 domain of Nck; (c) peptides which bind the SH3

```

CC domain of Abl; (d) peptides which bind the SH3 domain of Src; (e)  
 CC peptides which bind the SH3 domain of PLC gamma; (f) peptides which bind  
 CC the SH3 domain of p53bp2; (g) peptides which bind the amino-terminal SH3  
 CC domain of Crk; (h) peptides which bind the SH3 domain of Yes; and (i)  
 CC peptides which bind the amino-terminal SH3 domain of Grb2. The purified  
 CC binding peptides can be used in the method to identify inhibitors of  
 CC their binding to their respective SH3 domains, which could be used to  
 CC modulate the pharmacological activity of proteins or polypeptide  
 CC containing the SH3 domain. The peptides can also be used to activate  
 CC Src or Src-related protein tyrosine kinases, to stimulate the immune  
 CC response by increasing the production of certain lymphokines, e.g.  
 CC tumour necrosis factor-alpha and interleukin-1, or to deliver a  
 CC conjugated molecule to certain cellular compartments containing Src or  
 CC Src related proteins.  
 XX  
 XX  
 SQ Sequence 15 AA;  
 Query Match 50.0%; Score 4; DB 18; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 FPIL 7  
 DB 1 FPIL 4  
 RESULT 72  
 ABB98785  
 ID ABB98785 standard; Peptide; 15 AA.  
 XX  
 AC ABB98785;  
 XX  
 DT 03-FEB-2003 (first entry)  
 XX  
 DE Human ribosomal protein S4-18.04 peptide fragment.  
 XX  
 KW Human; ribosomal protein S4-18.04; tumour; haemopathy; HIV infection;  
 KW immunological disease; inflammation; cytostatic; anti-HIV.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1345823-A.  
 XX  
 PD 24-APR-2002.  
 XX  
 PF 29-SEP-2000; 2000CN-0125506.  
 XX  
 PR 29-SEP-2000; 2000CN-0125506.  
 XX  
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-584314/63.  
 XX  
 PT Novel polypeptide-human ribosomal protein S4-18.04 and polynucleotide  
 PT for encoding said polypeptide -  
 XX  
 PS Example 5; Page 19 (Disclosure); 33pp; Chinese.  
 XX  
 CC The present invention relates to human ribosomal protein S4-18.04 (see  
 CC ABB98784). The protein and its coding sequence can be used for treating  
 CC several diseases, such as malignant tumours, haemopathy, HIV infection,  
 CC immunological disease and various inflammations. The present sequence is  
 CC an N-terminal peptide fragment of the protein, which was used in an  
 CC example from the invention.  
 XX  
 XX  
 SQ Sequence 15 AA;  
 Query Match 50.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PILV 8  
 DB 2 PILV 5  
 RESULT 74  
 ABR41125  
 ID ABR41125 standard; peptide; 15 AA.  
 XX  
 AC ABR41125;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE LRP6 specific polyclonal antibody peptide 7.  
 XX  
 KW High bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;

QY 5 PILV 8  
 DB 7 PILV 10  
 RESULT 73  
 AAU77172  
 ID AAU77172 standard; Peptide; 15 AA.  
 XX  
 AC AAU77172;  
 XX  
 DT 02-JUL-2002 (first entry)  
 XX  
 DE Transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide.  
 XX  
 KW Human; transcriptional control factor ZFM1 isomer 25.63; HIV;  
 KW malignant tumour; haemopathy; human immunodeficiency virus; cancer;  
 KW immunological disease; inflammation; cytostatic; haemostatic; virucide;  
 KW immunomodulatory; antiinflammatory; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200220588-A1.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 02-JUL-2001; 2001WO-CN01127.  
 XX  
 PR 07-JUL-2000; 2000CN-0117050.  
 XX  
 PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-339796/37.  
 XX  
 PT Human transcriptional control factor ZFM1 isomer 25.63 and encoding  
 PT polynucleotide, used in diagnosis and treatment of malignant tumours,  
 PT haemopathy, human immunodeficiency virus infection, immunological  
 PT diseases and inflammation -  
 XX  
 PS Example 5; Page 14; 38pp; Chinese.  
 XX  
 CC The invention relates to the human transcriptional control factor ZFM1  
 CC isomer 25.63 and the polynucleotide encoding it. The sequences of the  
 CC invention are used in diagnosis and treatment of malignant tumours,  
 CC haemopathy, human immunodeficiency virus (HIV) infection, immunological  
 CC diseases and various inflammations. This sequence represents the human  
 CC transcriptional control factor ZFM1 isomer 25.63 N-terminal peptide, used  
 CC in ELISA.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 50.0%; Score 4; DB 23; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5 PILV 8  
 DB 2 PILV 5  
 RESULT 74  
 ABR41125  
 ID ABR41125 standard; peptide; 15 AA.  
 XX  
 AC ABR41125;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE LRP6 specific polyclonal antibody peptide 7.  
 XX  
 KW High bone mass; HBM; LRP5; LRP6; transgenic; bone mass modulation;

KW gene therapy; bone density modulation; bone strength; trabecular number;  
 KW bone size; bone tissue connectivity; bone disease; osteoporosis;  
 KW osteomalacia; rickets; Paget's disease; neoplasm of the bone.

XX Unidentified.

XX WO200292764-A2.

XX 21-NOV-2002.

XX 13-MAY-2002; 2002WO-US14876.

XX 11-MAY-2001; 2001US-290071P.

XX 17-MAY-2001; 2001US-291311P.

XX 01-FEB-2002; 2002US-353058P.

XX 04-MAR-2002; 2002US-361293P.

XX (GENO-) GENOME THERAPEUTICS CORP.

XX (AMHP) WYETH.

XX Babij P, Bex FJ, Yaworsky PJ, Bodine PV;

XX WPI; 2003-129278/12.

XX New transgenic animals (e.g. mice), useful as models for studying bone  
 PT density modulation, developing drugs for treating or preventing bone  
 PT diseases (e.g. osteoporosis), or diagnosing diseases characterized by  
 PT reduced bone density -

XX Disclosure; Page 131; 603pp; English.

XX The invention relates to novel transgenic animals expressing the high  
 CC bone mass (HBM) gene, expressing the corresponding wild type HBM gene,  
 CC comprising an alteration of the gene encoding LRP5 or LRP6, or  
 CC expressing an LRP5 that is modulated by an altered gene control  
 CC sequence introduced by homologous or non-homologous recombination. The  
 CC transgenic animals are for the study of bone density modulation or bone  
 CC mass modulation. The invention has osteopathic and cytostatic activity.  
 CC The polynucleotides of the invention may have a use in gene therapy.  
 CC The transgenic animals and nucleic acids are for the study of  
 CC bone density modulation, where the bone mass is modulated relative to  
 CC non-transgenic animals of the same species in more than one parameter  
 CC selected from bone density, bone strength, trabecular number, bone  
 CC size, or bone tissue connectivity. The transgenic animals, nucleic  
 CC acids and methods are useful for identifying molecules involved in bone  
 CC development, and for developing pharmaceutical compositions, which may  
 CC be employed for treating or preventing bone diseases, e.g.  
 CC osteoporosis, osteomalacia, rickets, Paget's disease, or neoplasms of  
 CC the bone. The transgenic animals and nucleic acids are also useful in  
 CC methods for diagnosing diseases involved in bone development, or  
 CC characterised by reduced bone density or mass. The present sequence is  
 CC used in the exemplification of the invention.

XX Sequence 15 AA;

Query Match 50.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPP 5

DB 6 GPPP 9

RESULT 75

ABR34952

ID ABR34952 standard; Peptide; 15 AA.

XX ABR34952;

XX ABR34952;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 18SP2C9 HLA peptide #4208.

XX

KW Human, cytostatic; vaccine; cancer; immune response; HLA;  
 KW human leukocyte antigen.

XX Homo sapiens.

XX WO200283921-A2.

XX 24-OCT-2002.

XX 10-APR-2002; 2002WO-US11654.

XX 10-APR-2001; 2001US-282739P.

XX 25-APR-2001; 2001US-283112P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response  
 PT in cancer patients -

XX Claim 13; Page 557; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABRO1789-ABRO1861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention.

XX Sequence 15 AA;

Query Match 50.0%; Score 4; DB 24; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPP 5

DB 2 GPPP 5

Search completed: November 25, 2003, 19:27:18

Job time : 21.4186 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 : Search time 12.8372 Seconds  
(without alignments)  
114.943 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGRPFILV 8

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 673684 seqs, 184443283 residues

Word size : 0

Total number of hits satisfying chosen parameters: 139996

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Published Applications AA:

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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	8	100.0	8	15	US-10-281-652-29
2	5	62.5	16	15	US-10-225-567A-1931
3	4	50.0	7	12	US-10-118-708-2
4	4	50.0	9	8	US-08-452-843A-10
5	4	50.0	9	10	US-09-824-787B-137
6	4	50.0	9	11	US-09-791-393-263
7	4	50.0	9	11	US-09-791-389-263
8	4	50.0	9	12	US-10-022-066-178
9	4	50.0	9	12	US-09-132-231-57
10	4	50.0	10	12	US-10-083-768-30
11	4	50.0	11	10	US-09-071-838-138
12	4	50.0	11	15	US-10-213-512-138
13	4	50.0	12	12	US-10-118-708-5
14	4	50.0	14	9	US-09-749-234A-7
15	4	50.0	15	11	US-09-774-639-257

15	50.0	4	16	US-09-969-730-339	Sequence 339, App
15	50.0	4	17	US-10-161-791-324	Sequence 324, App
16	50.0	4	18	US-10-225-567A-1018	Sequence 1018, App
20	50.0	4	19	US-09-736-076-8	Sequence 8, Appli
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4	37.5	4	21	US-09-040-518-8	Sequence 8, Appli
4	37.5	4	22	US-09-784-810A-20	Sequence 20, Appli
4	37.5	4	23	US-10-237-160-1	Sequence 1, Appli
4	37.5	4	24	US-10-313-338A-1	Sequence 1, Appli
4	37.5	4	25	US-10-313-790A-1	Sequence 1, Appli
4	37.5	4	26	US-10-158-742A-19	Sequence 19, Appli
4	37.5	4	27	US-10-028-075B-123	Sequence 123, App
4	37.5	4	28	US-10-029-206A-123	Sequence 123, App
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5	37.5	4	30	US-10-122-246-34	Sequence 34, Appli
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5	37.5	4	32	US-10-145-206-110	Sequence 110, App
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5	37.5	4	36	US-10-200-923-10	Sequence 10, Appli
6	37.5	4	37	US-08-996-140-8	Sequence 8, Appli
6	37.5	4	38	US-09-729-873-19	Sequence 19, Appli
6	37.5	4	39	US-09-767-395-28	Sequence 28, Appli
6	37.5	4	40	US-09-947-387-81	Sequence 81, Appli
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6	37.5	4	42	US-09-947-387-123	Sequence 123, App
6	37.5	4	43	US-09-974-879-411	Sequence 411, App
6	37.5	4	44	US-09-997-961-39	Sequence 39, Appli
6	37.5	4	45	US-09-305-736-411	Sequence 411, App
6	37.5	4	46	US-10-349-023-17	Sequence 17, Appli
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6	37.5	4	50	US-10-138-375-123	Sequence 123, App
6	37.5	4	51	US-09-818-683-411	Sequence 411, App
6	37.5	4	52	US-10-023-282-682	Sequence 682, App
6	37.5	4	53	US-10-211-088-242	Sequence 242, App
7	37.5	4	54	US-09-734-002-9	Sequence 9, Appli
7	37.5	4	55	US-09-729-873-17	Sequence 17, Appli
7	37.5	4	56	US-09-731-242A-22	Sequence 22, Appli
7	37.5	4	57	US-09-989-789-700	Sequence 700, App
7	37.5	4	58	US-09-989-789-701	Sequence 701, App
7	37.5	4	59	US-09-989-789-702	Sequence 702, App
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7	37.5	4	61	US-09-832-723-14	Sequence 14, Appli
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7	37.5	4	63	US-09-947-387-80	Sequence 80, Appli
7	37.5	4	64	US-09-931-325A-128	Sequence 128, App
7	37.5	4	65	US-09-990-186-700	Sequence 700, App
7	37.5	4	66	US-09-990-186-701	Sequence 701, App
7	37.5	4	67	US-09-990-186-702	Sequence 702, App
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7	37.5	4	69	US-09-865-548A-62	Sequence 62, Appli
7	37.5	4	70	US-09-989-994-700	Sequence 700, App
7	37.5	4	71	US-09-989-994-701	Sequence 701, App
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7	37.5	4	73	US-09-930-915A-169	Sequence 169, App
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7	37.5	4	80	US-10-293-371-40	Sequence 40, Appli
7	37.5	4	81	US-10-293-371-41	Sequence 41, Appli
7	37.5	4	82	US-10-293-371-42	Sequence 42, Appli
7	37.5	4	83	US-10-197-927-55	Sequence 55, Appli
7	37.5	4	84	US-10-412-203-17	Sequence 17, Appli
7	37.5	4	85	US-10-138-375-34	Sequence 34, Appli
7	37.5	4	86	US-10-138-375-80	Sequence 80, Appli
7	37.5	4	87	US-10-251-947-10	Sequence 10, Appli
7	37.5	4	88	US-10-214-932-70	Sequence 70, Appli



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89      3 37.5 7 15 US-10-214-932-118 Sequence 118, Appl
90      3 37.5 7 15 US-10-099-278-17 Sequence 17, Appl
91      3 37.5 8 9 US-09-839-666-6 Sequence 6, Appl
92      3 37.5 8 10 US-09-954-166-12 Sequence 12, Appl
93      3 37.5 8 10 US-09-761-534A-3 Sequence 3, Appl
94      3 37.5 8 10 US-09-756-875-11 Sequence 11, Appl
95      3 37.5 8 10 US-09-756-875-21 Sequence 21, Appl
96      3 37.5 8 10 US-09-756-875-22 Sequence 22, Appl
97      3 37.5 8 10 US-09-756-875-23 Sequence 23, Appl
98      3 37.5 8 10 US-09-756-875-24 Sequence 24, Appl
99      3 37.5 8 10 US-09-756-875-25 Sequence 25, Appl
100     3 37.5 8 10 US-09-756-875-26 Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-10-281-652-29
; Sequence 29, Application US/10281652
; Publication No. US20030091606A1
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-29

Query Match 100.0%; Score 8; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPFPILV 8
   |||||
Db 1 RGPFPILV 8

RESULT 2
US-10-225-567A-1931
; Sequence 1931, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1931
; LENGTH: 16

Sequence 118, Appl
Sequence 17, Appl
Sequence 6, Appl
Sequence 12, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 26, Appl

US-10-225-567A-1931
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1931

Query Match 62.5%; Score 5; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPIL 7
   |||||
Db 1 PPPIL 5

RESULT 3
US-10-118-708-2
; Sequence 2, Application US/10118708
; Publication No. US20030165991A1
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/10/118,708
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2
; OTHER INFORMATION: peptide mimotope of deoxynivalenol
US-10-118-708-2

Query Match 50.0%; Score 4; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
   ||||
Db 3 GPFP 6

RESULT 4
US-08-452-843A-10
; Sequence 10, Application US/08452843A
; Publication No. US20020098197A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 399632001321
; CURRENT APPLICATION NUMBER: US/08/452,843A
; CURRENT FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cw6 consensus
US-08-452-843A-10
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```

Query Match          50.0%; Score 4; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6
Db 2 PFPI 5

RESULT 5
US-09-824-787B-137
; Sequence 137, Application US/09824787B
; Patent No. US20020155447A1
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice E.
; APPLICANT: Evans, Elizabeth E.
; APPLICANT: Borrello, Melinda A.
; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
; FILE REFERENCE: 1821.0040001
; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 137
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-137

Query Match          50.0%; Score 4; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPEP 5
Db 1 GPEP 4

RESULT 6
US-09-791-393-263
; Sequence 263, Application US/09791393
; Publication No. US20030032200A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Rajesh Bhikhu
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N1
; CURRENT APPLICATION NUMBER: US/09/791,393
; CURRENT FILING DATE: 2002-01-02
; EARLIER APPLICATION NUMBER: GB 0004412.3
; EARLIER FILING DATE: 2000-02-24
; EARLIER APPLICATION NUMBER: GB 0030050.9
; EARLIER FILING DATE: 2000-12-08
; EARLIER APPLICATION NUMBER: US 60/254,830
; EARLIER FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-393-263

Query Match          50.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6
Db 2 PFPI 5

RESULT 7
US-09-791-389-263
; Sequence 263, Application US/09791389
; Publication No. US20030032773A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Rajesh Bhikhu
; APPLICANT: Parekh, Rajesh Bhikhu
; APPLICANT: Rohlf, Christian
; APPLICANT: Terrett, Jonathan Alexander
; APPLICANT: Tyson, Kerry Louise
; TITLE OF INVENTION: Proteins, Genes and Their Use for
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
; FILE REFERENCE: 2543-1-001 N2
; CURRENT APPLICATION NUMBER: US/09/791,389
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: GB 0004412.3
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: GB 0030050.9
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/254,830
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: homo sapien
US-09-791-389-263

Query Match          50.0%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6
Db 2 PFPI 5

RESULT 8
US-10-022-066-178
; Sequence 178, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLIMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;

```

US-10-022-066-178

Query Match 50.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4  
DB 6 RGPF 9

RESULT 9

US-09-132-231-57  
; Sequence 57, Application US/09132231A  
; Publication No. US20030198950A1  
; GENERAL INFORMATION:  
; APPLICANT: HORWITZ, Marshall S.  
; APPLICANT: LOEB, Lawrence A.  
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH  
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY  
; FILE REFERENCE: 032425-001  
; CURRENT APPLICATION NUMBER: US/09/132,231A  
; PRIOR FILING DATE: 1998-08-11  
; PRIOR APPLICATION NUMBER: US 08/316,415  
; PRIOR FILING DATE: 1994-09-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 57  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-09-132-231-57

Query Match 50.0%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7  
DB 2 FPIL 5

RESULT 10

US-10-083-768-30  
; Sequence 30, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven E.  
; Dufin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Matheakis, Larry C.  
; Schatz, Peter J.  
; Wegstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-10-083-768-30

Query Match 50.0%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4  
DB 2 RGPF 5

RESULT 11

US-09-071-838-138  
; Sequence 138, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Vadesari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 138:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-138

Query Match 50.0%; Score 4; DB 10; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7  
 ||||  
 Db 5 FPIL 8

## RESULT 12

US-10-213-512-138  
 ; Sequence 138, Application US/10213512  
 ; Publication No. US20030110536A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fischer, Robert L.  
 ; APPLICANT: Chad, Nir  
 ; APPLICANT: Kiyosue, Tomohiro  
 ; APPLICANT: Yadegari, Ramin  
 ; APPLICANT: Margossian, Linda  
 ; APPLICANT: Harada, John  
 ; APPLICANT: Goldberg, Robert B.  
 ; APPLICANT: The Regents of the University of California  
 ; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
 ; FILE OF INVENTION: Fruit Development in Plants  
 ; FILE REFERENCE: 023070-086110US  
 ; CURRENT APPLICATION NUMBER: US/10/213,512  
 ; CURRENT FILING DATE: 2002-08-06  
 ; PRIOR APPLICATION NUMBER: US/09/177,206  
 ; PRIOR FILING DATE: 1998-10-22  
 ; PRIOR APPLICATION NUMBER: US 09/071,838  
 ; PRIOR FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 324  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 138  
 ; LENGTH: 11  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis sp.  
 US-10-213-512-138

Query Match 50.0%; Score 4; DB 15; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7  
 ||||  
 Db 5 FPIL 8

## RESULT 13

US-10-118-708-5  
 ; Sequence 5, Application US/10118708  
 ; Publication No. US20030165991A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hart, L P  
 ; APPLICANT: Pestka, James J  
 ; APPLICANT: Yuan, Qiaoping  
 ; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
 ; FILE OF INVENTION: THEREOF  
 ; FILE REFERENCE: MSU 4.1-447  
 ; CURRENT APPLICATION NUMBER: US/10/118,708  
 ; CURRENT FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/146,643  
 ; PRIOR FILING DATE: 1999-07-30  
 ; NUMBER OF SEQ ID NOS: 8  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 12  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: C430, the  
 ; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a  
 ; OTHER INFORMATION: cysteine residue

## US-10-118-708-5

Query Match 50.0%; Score 4; DB 12; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPPP 5  
 ||||  
 Db 3 GPPP 6

## RESULT 14

US-09-749-234A-7  
 ; Sequence 7, Application US/09749234A  
 ; Patent No. US20020068817A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HOFMANN, Joachim  
 ; APPLICANT: SCHMID, Karlheinz  
 ; APPLICANT: PAULI, Annette  
 ; TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR THE  
 ; DIAGNOSIS OF LUNGWORM INFESTATION AND FOR VACCINATION  
 ; NUMBER OF SEQUENCES: 30  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: FOLEY & LARDNER  
 ; STREET: 3000 K Street, N.W.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/749,234A  
 ; FILING DATE: 27-Dec-2000  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/403,092  
 ; FILING DATE: 199-10-15  
 ; APPLICATION NUMBER: DE 197 15 586.3  
 ; FILING DATE: 15-APR-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Granados, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 038311/0103  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 672-5300  
 ; TELEFAX: (202) 672-5399  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: <Unknown>  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 US-09-749-234A-7

Query Match 50.0%; Score 4; DB 9; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7  
 ||||  
 Db 2 FPIL 5

## RESULT 15

US-09-774-639-257  
 ; Sequence 257, Application US/09774639  
 ; Publication No. US20030003555A1

```
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 257
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-257

Query Match          50.0%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPIL 7
      ||||
Db      8 FPIL 11

RESULT 16
US-09-969-730-339
; Sequence 339, Application US/09969730
; Publication No. US2003005443A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P2
; CURRENT APPLICATION NUMBER: US/09/969,730
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/774,639
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/238,291
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: PCT/US98/16235
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/056,371
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,732
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,366
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,364
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,370
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,367
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,365
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,731
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,557
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/056,563
; PRIOR FILING DATE: 1997-08-19
; PRIOR APPLICATION NUMBER: 60/055,970
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,986
; PRIOR FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: 60/055,311
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,808
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,803
; PRIOR FILING DATE: 1997-08-05
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; PRIOR APPLICATION NUMBER: 60/054,804
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,809
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,806
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,310
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,798
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,309
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,312
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/054,807
; PRIOR FILING DATE: 1997-08-05
; PRIOR APPLICATION NUMBER: 60/055,386
; PRIOR FILING DATE: 1997-08-05
; NUMBER OF SEQ ID NOS: 373
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 339
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-730-339

Query Match          50.0%; Score 4; DB 11; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPIL 7
      ||||
Db      8 FPIL 11

RESULT 17
US-10-161-791-324
; Sequence 324, Application US/10161791
; Publication No. US2003018683A1
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; TITLE OF INVENTION: ISOLATING AND USING SAME
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pernie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/161,791
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-3741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-10-161-791-324

Query Match      50.0%; Score 4; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 FPIL 7
Db      1 FPIL 4

RESULT 18
US-10-225-567A-1018
; Sequence 1018, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn A.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2392
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1018
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1018

Query Match      50.0%; Score 4; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGPF 4
Db      3 RGPF 6

RESULT 19
US-09-736-076-8
; Sequence 8, Application US/09736076
; Patent No. US20020049301A1
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson Shmuel A.
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY
; FILE REFERENCE: 1242.1015-009
; CURRENT APPLICATION NUMBER: US/09/736,076
; CURRENT FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 08/861,338
; PRIOR FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

;
; TELECOMMUNICATION INFORMATION: GRK1
; OTHER INFORMATION: GRK1
US-09-736-076-8

Query Match      50.0%; Score 4; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGPF 4
Db      7 RGPF 10

RESULT 20
US-09-759-584-16
; Sequence 16, Application US/09759584
; Patent No. US20010014732A1
; GENERAL INFORMATION:
; APPLICANT: BROSKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,584
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/377,687
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-759-584-16

Query Match      37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 ILV 8
Db      2 ILV 4

RESULT 21
US-09-040-518-8
; Sequence 8, Application US/09040518
; Patent No. US20010042255A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Karatzas, Costas N.
; TITLE OF INVENTION: PRODUCTION OF BIOFILAMENTS IN TRANSGENIC
; FILE OF INVENTION: ANIMALS
; FILE REFERENCE: 06632/011001
; CURRENT APPLICATION NUMBER: US/09/040,518
; CURRENT FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Designed peptide to act as a recognition site for
; OTHER INFORMATION: an enzyme
US-09-040-518-8

```

```

Query Match          37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

QY      1 RGP 3
      |||
Db      1 RGP 3

```

```

RESULT 22
US-09-784-810A-20
; Sequence 20, Application US/09784810A
; Patent No. US20020082203A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; TITLE OF INVENTION: NOVEL SPHINGOSINE KINASES AND NUCLEIC ACIDS ENCODING
; FILE OF INVENTION: SAME
; FILE REFERENCE: 10716-08
; CURRENT APPLICATION NUMBER: US/09/784,810A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,360
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 60/191,261
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: motif
US-09-784-810A-20

```

```

Query Match          37.5%; Score 3; DB 9; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

QY      6 ILV 8
      |||
Db      2 ILV 4

```

```

RESULT 23
US-10-237-160-1
; Sequence 1, Application US/10237160
; Publication No. US20030133926A1
; GENERAL INFORMATION:
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of
; Symptoms Of Autism
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley

```

```

; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,160
; FILING DATE: 09-Dec-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-237-160-1

```

```

Query Match          37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

QY      3 PFP 5
      |||
Db      2 PFP 4

```

```

RESULT 24
US-10-313-338A-1
; Sequence 1, Application US/10313338A
; Publication No. US20030170226A1
; GENERAL INFORMATION:
; APPLICANT: Klaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF
; FILE REFERENCE: 1776-1-7
; CURRENT APPLICATION NUMBER: US/10/313,338A
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: US 09/411,605
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-313-338A-1

```

```

Query Match          37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

```

```

QY      3 PFP 5
      |||
Db      2 PFP 4

```

```

RESULT 25

```

```
US-10-313-790A-1
; Sequence 1, Application US/10313790A
; Publication No. US20030170227A1
; GENERAL INFORMATION:
; APPLICANT: Kilaire Laboratories, Inc.
; APPLICANT: Houston, Devin B.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO REDUCTION OF SYMPTOMS OF AL
; FILE REFERENCE: 1776-1-6
; CURRENT APPLICATION NUMBER: US/10/313,790A
; CURRENT FILING DATE: 2002-12-06
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-313-790A-1

Query Match      37.5%; Score 3; DB 12; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 PFP 5
Db      2 PFP 4

RESULT 26
US-10-158-742A-19
; Sequence 19, Application US/10158742A
; Publication No. US20030104581A1
; GENERAL INFORMATION:
; APPLICANT: Hoess, Eva
; APPLICANT: Meier, Thomas
; APPLICANT: Pestlin, Gabriele
; APPLICANT: Popp, Friedrich
; APPLICANT: Reichert, Klaus
; APPLICANT: Schmuck, Rainer
; APPLICANT: Schneider, Bernd
; APPLICANT: Seidel, Christoph
; APPLICANT: Tischer, Wilhelm
; TITLE OF INVENTION: PROCESS FOR MAKING ANTIFUSOGENIC FUSION PEPTIDES THAT FORM
; FILE REFERENCE: 20904
; CURRENT APPLICATION NUMBER: US/10/158,742A
; CURRENT FILING DATE: 2002-05-30
; PRIOR FILING DATE: EP 01114497.9
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE:
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cleavage
; US-10-158-742A-19

Query Match      37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGP 3
Db      1 RGP 3

RESULT 27
US-10-028-075B-123
; Sequence 123, Application US/10028075B
```

```
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 2183-5223US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: EP 01203748.7
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sptrembl/Q9PVM5/Q9PVM5
; US-10-028-075B-123

Query Match      37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGP 3
Db      2 RGP 4

RESULT 28
US-10-029-206A-123
; Sequence 123, Application US/10029206A
; Publication No. US20030119720A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: sptrembl/Q9PVM5/Q9PVM5
; US-10-029-206A-123

Query Match      37.5%; Score 3; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RGP 3
Db      2 RGP 4

RESULT 29
US-09-947-387-84
; Sequence 84, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
```



```
; TITLE OF INVENTION: No. US2002015085A1 Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-84

Query Match          37.5%; Score 3; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
      |||
Db      3 FPI 5

RESULT 30
US-10-122-246-34
; Sequence 34, Application US/10122246
; Publication No. US20030176354A1
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; Feighner, John P.
; Hlavka, Joseph J.
; TITLE OF INVENTION: NEW THERAPEUTIC USES OF TRI-, TETRA-,
; AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stepan P. Gribok, Esq.
; STREET: Duane Morris, LLP; 1650 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word Perfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/122,246
; FILING DATE: 11-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gribok, Stephan P.
; REGISTRATION NUMBER: 29,643
; REFERENCE/DOCKET NUMBER: D4850-00021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 979-1000
; TELEFAX: (215) 979-1020
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified_site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp_NH2
; /note= "A modified Trp residue: an amine group replaces a
; hydroxyl group at the carboxy terminus."
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-122-246-34

Query Match          37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
      |||
Db      1 FPI 3

RESULT 31
US-10-122-246-44
; Sequence 44, Application US/10122246
; Publication No. US20030176354A1
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; Feighner, John P.
; Hlavka, Joseph J.
; TITLE OF INVENTION: NEW THERAPEUTIC USES OF TRI-, TETRA-,
; AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 128
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stepan P. Gribok, Esq.
; STREET: Duane Morris, LLP; 1650 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Word Perfect 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/122,246
; FILING DATE: 11-Apr-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gribok, Stephan P.
; REGISTRATION NUMBER: 29,643
; REFERENCE/DOCKET NUMBER: D4850-00021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 979-1000
; TELEFAX: (215) 979-1020
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified_site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp_NH2
; /note= "A modified Trp residue: an amine group replaces a
; hydroxyl group at the carboxy terminus."
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-122-246-44

Query Match          37.5%; Score 3; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
      |||
Db      1 FPI 3
```

QY 5 PIL 7  
|||  
Db 1 PIL 3

RESULT 32  
US-10-145-206-110  
; Sequence 110, Application US/10145206  
; Publication No. US20030195158A1  
; GENERAL INFORMATION:  
; APPLICANT: MIN, HOSUNG  
; APPLICANT: HSU, HAILING  
; APPLICANT: ZHONG, FEI  
; TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1  
; FILE REFERENCE: A-743  
; CURRENT APPLICATION NUMBER: US/10/145,206  
; CURRENT FILING DATE: 2002-05-13  
; PRIOR APPLICATION NUMBER: US 60/290,196  
; PRIOR FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 110  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Modulator of TALL-1  
US-10-145-206-110

Query Match 37.5%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFP 5  
|||  
Db 1 PFP 3

RESULT 33  
US-10-138-375-84  
; Sequence 84, Application US/10138375  
; Publication No. US20030208037A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/10/138,375  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-07-21  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-138-375-84

Query Match 37.5%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

---

Db |||  
3 FPI 5

RESULT 34  
US-10-168-758-19  
; Sequence 19, Application US/10168758  
; Publication No. US20030207812A1  
; GENERAL INFORMATION:  
; APPLICANT: Chapdelaine, Marc J  
; APPLICANT: Katherline, Knappenberger  
; APPLICANT: Steelman, Gary  
; APPLICANT: Suchard, Suzanne  
; APPLICANT: Sygowski, Linda  
; TITLE OF INVENTION: CD45  
; FILE REFERENCE: Z70624-1P US  
; CURRENT APPLICATION NUMBER: US/10/168,758  
; CURRENT FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-168-758-19

Query Match 37.5%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
Db 1 RGP 3

RESULT 35  
US-10-168-758-28  
; Sequence 28, Application US/10168758  
; Publication No. US20030207812A1  
; GENERAL INFORMATION:  
; APPLICANT: Chapdelaine, Marc J  
; APPLICANT: Katherline, Knappenberger  
; APPLICANT: Steelman, Gary  
; APPLICANT: Suchard, Suzanne  
; APPLICANT: Sygowski, Linda  
; TITLE OF INVENTION: CD45  
; FILE REFERENCE: Z70624-1P US  
; CURRENT APPLICATION NUMBER: US/10/168,758  
; CURRENT FILING DATE: 2000-12-18  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-168-758-28

Query Match 37.5%; Score 3; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
Db 1 RGP 3

RESULT 36  
US-10-200-923-10  
; Sequence 10, Application US/10200923

Publication No. US20030104976A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVAR, GUDARZ  
; APPLICANT: STRICHARTZ, GARY  
; APPLICANT: FAREED, MOIN  
; APPLICANT: KHODOROVA, ALIA  
; TITLE OF INVENTION: ANALGESIC METHODS USING ENDOTHELIN  
; FILE OF INVENTION: RECEPTOR LIGANDS  
; CURRENT APPLICATION NUMBER: US/010002  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: US 60/307,228  
; PRIOR FILING DATE: 2001-07-23  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-200-923-10

Query Match 37.5%; Score 3; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 P1L 7  
|||  
Db 2 P1L 4

RESULT 37  
US-08-996-140-8  
; Sequence 8, Application US/08996140  
; Publication No. US20030190318A1  
; GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: USHIO, Shimpei  
; APPLICANT: KUNIKATA, Toshio  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,140  
; FILING DATE: 22-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 356,426/1996  
; FILING DATE: 26-DEC-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 52,526/1997  
; FILING DATE: 21-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 163,490/1997  
; FILING DATE: 6-JUN-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 215,490/1997  
; FILING DATE: 28-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: TORIGOE-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
US-08-996-140-8

Query Match 37.5%; Score 3; DB 7; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
|||  
Db 3 ILV 5

RESULT 38  
US-09-729-873-19  
; Sequence 19, Application US/09729873  
; Patent No. US20010036921A1  
; GENERAL INFORMATION:  
; APPLICANT: Samy Ashkar  
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents  
; TITLE OF INVENTION: and Uses Therefor  
; FILE REFERENCE: CMZ-123CP  
; CURRENT APPLICATION NUMBER: US/09/729,873  
; CURRENT FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: 60/129,764  
; PRIOR FILING DATE: 1999-04-15  
; PRIOR APPLICATION NUMBER: PCT/US00/10344  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-729-873-19

Query Match 37.5%; Score 3; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
|||  
Db 1 ILV 3

RESULT 39  
US-09-767-395-28  
; Sequence 28, Application US/09767395  
; Patent No. US20020004215A1  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, Jane K  
; Derbyshire, Elaine J  
; McCafferty, John G  
; Vaughan, Tristan J  
; Johnson, Kevin S  
; TITLE OF INVENTION: Labelling and selection of molecules  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears tower, 233 South Wacker Drive  
; CITY: Chicago

/ STATE: Illinois  
/ COUNTRY: USA  
/ ZIP: 60606-6402  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/09/767,395  
/ FILING DATE: 23-Jan-2001  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 09/098,244  
/ FILING DATE: <Unknown>  
/ APPLICATION NUMBER: PCT/GB97/01835  
/ FILING DATE: 08-JUL-1997  
/ APPLICATION NUMBER: GB 9614292.2  
/ FILING DATE: 08-JUL-1996  
/ APPLICATION NUMBER: GB 9624880.2  
/ FILING DATE: 29-NOV-1996  
/ APPLICATION NUMBER: GB 9712818.5  
/ FILING DATE: 18-JUN-1997  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: David W. Clough  
/ REGISTRATION NUMBER: 36,107  
/ REFERENCE/DOCKET NUMBER: 28111/34800  
/ INFORMATION FOR SEQ ID NO: 28:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 6 amino acids  
/ TYPE: amino acid  
/ TOPOLOGY: linear  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
US-09-767-395-28

Query Match 37.5%; Score 3; DB 9; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PII 7  
///  
Db 2 PII 4

RESULT 40  
US-09-947-387-81  
/ Sequence 81, Application US/09947387  
/ Patent No. US20020150885A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Weber, Eckard  
/ APPLICANT: Cai, Sui Xiong  
/ APPLICANT: Keana, John F.W.  
/ APPLICANT: Drewe, John A.  
/ APPLICANT: Zhang, Han-Zhong  
/ TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molec  
/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
/ TITLE OF INVENTION: Use Thereof  
/ FILE REFERENCE: 1735.0290005  
/ CURRENT APPLICATION NUMBER: US/09/947,387  
/ CURRENT FILING DATE: 2001-09-07  
/ PRIOR APPLICATION NUMBER: US 60/061,582  
/ PRIOR FILING DATE: 1997-10-10  
/ PRIOR APPLICATION NUMBER: US 60/145,746  
/ PRIOR FILING DATE: 1998-03-03  
/ PRIOR APPLICATION NUMBER: US 09/168,888  
/ PRIOR FILING DATE: 1998-10-09  
/ NUMBER OF SEQ ID NOS: 142  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 81  
/ LENGTH: 6  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence

/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
/ OTHER INFORMATION: Peptide  
US-09-947-387-81

Query Match 37.5%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
///  
Db 4 FPI 6

RESULT 41  
US-09-947-387-83  
/ Sequence 83, Application US/09947387  
/ Patent No. US20020150885A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Weber, Eckard  
/ APPLICANT: Cai, Sui Xiong  
/ APPLICANT: Keana, John F.W.  
/ APPLICANT: Drewe, John A.  
/ APPLICANT: Zhang, Han-Zhong  
/ TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molec  
/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
/ TITLE OF INVENTION: Use Thereof  
/ FILE REFERENCE: 1735.0290005  
/ CURRENT APPLICATION NUMBER: US/09/947,387  
/ CURRENT FILING DATE: 2001-09-07  
/ PRIOR APPLICATION NUMBER: US 60/061,582  
/ PRIOR FILING DATE: 1997-10-10  
/ PRIOR APPLICATION NUMBER: US 60/145,746  
/ PRIOR FILING DATE: 1998-03-03  
/ PRIOR APPLICATION NUMBER: US 09/168,888  
/ PRIOR FILING DATE: 1998-10-09  
/ NUMBER OF SEQ ID NOS: 142  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 83  
/ LENGTH: 6  
/ TYPE: PRT  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
/ OTHER INFORMATION: Peptide  
US-09-947-387-83

Query Match 37.5%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
///  
Db 3 FPI 5

RESULT 42  
US-09-947-387-123  
/ Sequence 123, Application US/09947387  
/ Patent No. US20020150885A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Weber, Eckard  
/ APPLICANT: Cai, Sui Xiong  
/ APPLICANT: Keana, John F.W.  
/ APPLICANT: Drewe, John A.  
/ APPLICANT: Zhang, Han-Zhong  
/ TITLE OF INVENTION: No. US20020150885A1 Fluorogenic or Fluorescent Reporter Molec  
/ TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
/ TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
/ TITLE OF INVENTION: Use Thereof  
/ FILE REFERENCE: 1735.0290005  
/ CURRENT APPLICATION NUMBER: US/09/947,387

; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 123  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-947-387-123

Query Match 37.5%; Score 3; DB 10; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6  
|||  
Db 4 FPI 6

RESULT 43  
US-09-974-879-411  
; Sequence 411, Application US/09974879  
; Publication No. US20030028003A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: PZ020P2  
; CURRENT APPLICATION NUMBER: US/09/974,879  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: US 60/239,893  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: US 09/818,683  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 09/305,736  
; PRIOR FILING DATE: 1999-05-05  
; PRIOR APPLICATION NUMBER: PCT/US98/23435  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: US 60/064,911  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,912  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,983  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,900  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,988  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,987  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,908  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,984  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/064,985  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: US 60/066,094  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,100  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,089  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,095  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: US 60/066,090  
; PRIOR FILING DATE: 1997-11-17

; NUMBER OF SEQ ID NOS: 611  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 411  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-974-879-411

Query Match 37.5%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PII 7  
|||  
Db 4 PII 6

RESULT 44  
US-09-997-961-39  
; Sequence 39, Application US/09997961  
; Publication No. US2003006013A1  
; GENERAL INFORMATION:  
; APPLICANT: DEDHAR, Shoukat  
; TITLE OF INVENTION: NOVEL USE OF CALRETICULIN IN MODULATING  
; HORMONE RESPONSIVENESS AND NEW PHARMACEUTICALS FOR  
; TREATING CANCER, OSTEOPOROSIS AND CHRONIC INFLAMMATORY  
; DISEASE  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/997,961  
; FILING DATE: 29-Jan-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/169,935  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: US/08/377,432  
; FILING DATE: 24-JAN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mooi, Leslie A  
; REGISTRATION NUMBER: 37,047  
; REFERENCE/DOCKET NUMBER: 007315-005  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-09-997-961-39

Query Match 37.5%; Score 3; DB 11; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPF 4  
|||  
Db 2 GPF 4

## RESULT 45

US-09-305-736-411  
 ; Sequence 411, Application US/09305736  
 ; Publication No. US20030088078A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Feng et al.  
 ; TITLE OF INVENTION: 125 Human Secreted Proteins  
 ; FILE REFERENCE: P2020P1  
 ; CURRENT APPLICATION NUMBER: US/09/305,736  
 ; EARLIER FILING DATE: 1999-05-05  
 ; EARLIER APPLICATION NUMBER: PCT/US98/23435  
 ; EARLIER FILING DATE: 1998-11-04  
 ; EARLIER APPLICATION NUMBER: 60/064,911  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,912  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,983  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,900  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,988  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,987  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,908  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,984  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/064,985  
 ; EARLIER FILING DATE: 1997-11-07  
 ; EARLIER APPLICATION NUMBER: 60/066,094  
 ; EARLIER FILING DATE: 1997-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,100  
 ; EARLIER FILING DATE: 1997-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,089  
 ; EARLIER FILING DATE: 1997-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,095  
 ; EARLIER FILING DATE: 1997-11-17  
 ; EARLIER APPLICATION NUMBER: 60/066,090  
 ; EARLIER FILING DATE: 1997-11-17  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 411  
 ; LENGTH: 6  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-305-736-411

Query Match 37.5%; Score 3; DB 11; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
 Db 4 PIL 6

## RESULT 46

US-10-349-023-17  
 ; Sequence 17, Application US/10349023  
 ; Publication No. US20030133919A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TORIGOE, Kakuji  
 ; OKURA, Takanori  
 ; KURIMOTO, Mutsashi  
 ; TITLE OF INVENTION: POLYPEPTIDES  
 ; NUMBER OF SEQUENCES: 37  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington

STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/349,023  
 FILING DATE: 23-Jan-2003  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/556,972  
 FILING DATE: 24-Apr-2000  
 APPLICATION NUMBER: US/08/996,338  
 FILING DATE: 22-DEC-1997  
 APPLICATION NUMBER: JP 74,697/1997  
 FILING DATE: 12-MAR-1997  
 APPLICATION NUMBER: JP 215,488/1997  
 FILING DATE: 28-JUL-1997  
 APPLICATION NUMBER: JP 291,837/1997  
 FILING DATE: 09-OCT-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BROWDY, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: TORIGOE-3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-628-5197  
 TELEFAX: 202-737-3528  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
 US-10-349-023-17

Query Match 37.5%; Score 3; DB 12; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 6e+05; Indels 0; Gaps 0;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8  
 Db 3 ILV 5

## RESULT 47

US-09-933-767-682  
 ; Sequence 682, Application US/09933767  
 ; Publication No. US20030181692A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ni et al.  
 ; TITLE OF INVENTION: 207 Human Secreted Proteins  
 ; FILE REFERENCE: P2007P2  
 ; CURRENT APPLICATION NUMBER: US/09/933,767  
 ; CURRENT FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: PCT/US01/05614  
 ; PRIOR FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: 60/184,836  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: 60/193,170  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: 09/205,258  
 ; PRIOR FILING DATE: 1998-12-04  
 ; PRIOR APPLICATION NUMBER: PCT/US98/11422  
 ; PRIOR FILING DATE: 1998-06-04  
 ; PRIOR APPLICATION NUMBER: 60/048,885  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/049,375  
 ; PRIOR FILING DATE: 1997-06-06  
 ; PRIOR APPLICATION NUMBER: 60/048,881

; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,880  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,896  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,020  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,876  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,895  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,884  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,894  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,971  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,882  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,899  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,893  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,900  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,901  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,892  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,915  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,019  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,970  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,972  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,916  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,373  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,875  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/049,374  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,917  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,949  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,883  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,897  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,898  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,962  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,963  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,877  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/048,878  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18

; PRIOR APPLICATION NUMBER: 60/070,923  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/073,160  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,159  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,165  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/073,164  
; PRIOR FILING DATE: 1998-01-30  
; PRIOR APPLICATION NUMBER: 60/085,925  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,921  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,923  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/085,922  
; PRIOR FILING DATE: 1998-05-18  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; NUMBER OF SEQ ID NOS: 1245  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 682  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-933-767-682

Query Match 37.5%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7  
Db 1 PIL 3

## RESULT 48

US-10-138-375-81  
; Sequence 81, Application US/10138375  
; Publication No. US20030208037A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. US20030208037A1 Fluorescence Dyes and Their Applications  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/10138,375  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 81  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-10-138-375-81

Query Match 37.5%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6  
Db 4 FPI 6

RESULT 49  
US-10-138-375-83  
; Sequence 83, Application US/10138375  
; Publication No. US20030208037A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/10/138,375  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-10-138-375-83

Query Match 37.5%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6  
Db 3 FPI 5

RESULT 50  
US-10-138-375-123  
; Sequence 123, Application US/10138375  
; Publication No. US20030208037A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/10/138,375  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642  
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 123  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
US-10-138-375-123

Query Match 37.5%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6  
Db 4 FPI 6

RESULT 51  
US-09-818-683-411  
; Sequence 411, Application US/09818693  
; Publication No. US20030211472A1  
; GENERAL INFORMATION:  
; APPLICANT: Feng et al.  
; TITLE OF INVENTION: 125 Human Secreted Proteins  
; FILE REFERENCE: P2020P1  
; CURRENT APPLICATION NUMBER: US/09/818,683  
; CURRENT FILING DATE: 2001-03-28  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 612  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 411  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-818-683-411

Query Match 37.5%; Score 3; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7  
Db 4 PIL 6

RESULT 52  
US-10-023-282-682  
; Sequence 682, Application US/10023282  
; Publication No. US20030092893A1  
; GENERAL INFORMATION:  
; APPLICANT: Young et al.  
; TITLE OF INVENTION: 207 Human Secreted Proteins  
; FILE REFERENCE: P2007P1  
; CURRENT APPLICATION NUMBER: US/10/023,282  
; CURRENT FILING DATE: 2001-12-20  
; EARLIER APPLICATION NUMBER: 09/205,258  
; EARLIER FILING DATE: 1998-12-04  
; EARLIER APPLICATION NUMBER: PCT/US98/11422  
; EARLIER FILING DATE: 1998-06-04  
; EARLIER APPLICATION NUMBER: 60/048,885  
; EARLIER FILING DATE: 1997-06-05  
; EARLIER APPLICATION NUMBER: 60/049,375  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,881  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,880  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,896  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/049,020  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,876  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,895  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,884  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,894  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/048,971



EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,882  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,899  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,893  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,900  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,901  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,892  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,915  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,019  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,970  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,972  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,916  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,373  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,875  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/049,374  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,917  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,949  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,974  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,883  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,962  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,963  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,877  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/048,878  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/070,923  
EARLIER FILING DATE: 1997-12-18  
EARLIER APPLICATION NUMBER: 60/092,921  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/094,657  
NUMBER OF SEQ ID NOS: 1227  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 682  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-023-282-682

Query Match 37.5%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
5 PIL 7  
1 PIL 3

RESULT 53  
US-10-211-088-242  
Sequence 242, Application US/10211088  
Publication No. US20030104479A1  
GENERAL INFORMATION:  
APPLICANT: Bright, Gary R.  
APPLICANT: Premkumar, D. David  
APPLICANT: Chen, Yih-Tai  
TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular  
FILE REFERENCE: 01-1022-US  
CURRENT APPLICATION NUMBER: US/10/211,088  
CURRENT FILING DATE: 2002-10-15  
PRIOR APPLICATION NUMBER: 60/309,395  
PRIOR FILING DATE: 2001-08-01  
PRIOR APPLICATION NUMBER: 60/341,589  
PRIOR FILING DATE: 2001-12-13  
NUMBER OF SEQ ID NOS: 366  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 242  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-242  
Query Match 37.5%; Score 3; DB 15; Length 6;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RGP 3  
Db 3 RGP 5  
RESULT 54  
US-09-734-002-9  
Sequence 9, Application US/09734002  
Patent No. US20010016333A1  
GENERAL INFORMATION:  
APPLICANT: Mochiharu SEIKI et al.  
TITLE OF INVENTION: NOVEL PROTEIN AND MONOCLONAL ANTIBODY SPECIFIC THERETO  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,002  
FILING DATE: 12-Dec-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/01956  
FILING DATE: July 12, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
REFERENCE/DOCKET NUMBER: <Unknown>  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:

```
; LENGTH: 7
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-734-002-9

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 5 ILV 7

RESULT 55
US-09-729-873-17
; Sequence 17, Application US/09729873
; Patent No. US20010036921A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Osteopontin-Derived Chemotactic and Inhibitory Agents
; FILE REFERENCE: CMZ-123CP
; CURRENT APPLICATION NUMBER: US/09/729,873
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/129,764
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PCT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-729-873-17

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 1 ILV 3

RESULT 56
US-09-731-242A-22
; Sequence 22, Application US/09731242A
; Patent No. US20020058253A1
; GENERAL INFORMATION:
; APPLICANT: KRANZ, DAVID
; APPLICANT: WITTRUP, K. DANE
; APPLICANT: HOLLER, PHILLIP
; TITLE OF INVENTION: HIGH AFFINITY TCR PROTEINS AND METHODS
; FILE REFERENCE: 89-99
; CURRENT APPLICATION NUMBER: US/09/731,242A
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,179
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/009,388
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 7
; TYPE: PRT

; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().()
; OTHER INFORMATION: CDR3alpha sequence
US-09-731-242A-22

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
Db 5 PIL 7

RESULT 57
US-09-989-789-700
; Sequence 700, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-700

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 58
US-09-989-789-701
; Sequence 701, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-789-701

Query Match          37.5%; Score 3; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3
```

Db 1 RGP 3

## RESULT 59

US-09-989-789-702  
; Sequence 702, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 702  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP  
US-09-989-789-702

Query Match 37.5%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3

Db 1 RGP 3

## RESULT 60

US-09-832-723-4  
; Sequence 4, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; APPLICANT: Chen, Yiyou  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: Peptide library  
US-09-832-723-4

Query Match 37.5%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7

Db 4 PIL 6

## RESULT 61

US-09-832-723-14  
; Sequence 14, Application US/09832723  
; Patent No. US20020098524A1  
; GENERAL INFORMATION:

; APPLICANT: Estell, David A.  
; APPLICANT: Chen, Yiyou  
; APPLICANT: Murray, Christopher J.  
; APPLICANT: Tijerina, Pilar  
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING  
; FILE REFERENCE: GC617-2  
; CURRENT APPLICATION NUMBER: US/09/832,723  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: Peptide library  
US-09-832-723-14

Query Match 37.5%; Score 3; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7

Db 2 PIL 4

## RESULT 62

US-09-947-387-34  
; Sequence 34, Application US/09947387  
; Patent No. US20020150885A1  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. US20020150885A1e1 Fluorogenic or Fluorescent Reporter Mole  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-947-387-34

Query Match 37.5%; Score 3; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6

Db 4 FPI 6

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RESULT 63
US-09-947-387-80
; Sequence 80, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-80

Query Match          37.5%; Score 3; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 FPI 6
Db      4 FPI 6

RESULT 64
US-09-931-325A-128
; Sequence 128, Application US/09931325A
; Publication No. US20030054337A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: MALARIA IMMUNOGEN AND VACCINE
; FILE REFERENCE: 4564/83503 ICC-103.1
; CURRENT APPLICATION NUMBER: US/09/931,325A
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: USSN NOT YET ASSIGNED
; PRIOR FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 128
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-325A-128

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
Db      2 RGP 4

RESULT 65
US-09-990-186-700
; Sequence 700, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-700

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
Db      1 RGP 3

RESULT 66
US-09-990-186-701
; Sequence 701, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-701

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
Db      1 RGP 3

RESULT 67
US-09-990-186-702
; Sequence 702, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 702
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-990-186-702

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
   |||
Db 1 RGP 3

RESULT 68
US-09-940-727B-41
; Sequence 41, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCR/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-41

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
   |||
Db 5 RGP 7

RESULT 69
US-09-865-548A-62
; Sequence 62, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-62

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
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Db 4 PFP 6

RESULT 70
US-09-989-994-700
; Sequence 700, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 700
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-700

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
   |||
Db 1 RGP 3

RESULT 71
US-09-989-994-701
; Sequence 701, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 701
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZFP
US-09-989-994-701

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
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Db 1 RGP 3
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RESULT 72
US-09-989-994-702
; Sequence 702, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 702
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example ZPP
US-09-989-994-702

Query Match          37.5%; Score 3; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
        |||
Db      1 RGP 3

RESULT 73
US-09-930-915A-169
; Sequence 169, Application US/09930915A
; Publication No. US20030138769A1
; GENERAL INFORMATION:
; APPLICANT: Birkett, Ashley J.
; TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES HAVING ENHANCED
; FILE REFERENCE: 4564/83501 ICC-102.2 PCT
; CURRENT APPLICATION NUMBER: US/09/930,915A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: 60/226,867
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,843
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 169
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-930-915A-169

Query Match          37.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RGP 3
        |||
Db      2 RGP 4

RESULT 74
US-10-146-999-16
; Sequence 16, Application US/10146999
; Publication No. US20030148942A1
; GENERAL INFORMATION:
; APPLICANT: Plotnikoff, Nicholas P.
; TITLE OF INVENTION: Methods for Inducing Sustained Immune Response
; FILE REFERENCE: 01-635-A
; CURRENT APPLICATION NUMBER: US/10/146,999
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US 60/291,237

RESULT 75
US-10-303-331-4
; Sequence 4, Application US/10303331
; Publication No. US20030152976A1
; GENERAL INFORMATION:
; APPLICANT: Janssen, Giselle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Winetzky, Deborah S.
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-3
; CURRENT APPLICATION NUMBER: US/10/303,331
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 09/832,723
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 60/197,259
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptides screened from a phage display random
; OTHER INFORMATION: peptide library
US-10-303-331-4

Query Match          37.5%; Score 3; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 PIL 7
        |||
Db      4 PIL 6

Search completed: November 25, 2003, 20:37:06
Job time : 13.9372 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 6.46512 Seconds  
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52.356 Million cell updates/sec

Title: US-09-641-801-29

Perfect score: 8

Sequence: 1 RGPFPILV 8

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 151837

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8	100.0	8	4	US-09-641-803-29
2	6	75.0	6	2	US-08-747-137-29
3	4	50.0	5	3	US-08-676-242-9
4	4	50.0	6	2	US-08-656-177A-16
5	4	50.0	6	3	US-09-286-797-16
6	4	50.0	7	3	US-09-365-861A-2
7	4	50.0	7	4	US-09-626-821A-2
8	4	50.0	9	6	US-09-626-821A-2
9	4	50.0	9	6	US-09-626-821A-2
10	4	50.0	10	2	US-08-764-640-30
11	4	50.0	10	3	US-08-973-225-30
12	4	50.0	10	3	US-09-244-298A-30
13	4	50.0	10	3	US-09-516-704-30
14	4	50.0	10	4	US-09-549-090-30
15	4	50.0	10	4	US-08-832-230A-30
16	4	50.0	11	3	US-08-451-946B-2
17	4	50.0	11	3	US-08-446-938B-2
18	4	50.0	11	3	US-08-311-703A-2
19	4	50.0	11	3	US-08-446-939B-2
20	4	50.0	11	3	US-09-183-543-2
21	4	50.0	11	3	US-08-446-936A-2
22	4	50.0	11	3	US-09-177-249-138
23	4	50.0	11	5	PCT-US92-09326-6
24	4	50.0	12	3	US-09-365-861A-5
25	4	50.0	12	4	US-09-147-208-58
26	4	50.0	12	4	US-09-550-117A-58
27	4	50.0	12	4	US-09-626-821A-5

28	4	50.0	13	2	US-08-752-852A-191	Sequence 191, App
29	4	50.0	13	4	US-09-431-705-30	Sequence 30, Appl
30	4	50.0	15	3	US-08-602-999A-324	Sequence 324, App
31	4	50.0	15	4	US-09-500-124-324	Sequence 324, App
32	4	50.0	19	4	US-09-441-502B-65	Sequence 65, Appl
33	4	50.0	19	4	US-09-441-502B-66	Sequence 66, Appl
34	4	50.0	19	4	US-09-441-502B-71	Sequence 71, Appl
35	4	50.0	20	3	US-08-861-338-8	Sequence 8, Appl
36	3	37.5	4	1	US-08-149-839B-20	Sequence 20, Appl
37	3	37.5	4	1	US-08-377-687-16	Sequence 16, Appl
38	3	37.5	4	1	US-07-734-434A-30	Sequence 30, Appl
39	3	37.5	4	1	US-07-734-434A-33	Sequence 33, Appl
40	3	37.5	4	1	US-08-206-789-1	Sequence 1, Appl
41	3	37.5	4	1	US-08-206-789-3	Sequence 3, Appl
42	3	37.5	4	1	US-08-451-568-20	Sequence 20, Appl
43	3	37.5	4	1	US-08-494-763-4	Sequence 4, Appl
44	3	37.5	4	1	US-08-294-434-4	Sequence 4, Appl
45	3	37.5	4	1	US-08-457-166-4	Sequence 4, Appl
46	3	37.5	4	1	US-08-358-160-175	Sequence 175, App
47	3	37.5	4	1	US-08-451-566-20	Sequence 20, Appl
48	3	37.5	4	1	US-08-224-868-4	Sequence 22, Appl
49	3	37.5	4	1	US-08-224-868-4	Sequence 4, Appl
50	3	37.5	4	2	US-08-777-192-16	Sequence 16, Appl
51	3	37.5	4	2	US-08-249-830-3	Sequence 3, Appl
52	3	37.5	4	2	US-08-777-113-20	Sequence 20, Appl
53	3	37.5	4	3	US-09-198-209-3	Sequence 3, Appl
54	3	37.5	4	3	US-08-927-128-10	Sequence 10, Appl
55	3	37.5	4	3	US-09-219-849-16	Sequence 16, Appl
56	3	37.5	4	3	US-08-971-982-16	Sequence 16, Appl
57	3	37.5	4	3	US-09-411-531A-1	Sequence 1, Appl
58	3	37.5	4	3	US-07-901-713A-23	Sequence 23, Appl
59	3	37.5	4	4	US-09-411-605A-1	Sequence 1, Appl
60	3	37.5	4	4	US-09-298-574-20	Sequence 20, Appl
61	3	37.5	4	5	PCT-US93-06591-4	Sequence 4, Appl
62	3	37.5	4	6	5215966-12	Patent No. 5215966
63	3	37.5	5	1	US-08-238-089-34	Sequence 34, Appl
64	3	37.5	5	1	US-08-238-089-44	Sequence 44, Appl
65	3	37.5	5	1	US-08-494-763-2	Sequence 2, Appl
66	3	37.5	5	1	US-08-494-763-5	Sequence 5, Appl
67	3	37.5	5	1	US-08-432-651A-34	Sequence 34, Appl
68	3	37.5	5	1	US-08-432-651A-44	Sequence 44, Appl
69	3	37.5	5	2	US-08-347-335A-4	Sequence 4, Appl
70	3	37.5	5	2	US-08-840-847C-33	Sequence 33, Appl
71	3	37.5	5	3	US-08-962-962C-34	Sequence 34, Appl
72	3	37.5	5	3	US-08-962-962C-44	Sequence 44, Appl
73	3	37.5	5	3	US-09-357-952-84	Sequence 84, Appl
74	3	37.5	5	4	US-09-521-650-84	Sequence 84, Appl
75	3	37.5	5	4	US-09-168-888-84	Sequence 84, Appl
76	3	37.5	5	4	US-09-295-996B-47	Sequence 47, Appl
77	3	37.5	5	4	US-09-209-676-41	Sequence 41, Appl
78	3	37.5	5	4	US-09-295-846B-50	Sequence 50, Appl
79	3	37.5	5	4	US-09-551-737C-50	Sequence 50, Appl
80	3	37.5	5	5	PCT-US95-05560-34	Sequence 34, Appl
81	3	37.5	5	5	PCT-US95-05560-44	Sequence 44, Appl
82	3	37.5	6	1	US-07-943-709-63	Sequence 63, Appl
83	3	37.5	6	1	US-08-179-481-24	Sequence 24, Appl
84	3	37.5	6	1	US-08-584-579-1	Sequence 1, Appl
85	3	37.5	6	1	US-08-456-424-141	Sequence 141, App
86	3	37.5	6	2	US-08-672-805-2	Sequence 2, Appl
87	3	37.5	6	2	US-08-672-805-4	Sequence 4, Appl
88	3	37.5	6	2	US-08-672-805-6	Sequence 6, Appl
89	3	37.5	6	2	US-08-377-432-39	Sequence 39, Appl
90	3	37.5	6	2	US-08-540-118-5	Sequence 5, Appl
91	3	37.5	6	2	US-08-889-291-28	Sequence 28, Appl
92	3	37.5	6	2	US-08-947-965-10	Sequence 10, Appl
93	3	37.5	6	3	US-08-860-248C-118	Sequence 118, App
94	3	37.5	6	3	US-08-996-338-17	Sequence 17, Appl
95	3	37.5	6	3	US-08-817-177-11	Sequence 11, Appl
96	3	37.5	6	3	US-09-098-244-28	Sequence 28, Appl
97	3	37.5	6	3	US-09-357-952-81	Sequence 81, Appl
98	3	37.5	6	3	US-09-357-952-83	Sequence 83, Appl
99	3	37.5	6	3	US-09-357-952-123	Sequence 123, App
100	3	37.5	6	4	US-09-521-650-81	Sequence 81, Appl

## ALIGNMENTS

RESULT 1  
US-09-641-803-29  
; Sequence 29, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265 00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-803-29

Query Match 100.0%; Score 8; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGPFPILV 8  
Db 1 RGPFPILV 8

RESULT 2  
US-08-747-137-29  
; Sequence 29, Application US/08747137  
; Patent No. 5945033  
; GENERAL INFORMATION:  
; APPLICANT: YEN, Richard C.K.  
; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE  
; NUMBER OF SEQUENCES: 184  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/747,137  
; FILING DATE: 12-NOV-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,546  
; FILING DATE: 14-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/069,831  
; FILING DATE: 01-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/959,560

; FILING DATE: 13-OCT-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/641,720  
; FILING DATE: 15-JAN-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Apple, Randolph T.  
; REGISTRATION NUMBER: 36,429  
; REFERENCE/DOCKET NUMBER: 016197-000840US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; INFORMATION FOR SEQ ID NO: 29:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
US-08-747-137-29

Query Match 75.0%; Score 6; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPFPPI 6  
Db 1 RGPFPPI 6

RESULT 3  
US-08-676-242-9  
; Sequence 9, Application US/08676242C  
; Patent No. 6143719  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of the University of Michigan  
; APPLICANT: Schmaier, Alvin H.  
; APPLICANT: Haeen, Ahmed A.K.  
; TITLE OF INVENTION: Bradykinin Analogs As Selective Thrombin Inhibitors  
; FILE REFERENCE: 8820-2 US  
; CURRENT APPLICATION NUMBER: US/08/676,242C  
; CURRENT FILING DATE: 2000-07-16  
; EARLIER APPLICATION NUMBER: 60/000,096  
; EARLIER FILING DATE: 1995-06-09  
; EARLIER APPLICATION NUMBER: PCT/US96/09940  
; EARLIER FILING DATE: 1996-06-07  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Scrambled  
; OTHER INFORMATION: peptide  
US-08-676-242-9

Query Match 50.0%; Score 4; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5  
Db 1 GPFP 4

RESULT 4  
US-08-656-177A-16  
; Sequence 16, Application US/08656177A  
; Patent No. 5882851  
; GENERAL INFORMATION:  
; APPLICANT: Koch, Birgit M.  
; APPLICANT: Sibbesen, Ole  
; APPLICANT: Halkier, Barbara Ann  
; APPLICANT: Moller, Birger L.  
; TITLE OF INVENTION: Cytochrome P-450 Monooxygenases



; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5882851artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/656,177A  
; APPLICATION NUMBER: US/08/656,177A  
; FILING DATE: 08-AUG-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19783/A/PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-08-656-177A-16

Query Match 50.0%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6  
Db 3 PFPI 6

RESULT 5  
US-09-256-797-16  
; Sequence 16, Application US/09256797  
; Patent No. 6133417  
; GENERAL INFORMATION:  
; APPLICANT: Koch, Birgit M.  
; APPLICANT: Sibbesen, Ole  
; APPLICANT: Halkier, Barbara Ann  
; APPLICANT: Moller, Birger L.  
; TITLE OF INVENTION: Cytochrome P-450 Monooxygenases  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6133417artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/256,797  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/656,177  
; FILING DATE: 08-AUG-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-19783/A/PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; US-09-256-797-16

Query Match 50.0%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6  
Db 3 PFPI 6

RESULT 6  
US-09-365-581A-2  
; Sequence 2, Application US/09365581A  
; Patent No. 6287776  
; GENERAL INFORMATION:  
; APPLICANT: Hart, L P  
; APPLICANT: Pestka, James J  
; APPLICANT: Yuan, Qiaoping  
; TITLE OF INVENTION: PEPTIDE MINOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
; FILE REFERENCE: MSU 4.1-447  
; CURRENT APPLICATION NUMBER: US/09/365,581A  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,643  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DONPBP.2  
; OTHER INFORMATION: peptide mimotope of deoxynivalenol  
; US-09-365-581A-2

Query Match 50.0%; Score 4; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPFP 5  
Db 3 GPFP 6

RESULT 7  
US-09-626-821A-2  
; Sequence 2, Application US/09626821A  
; Patent No. 6537762  
; GENERAL INFORMATION:  
; APPLICANT: Hart, L P  
; APPLICANT: Pestka, James J  
; APPLICANT: Yuan, Qiaoping

; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES

; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: MSU 4.1-447  
; CURRENT APPLICATION NUMBER: US/09/626,821A  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,643  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DONPEP.2  
; OTHER INFORMATION: peptide mimotope of deoxynivalenol  
US-09-626-821A-2

Query Match 50.0%; Score 4; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPP 5  
Db 3 GPP 6

## RESULT 8

5310667-13  
; Patent No. 5310667  
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,  
; GANESH M.  
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL  
; -3-PHOSPHOSHIKIMATE SYNTHASES  
; NUMBER OF SEQUENCES: 37  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/380,963  
; FILING DATE: 17-JUL-1989  
; SEQ ID NO:13:  
; LENGTH: 9  
5310667-13

Query Match 50.0%; Score 4; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8  
Db 3 PILV 6

## RESULT 9

5310667-14  
; Patent No. 5310667  
; APPLICANT: EICHHOLTZ, DAVID A.; GASSER, CHARLES S.; KISHORE,  
; GANESH M.  
; TITLE OF INVENTION: GLYPHOSATE-TOLERANT 5-ENOLPYRUVYL  
; -3-PHOSPHOSHIKIMATE SYNTHASES  
; NUMBER OF SEQUENCES: 37  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/380,963  
; FILING DATE: 17-JUL-1989  
; SEQ ID NO:14:  
; LENGTH: 9  
5310667-14

Query Match 50.0%; Score 4; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PILV 8  
Db 3 PILV 6

## RESULT 10

US-08-764-640-30  
; Sequence 30; Application US/08764640  
; Patent No. 5869451  
; Patent No. 5869451 5837683  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirila, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Depince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,640  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-764-640-30

Query Match 50.0%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4  
Db 2 RGPF 5

## RESULT 11

US-08-973-225-30  
; Sequence 30; Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirila, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.

Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,225A  
FILING DATE: 04-Dec-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 30:  
US-08-973-225-30  
Query Match 50.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGPF 4  
Db 2 RGPF 5  
RESULT 12  
US-09-244-298A-30  
; Sequence 30, Application US/09244298A  
; Patent No. 6121238  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/244,298A  
FILING DATE: 11-Dec-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-244-298A-30  
Query Match 50.0%; Score 4; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGPF 4  
Db 2 RGPF 5  
RESULT 13  
US-09-516-704-30  
; Sequence 30, Application US/09516704  
; Patent No. 6251864  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Surekha  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/516,704  
FILING DATE: 01-Mar-2000  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000

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; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-516-704-30

Query Match          50.0%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 2 RGPF 5

RESULT 14
US-09-549-090-30
; Sequence 30, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
;   Barrett, Ronald W.
;   Cwiria, Steven E.
;   Duffin, David J.
;   Gates, Christian
;   Haselden, Sherril S.
;   Mattheakis, Larry C.
;   Schatz, Peter J.
;   Wagstrom, Christopher R.
;   Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;   THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-549-090-30

Query Match          50.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 2 RGPF 5

RESULT 15
US-09-832-230A-30
; Sequence 30, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;   RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-832-230A-30

Query Match          50.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 2 RGPF 5

RESULT 16
US-08-451-946B-2
; Sequence 2, Application US/08451946B
; Patent No. 6001969
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
;   NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
```

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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 2 RGPF 5

RESULT 15
US-09-832-230A-30
; Sequence 30, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
;   RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-832-230A-30

Query Match          50.0%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGPF 4
DB 2 RGPF 5

RESULT 16
US-08-451-946B-2
; Sequence 2, Application US/08451946B
; Patent No. 6001969
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
;   NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
```

```
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451.946B
; FILING DATE: 26-MAY-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI91-09V
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-451-946B-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6
Db 3 PFPI 6

RESULT 17
US-08-446-938B-2
; Sequence 2, Application US/08446938B
; Patent No. 6008011
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,938B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI91-09PFZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-446-938B-2

Query Match 50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFPI 6
Db 3 PFPI 6

RESULT 18
US-08-311-703A-2
; Sequence 2, Application US/08311703A
; Patent No. 6010872
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Fan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,703A
; FILING DATE: 23-SEP-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hogle, Doreen
; REGISTRATION NUMBER: 36,361
; REFERENCE/DOCKET NUMBER: WHI91-09F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-311-703A-2
```

```
Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY      3 PPPI 6
Db      3 PPPI 6

RESULT 19
US-08-446-939B-2
; Sequence 2, Application US/08446939B
; Patent No. 6046157
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Pan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,939B
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 23-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI91-09FX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
US-08-446-939B-2

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Gaps 0; Indels 0;

QY      3 PPPI 6
Db      3 PPPI 6

RESULT 20
US-09-183-543-2
; Sequence 2, Application US/09183543A
; Patent No. 6086867
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
```

```
; APPLICANT: Wang, Xiao-Pan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Modulation of TGF-Beta by TGF-Beta Type III Receptor Polypeptide
; FILE REFERENCE: WHI91-09FXA
; CURRENT APPLICATION NUMBER: US/09/183,543A
; CURRENT FILING DATE: 1998-10-30
; EARLIER APPLICATION NUMBER: US 08/446,939
; EARLIER FILING DATE: 1995-05-23
; EARLIER APPLICATION NUMBER: US 08/311,703
; EARLIER FILING DATE: 1994-09-23
; EARLIER APPLICATION NUMBER: US 07/786,063
; EARLIER FILING DATE: 1991-10-31
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide sequence
US-09-183-543-2

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 PPPI 6
Db      3 PPPI 6

RESULT 21
US-08-446-936A-2
; Sequence 2, Application US/08446936A
; Patent No. 6201108
; GENERAL INFORMATION:
; APPLICANT: Lin, Herbert Y.
; APPLICANT: Wang, Xiao-Pan
; APPLICANT: Weinberg, Robert A.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: TGF-Beta Type Receptor cDNAs Encoded
; TITLE OF INVENTION: Products and Uses Therefor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,936A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/311,703
; FILING DATE: 23-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI91-09FY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
```

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 11 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
US-08-446-936A-2

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 22
US-09-177-249-138
; Sequence 138, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; TITLE OF INVENTION: Development in Plants
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; CURRENT FILING DATE: 1998-10-22
; EARLIER APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 138
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-138

Query Match          50.0%; Score 4; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPIL 7
Db 5 FPIL 8

RESULT 23
PCT-US92-09326-6
; Sequence 6, Application PC/TUS9209326
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; TITLE OF INVENTION: TGF-BETA TYPE RECEPTOR cDNAs ENCODED
; TITLE OF INVENTION: PRODUCTS AND USES THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09326
; FILING DATE: 19921030
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/786,063
; FILING DATE: 31-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI91-09 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-09326-6

Query Match          50.0%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PPPI 6
Db 3 PPPI 6

RESULT 24
US-09-365-581A-5
; Sequence 5, Application US/09365581A
; Patent No. 6287776
; GENERAL INFORMATION:
; APPLICANT: Hart, L P
; APPLICANT: Pestka, James J
; APPLICANT: Yuan, Qiaoping
; TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: MSU 4.1-447
; CURRENT APPLICATION NUMBER: US/09/365,581A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,643
; PRIOR FILING DATE: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: C430, the
; OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a
; OTHER INFORMATION: cysteine residue
US-09-365-581A-5

Query Match          50.0%; Score 4; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPFP 5
Db 3 GPFP 6

RESULT 25
US-09-147-208-58
; Sequence 58, Application US/09147208
; Patent No. 6333303
; GENERAL INFORMATION:
```

APPLICANT:  
TITLE OF INVENTION: Antiviral Ricin-Like Proteins  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BERESKIN & PARR  
STREET: 40 King Street West  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: M5H 3Y2  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/147,208  
FILING DATE: 02-MAR-1999  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Rudolph, John R.  
REGISTRATION NUMBER: 38,003  
REFERENCE/DOCKET NUMBER: 7841-76  
TELEPHONE: (416) 364-7311  
TELEFAX: (416) 361-1398  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-147-208-58

Query Match 50.0%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7  
Db 6 FPIL 9

RESULT 26  
US-09-550-117A-58  
Sequence 58 Application US/09550117A  
Patent No. 6531125  
GENERAL INFORMATION:  
APPLICANT: Borgford, Thor  
TITLE OF INVENTION: Antiviral Ricin-Like Proteins  
FILE REFERENCE: 10447-10  
CURRENT APPLICATION NUMBER: US/09/550,117A  
CURRENT FILING DATE: 2000-04-14  
PRIOR FILING DATE: 1999-03-02  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 58  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: PAP-211/PAP-212  
US-09-550-117A-58

Query Match 50.0%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7  
Db 6 FPIL 9

RESULT 27  
US-09-626-821A-5  
Sequence 5, Application US/09626821A  
Patent No. 6537762  
GENERAL INFORMATION:  
APPLICANT: Hart, L P  
APPLICANT: Pestka, James J  
APPLICANT: Yuan, Qiaoping  
TITLE OF INVENTION: PEPTIDE MIMOTOPE TO MYCOTOXIN DEOXYNIVALENOL AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: MSU 4.1-447  
CURRENT APPLICATION NUMBER: US/09/626,821A  
CURRENT FILING DATE: 2000-07-27  
PRIOR APPLICATION NUMBER: 60/146,643  
PRIOR FILING DATE: 1999-07-30  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: C430, the  
OTHER INFORMATION: DONPEP.2 with a structurally flexible linker and a  
OTHER INFORMATION: cysteine residue  
US-09-626-821A-5

Query Match 50.0%; Score 4; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPPF 5  
Db 3 GPPF 6

RESULT 28  
US-08-752-852A-191  
Sequence 191, Application US/08752852A  
Patent No. 5994306  
GENERAL INFORMATION:  
APPLICANT: Chang, Conway  
APPLICANT: Gu, Chee-Liang  
APPLICANT: Chen, Jie  
APPLICANT: Steinberg, Deborah  
APPLICANT: Lehrner, Robert  
APPLICANT: Harwig, Sylvia  
TITLE OF INVENTION: FINE-TUNED PROTEGRINS  
NUMBER OF SEQUENCES: 242  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/752,852A  
FILING DATE: 21-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742



```

; REFERENCE/DOCKET NUMBER: 8067-034-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-191

Query Match 50.0%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 6 RGPF 9

RESULT 29
US-09-431-705-30
; Sequence 30, Application US/09431705
; Patent No. 6585975
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Londono-Arcila, Patricia
; APPLICANT: Freeman, Donna
; TITLE OF INVENTION: Use of salmonella vectors for
; FILE REFERENCE: 06132/060001
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-09-431-705-30

Query Match 50.0%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 8 RGPF 11

RESULT 30
US-08-602-999A-324
; Sequence 324, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

; REFERENCE/DOCKET NUMBER: 8067-034-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-752-852A-191

Query Match 50.0%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 6 RGPF 9

RESULT 29
US-09-431-705-30
; Sequence 30, Application US/09431705
; Patent No. 6585975
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Londono-Arcila, Patricia
; APPLICANT: Freeman, Donna
; TITLE OF INVENTION: Use of salmonella vectors for
; FILE REFERENCE: 06132/060001
; CURRENT FILING DATE: 1999-11-01
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-09-431-705-30

Query Match 50.0%; Score 4; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4
Db 8 RGPF 11

RESULT 30
US-08-602-999A-324
; Sequence 324, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York

```

```

; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,999A
; FILING DATE: 16-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 324:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-602-999A-324

Query Match 50.0%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPIL 7
Db 1 FPIL 4

RESULT 31
US-09-500-124-324
; Sequence 324, Application US/09500124
; Patent No. 6432920
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.
; APPLICANT: QUILLIAM, Lawrence A.
; APPLICANT: DER, Channing J.
; APPLICANT: FOWLKES, Dana M.
; APPLICANT: RIDER, James E.
; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
; NUMBER OF SEQUENCES: 467
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/500,124
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/602,999
; FILING DATE: 16-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

```

Query Match 50.0%; Score 4; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPF 4  
|||  
Db 7 RGPF 10

RESULT 36  
US-08-149-839B-20  
; Sequence 20, Application US/08149839B  
; Patent No. 5514779  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/149.839B  
; FILING DATE: 10-NOV-1993  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9112300.0  
; FILING DATE: 07-JUN-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00999  
; FILING DATE: 03-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9223708.0  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002842  
; FILING DATE: 14-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9303564.0  
; FILING DATE: 23-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/02179  
; FILING DATE: 22-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 3893/99204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-149-839B-20

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
|||  
Db 2 ILV 4

RESULT 37  
US-08-377-687-16  
; Sequence 16, Application US/08377687  
; Patent No. 5538525  
; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, SARAH B.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/377.687  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-377-687-16

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8  
|||  
Db 2 ILV 4

RESULT 38  
US-07-734-434A-30  
; Sequence 30, Application US/07734434A  
; Patent No. 5554728  
; GENERAL INFORMATION:  
; APPLICANT: Basava, Channa Y.  
; APPLICANT: Hosteler, Karl  
; TITLE OF INVENTION: LIPID CONJUGATES OF THERAPEUTIC  
; TITLE OF INVENTION: PEPTIDES AND PROTEASE INHIBITORS  
; NUMBER OF SEQUENCES: 35

/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: VICAL, INC.  
/ STREET: 9373 Towne Centre Drive  
/ CITY: San Diego,  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 92121  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/734,434A  
/ FILING DATE: 19910723  
/ CLASSIFICATION: 530  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kirkpatrick, Anita M.  
/ REGISTRATION NUMBER: 32,617  
/ REFERENCE/DOCKET NUMBER: VICAL.019A  
/ INFORMATION FOR SEQ ID NO: 30:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 4 amino acids  
/ TYPE: AMINO ACID  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ FRAGMENT TYPE: internal  
/ FEATURE:  
/ NAME/KEY: Misc. differences  
/ LOCATION: 1-2, 4  
/ OTHER INFORMATION: Phe-1 is joined to Phe-2 by an  
/ isosteric linkage having the structure -CHOH-CH2-N-; carboxy  
/ terminal Val-4 is an amide.  
/ US-07-734-434A-30

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
Db 1 FPI 3

RESULT 39  
US-07-734-434A-33  
/ Sequence 33, Application US/07734434A  
/ Patent No. 5554728  
/ GENERAL INFORMATION:  
/ APPLICANT: Basava, Channa  
/ APPLICANT: Hosteler, Karl V.  
/ TITLE OF INVENTION: LIPID CONJUGATES OF THERAPEUTIC  
/ TITLE OF INVENTION: PEPTIDES AND PROTEASE INHIBITORS  
/ NUMBER OF SEQUENCES: 35  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: VICAL, INC.  
/ STREET: 9373 Towne Centre Drive  
/ CITY: San Diego,  
/ STATE: California  
/ COUNTRY: USA  
/ ZIP: 92121  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/07/734,434A  
/ FILING DATE: 19910723  
/ CLASSIFICATION: 530

/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Kirkpatrick, Anita M.  
/ REGISTRATION NUMBER: 32,617  
/ REFERENCE/DOCKET NUMBER: VICAL.019A  
/ INFORMATION FOR SEQ ID NO: 33:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 4 amino acids  
/ TYPE: AMINO ACID  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: peptide  
/ HYPOTHETICAL: NO  
/ ANTI-SENSE: NO  
/ FRAGMENT TYPE: internal  
/ FEATURE:  
/ NAME/KEY: Unusual amino acids; misc. differences  
/ LOCATION: 1, 1-2, 4  
/ OTHER INFORMATION: amino terminal Ala-1 residue is a  
/ t-butyloxycarbonyl derivative; Phe-1 and Pro-2 are joined  
/ isosteric link having the structure -CHOH-CH2-N-; carboxy  
/ terminal Val-4 is an amide.  
/ US-07-734-434A-33

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
Db 1 FPI 3

RESULT 40  
US-08-206-789-1  
/ Sequence 1, Application US/08206789  
/ Patent No. 5580854  
/ GENERAL INFORMATION:  
/ APPLICANT: Orlowski, Marian  
/ APPLICANT: Cardozo, Christopher  
/ APPLICANT: Vinitzky, Alexander  
/ TITLE OF INVENTION: SUBSTRATE-RELATED  
/ TITLE OF INVENTION: PEPTIDYL-ALDEHYDE  
/ TITLE OF INVENTION: INHIBITORS OF THE PROTEOLYTIC ACTIVITY OF THE  
/ MULTICATALYTIC PROTEINASE COMPLEX  
/ NUMBER OF SEQUENCES: 5  
/ CORRESPONDENCE ADDRESS:  
/ ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE &  
/ STREET: 30 Rockefeller Plaza  
/ CITY: New York  
/ STATE: New York  
/ COUNTRY: USA  
/ ZIP: 10112-2500  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/206,789  
/ FILING DATE:  
/ CLASSIFICATION: 530  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Seide, Rochelle K.  
/ REGISTRATION NUMBER: 32,300  
/ REFERENCE/DOCKET NUMBER: A29525 - 165/25989  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 212-408-2626  
/ TELEFAX: 212-765-2519  
/ INFORMATION FOR SEQ ID NO: 1:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 4 amino acids  
/ TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; US-08-206-789-1
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GPF 4
Db 1 GPF 3

RESULT 41
US-08-206-789-3
; Sequence 3, Application US/08206789
; Patent No. 5580854
; GENERAL INFORMATION:
; APPLICANT: Orłowski, Marian
; APPLICANT: Cardozo, Christopher
; APPLICANT: Vinitzky, Alexander
; TITLE OF INVENTION: SUBSTRATE-RELATED
; TITLE OF INVENTION: PEPTIDYL-ALDEHYDE
; TITLE OF INVENTION: INHIBITORS OF THE PROTEOLYTIC ACTIVITY OF THE
; TITLE OF INVENTION: MULTICATALYTIC PROTEINASE COMPLEX
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BRUMBAUGH, GRAVES, DONOHUE &
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112-2500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,789
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Seide, Rochelle K.
; REGISTRATION NUMBER: 32,300
; REFERENCE/DOCKET NUMBER: A29525 - 165/25989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-408-2626
; TELEFAX: 212-765-2519
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; US-08-206-789-3
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GPF 4
Db 1 GPF 3

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; US-08-206-789-1
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GPF 4
Db 1 GPF 3

RESULT 42
US-08-451-568-20
; Sequence 20, Application US/08451568
; Patent No. 5597801
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBAY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,568
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,839
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002842
; FILING DATE: 14-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9303564.0
; FILING DATE: 23-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02179
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 3893/99204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-451-568-20
Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 ILV 8
Db 2 ILV 4
```

```
RESULT 43
US-08-494-763-4
; Sequence 4, Application US/08494763
; Patent No. 5627035
; GENERAL INFORMATION:
; APPLICANT: Vahlne, Anders
; APPLICANT: Svennerholm, Bo
; APPLICANT: Rymo, Lars
; APPLICANT: Jeansson, Stig
; APPLICANT: Horal, Peter
; TITLE OF INVENTION: Peptides That Block Human
; TITLE OF INVENTION: Immunodeficiency Virus Infections and Methods of Use Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brumbaugh, Graves, Donohue &
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette
; COMPUTER: IBM OR COMPATIBLE
; OPERATING SYSTEM: DOS VER. 5.0
; SOFTWARE: WP 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,763
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/988,127
; FILING DATE: 12-FEB-1993
; APPLICATION NUMBER: 07/571,080
; FILING DATE: 22-AUG-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Kay-Ellen
; REGISTRATION NUMBER: 36,364
; REFERENCE/DOCKET NUMBER: 28391A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 408-2500
; TELEFAX: (212) 765-2519
; TELEX: 238555
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
US-08-494-763-4

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
Db 1 RGP 3

RESULT 44
US-08-294-434-4
; Sequence 4, Application US/08294434
; Patent No. 5635371
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5656456west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
```

```
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; TITLE OF INVENTION: POLYPEPTIDE OR A PORTION THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5635371west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/294,434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,798
; FILING DATE: 13-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.29-US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-294-434-4

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
Db 1 RGP 3

RESULT 45
US-08-457-166-4
; Sequence 4, Application US/08457166
; Patent No. 5656456
; GENERAL INFORMATION:
; APPLICANT: Stout, Jay
; APPLICANT: Wagner, Fred W.
; APPLICANT: Coolidge, Thomas R.
; APPLICANT: Holmquist, Barton
; TITLE OF INVENTION: CHEMICAL METHOD FOR SELECTIVE
; TITLE OF INVENTION: MODIFICATION OF THE N- AND/OR C-TERMINAL AMINO ACID
; TITLE OF INVENTION: ALPHA-CARBON REACTIVE GROUP OF A RECOMBINANT
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5656456west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,166
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/091,751
; FILING DATE:
; APPLICATION NUMBER: US 07/912,798
; FILING DATE: 13-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.35-US-01
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-457-166-4

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 46
US-08-358-160-175
; Sequence 175, Application US/08358160
; Patent No. 5663143
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur C.
; APPLICANT: LADNER, Robert C.
; APPLICANT: GUTERMAN, Sonia K.
; APPLICANT: ROBERTS, Bruce L.
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel B.
; TITLE OF INVENTION: ENGINEERED HUMAN-DERIVED KUNITZ
; NUMBER OF SEQUENCES: 234
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W. Suite 300
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/358,160
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,031
; FILING DATE: 13-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,319
; FILING DATE: 26-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/664,989
; FILING DATE: 01-MAR-1991

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/487,063
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/240,160
; FILING DATE: 02-SEP-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: LEY=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-358-160-175

Query Match 37.5%; Score 3; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 2 RGP 4

RESULT 47
US-08-451-566-20
; Sequence 20, Application US/08451566
; Patent No. 5691199
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,566
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149839
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002842

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Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 6 ILV 8  
Db 2 ILV 4

RESULT 48  
US-08-213-124-22  
; Sequence 22, Application US/08213124  
; Patent No. 5693325  
; GENERAL INFORMATION:  
; APPLICANT: Kahn, Michael  
; TITLE OF INVENTION: PEPTIDE VACCINES AND METHODS RELATING  
; TO THE INVENTION: THEREO  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/213,124  
; FILING DATE: 15-MAR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hermans, Karl R.  
; REGISTRATION NUMBER: 33,507  
; REFERENCE/DOCKET NUMBER: 67063.411  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANBERRY  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-451-566-20

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 6 ILV 8  
Db 2 ILV 4

RESULT 48  
US-08-213-124-22  
; Sequence 22, Application US/08213124  
; Patent No. 5693325  
; GENERAL INFORMATION:  
; APPLICANT: Kahn, Michael  
; TITLE OF INVENTION: PEPTIDE VACCINES AND METHODS RELATING  
; TO THE INVENTION: THEREO  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED AND BERRY  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/213,124  
; FILING DATE: 15-MAR-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hermans, Karl R.  
; REGISTRATION NUMBER: 33,507  
; REFERENCE/DOCKET NUMBER: 67063.411  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; TELEX: 3723836 SEEDANBERRY  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-213-124-22

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;

QY 1 RGP 3  
Db 1 RGP 3

RESULT 49  
US-08-224-868-4  
; Sequence 4, Application US/08224868  
; Patent No. 5698448  
; GENERAL INFORMATION:  
; APPLICANT: Soldin, Steven J.  
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE DRUG BINDING PROTEINS  
; AND USE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Hardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/224,868  
; FILING DATE: 08-APR-1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/200,404  
; FILING DATE: 23-FEB-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/782,761  
; FILING DATE: 22-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/487,115  
; FILING DATE: 02-MAR-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/279,176  
; FILING DATE: 02-DEC-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/841,792  
; FILING DATE: 26-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/521,074  
; FILING DATE: 09-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 64688/125/CHRE  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-224-868-4

Query Match 37.5%; Score 3; DB 1; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;



Qy 2 GPF 4  
|||  
Db 2 GPF 4

## RESULT 50

US-08-777-192-16  
; Sequence 16, Application US/08777192  
; Patent No. 5824869

; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEIDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,192  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SER.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-777-192-16

Query Match 37.5%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 6 ILV 8  
|||  
Db 2 ILV 4

## RESULT 51

US-08-249-830-3  
; Sequence 3, Application US/08249830  
; Patent No. 5840485

; GENERAL INFORMATION:  
; APPLICANT: Lebl, Michal  
; APPLICANT: Lam, Kit S.  
; APPLICANT: Salmon, Sydney E.  
; APPLICANT: Krchnak, Victor  
; APPLICANT: Sepetov, Nikolai

; APPLICANT: Kocis, Peter  
; TITLE OF INVENTION: TOPOLOGICALLY SEGREGATED, ENCODED  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/249,830  
; FILING DATE: 26-MAY-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Baldwin, Geraldine F.  
; REGISTRATION NUMBER: 31,232  
; REFERENCE/DOCKET NUMBER: 7156-057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090  
; TELEFAX: 212-869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-249-830-3

Query Match 37.5%; Score 3; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0;

Qy 2 GPF 4  
|||  
Db 2 GPF 4

## RESULT 52

US-08-777-113-20  
; Sequence 20, Application US/08777113  
; Patent No. 5986176

; GENERAL INFORMATION:  
; APPLICANT: BROEKAERT, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: VANDERLEIDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,113  
; FILING DATE: 30-DEC-1996

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; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/451,566
; FILING DATE: 26-MAY-1995
; APPLICATION NUMBER: US 08/149839
; FILING DATE: 10-NOV-1993
; APPLICATION NUMBER: GB 9112300.0
; FILING DATE: 07-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00999
; FILING DATE: 03-JUN-1992
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9223708.0
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002842
; FILING DATE: 14-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9303564.0
; FILING DATE: 23-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/02179
; FILING DATE: 22-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 3893/99204
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-777-113-20

Query Match 37.5%; Score 3; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8
DB 2 ILV 4

RESULT 53
US-09-198-209-3
; Sequence 3, Application US/09198209A
; Patent No. 6090912
; GENERAL INFORMATION:
; APPLICANT: Lebl, Michal
; APPLICANT: Lam, Kit S.
; APPLICANT: Salmon, Sydney B.
; APPLICANT: Krchnak, Victor
; APPLICANT: Sepetov, Nikolai
; APPLICANT: Kocis, Peter
; TITLE OF INVENTION: TOPOLOGICALLY SEGREGATED, ENCODED SOLID PHASE LIBRARIES
; FILE REFERENCE: 7156-079
; CURRENT APPLICATION NUMBER: US/09/198,209A
; CURRENT FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: 08/249,830
; EARLIER FILING DATE: 1994-05-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-198-209-3

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4
DB 2 GPF 4

RESULT 54
US-08-927-128-10
; Sequence 10, Application US/08927128
; Patent No. 6127150
; GENERAL INFORMATION:
; APPLICANT: Coolidge, Thomas
; APPLICANT: Wagner, Fred
; APPLICANT: ven Heeke, Gino
; APPLICANT: Schuster, Sheldon
; APPLICANT: Stout, Jay
; APPLICANT: Wylie, Dwane
; TITLE OF INVENTION: PURIFICATION DIRECTED CLOSING OF PEPTIDES
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 6127150 West Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/927,128
; FILING DATE: 05-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/680,004
; FILING DATE: 15-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.2USD1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORIGINAL SOURCE:
US-08-927-128-10

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3
DB 1 RGP 3
```

```

RESULT 55
US-09-219-849-16
; Sequence 16, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOWSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHELIE D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; TITLE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Murine sp.
US-09-219-849-16

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 56
US-08-971-982-16
; Sequence 16, Application US/08971982
; Patent No. 6187904
; GENERAL INFORMATION:
; APPLICANT: BROEKAERT, WILLEM F.
; APPLICANT: CAMMUE, BRUNO P.A.
; APPLICANT: OSBORN, RUPERT W.
; APPLICANT: REES, SARAH B.
; APPLICANT: TERRAS, FRANKY R.G.
; APPLICANT: VANDERLEYDEN, JOZEF
; TITLE OF INVENTION: BIOCIDAL PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,982
; FILING DATE: 17-Jan-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/002,480
; FILING DATE: 04-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

US-09-641-801-29.oligo.ra1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-971-982-16

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ILV 8
Db 2 ILV 4

RESULT 57
US-09-411-531A-1
; Sequence 1, Application US/09411531A
; Patent No. 6251391
; GENERAL INFORMATION:
; APPLICANT: Wilkinson, Randall
; APPLICANT: Houston, Devin
; TITLE OF INVENTION: Inhibition of casomorphin and glutomorphin
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Graybeal Jackson Haley
; STREET: 777-108th Ave. NE, Suite 2460
; CITY: Bellevue
; STATE: Washington
; COUNTRY: USA
; ZIP: 98004-5117
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: Microsoft word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,531A
; FILING DATE: 01-Oct-1999
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: King, Joshua
; REGISTRATION NUMBER: 35,570
; REFERENCE/DOCKET NUMBER: 1776-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (425) 455-5575
; TELEFAX: (425) 455-1046
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-411-531A-1

Query Match 37.5%; Score 3; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 3 PFP 5
```

Db 2 PFF 4

## RESULT 58

US-07-901-713A-23

; Sequence 23, Application US/07901713A

; Patent No. 6291205

; GENERAL INFORMATION:

; APPLICANT: Tuite, Michael F.

; APPLICANT: Freedman, Robert B.

; APPLICANT: Markus, Henry Z.

; APPLICANT: Schultz, Loren D.

; APPLICANT: Montgomery, Donna L.

; APPLICANT: Ellis, Ronald W.

; TITLE OF INVENTION: METHOD FOR INCREASING PRODUCTION OF

; TITLE OF INVENTION: DISULFIDE BONDED RECOMBINANT PROTEINS BY SACCAROMYCES

; FILE REFERENCE: CERESISIAE

; FILE REFERENCE: 18469

; CURRENT APPLICATION NUMBER: US/07/901,713A

; CURRENT FILING DATE: 1992-06-12

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 23

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: portion of antistasin coding sequence (Figure 8)

US-07-901-713A-23

Query Match

Best Local Similarity 37.5%; Score 3; DB 3; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GPF 4

Db 2 GPF 4

## RESULT 59

US-09-411-605A-1

; Sequence 1, Application US/09411605A

; Patent No. 6447772

; GENERAL INFORMATION:

; APPLICANT: Houston, Devin

; TITLE OF INVENTION: Compositions And Methods Relating To Reduction Of Symptoms Of Au

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/411,605A

; CURRENT FILING DATE: 1999-10-01

; NUMBER OF SEQ ID NOS: 5

; SEQ ID NO 1

; LENGTH: 4

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-411-605A-1

Query Match

Best Local Similarity 37.5%; Score 3; DB 4; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFF 5

Db 2 PFF 4

## RESULT 60

US-09-298-574-20

; Sequence 20, Application US/09298574

; Patent No. 6521590

; GENERAL INFORMATION:

; APPLICANT: BROEKERT, WILLEM F.

; APPLICANT: CAMMUE, BRUNO P.A.

; APPLICANT: OSBORN, RUPERT W.

; TITLE OF INVENTION: METHOD FOR MODIFICATION OF

; APPLICANT: REES, SARAH B.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3918  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/298,574  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/149,839  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB92/00999  
; FILING DATE: 03-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9223708.0  
; FILING DATE: 12-NOV-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002842  
; FILING DATE: 14-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9303564.0  
; FILING DATE: 23-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB93/02179  
; FILING DATE: 22-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 3893/99204  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 861-3000  
; TELEFAX: (202) 822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-298-574-20

Query Match

Best Local Similarity 37.5%; Score 3; DB 4; Length 4;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ILV 8

Db 2 ILV 4

## RESULT 61

PCT-US93-06591-4

; Sequence 4, Application PC/TUS9306591

; GENERAL INFORMATION:

; APPLICANT: Stout, Jay

; APPLICANT: Wagner, Fred W.

; APPLICANT: Coolidge, Thomas R.

; APPLICANT: Holmquist, Barton

; TITLE OF INVENTION: METHOD FOR MODIFICATION OF

```
; TITLE OF INVENTION: RECOMBINANT POLYPEPTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 Northwest Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE:
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06591
; FILING DATE: 19930713
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 8648.35-WO-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-06591-4

Query Match 37.5%; Score 3; DB 5; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
Db 1 RGP 3

RESULT 62
5215966-12
; Patent No. 5215966
; APPLICANT: HOLZMANN, GUNTER; RADDATZ, PETER; SCHMITGES,
; CLAUS J.; MINCK, KLAUS OTTO; JONCZYK, ALFRED; SOMEROEK,
; JOHANNES; GANTE, JOACHIM
; TITLE OF INVENTION: PEPTIDE AND RENIN INHIBITORS
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/126,060
; FILING DATE: 27-NOV-1987
; SEQ ID NO: 12:
; LENGTH: 4
; 5215966-12

Query Match 37.5%; Score 3; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PFP 5
Db 2 PFP 4

RESULT 63
US-08-238-089-34
; Sequence 34, Application US/08238089
; Patent No. 5589460
; GENERAL INFORMATION:
; APPLICANT: Abajian, Herny B.
; APPLICANT: No. 55894601e, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; AND THEIR THERAPEUTIC USE AS AN ANTI-DEPRESSANT AGENT
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```
; APPLICANT: Abajian, Herny B.
; APPLICANT: No. 55894601e, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; AND THEIR THERAPEUTIC USE AS AN ANTI-DEPRESSANT AGENT
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/238,089
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 3297-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Trp-NH2
; OTHER INFORMATION: /note= "A modified Trp residue: an amine group
; OTHER INFORMATION: replaces a hydroxyl group at the carboxy terminus."
; US-08-238-089-34

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6
Db 1 FPI 3

RESULT 64
US-08-238-089-44
; Sequence 44, Application US/08238089
; Patent No. 5589460
; GENERAL INFORMATION:
; APPLICANT: Abajian, Herny B.
; APPLICANT: No. 55894601e, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; AND THEIR THERAPEUTIC USE AS AN ANTI-DEPRESSANT AGENT
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,089  
FILING DATE: 04-MAY-1994  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gould, Jr., Lewis F.  
REGISTRATION NUMBER: 25,057  
REFERENCE/DOCKET NUMBER: 3297-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 575-6020  
TELEFAX: (215) 575-6015  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: /label= Trp-NH2  
OTHER INFORMATION: /note= "A modified Trp residue: an amine group  
OTHER INFORMATION: replaces a hydroxyl group at the carboxy terminus."  
US-08-238-089-44  
Query Match 37.5%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 5 PIL 7  
Db 1 PIL 3  
RESULT 65  
US-08-494-763-2  
Sequence 2, Application US/08494763  
Patent No. 5627035  
GENERAL INFORMATION:  
APPLICANT: Vahline, Anders  
APPLICANT: Svennerholm, Bo  
APPLICANT: Rymo, Lars  
APPLICANT: Jeansson, Stig  
APPLICANT: Horal, Peter  
TITLE OF INVENTION: Peptides That Block Human  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue &  
ADDRESSEE: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette  
COMPUTER: IBM OR COMPATIBLE  
OPERATING SYSTEM: DOS VER. 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,763  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/988,127  
FILING DATE: 12-FEB-1993  
APPLICATION NUMBER: 07/571,080  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Kay-Ellen  
REGISTRATION NUMBER: 36,364  
REFERENCE/DOCKET NUMBER: 28391A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2500  
TELEFAX: (212) 765-2519  
TELEX: 238555  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid

ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Kay-Ellen  
REGISTRATION NUMBER: 36,364  
REFERENCE/DOCKET NUMBER: 28391A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2500  
TELEFAX: (212) 765-2519  
TELEX: 238555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
DESCRIPTION: peptide  
US-08-494-763-2  
Query Match 37.5%; Score 3; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 RGP 3  
Db 2 RGP 4  
RESULT 66  
US-08-494-763-5  
Sequence 5, Application US/08494763  
Patent No. 5627035  
GENERAL INFORMATION:  
APPLICANT: Vahline, Anders  
APPLICANT: Svennerholm, Bo  
APPLICANT: Rymo, Lars  
APPLICANT: Jeansson, Stig  
APPLICANT: Horal, Peter  
TITLE OF INVENTION: Peptides That Block Human  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Brumbaugh, Graves, Donohue &  
ADDRESSEE: Raymond  
STREET: 30 Rockefeller Plaza  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10112  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2 inch 1.44 MB diskette  
COMPUTER: IBM OR COMPATIBLE  
OPERATING SYSTEM: DOS VER. 5.0  
SOFTWARE: WP 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,763  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/988,127  
FILING DATE: 12-FEB-1993  
APPLICATION NUMBER: 07/571,080  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, Kay-Ellen  
REGISTRATION NUMBER: 36,364  
REFERENCE/DOCKET NUMBER: 28391A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 408-2500  
TELEFAX: (212) 765-2519  
TELEX: 238555  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5  
TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: peptide
US-08-494-763-5

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
   |||
Db 1 RGP 3

RESULT 67
US-08-432-651A-34
; Sequence 34, Application US/08432651A
; Patent No. 5767083
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; APPLICANT: No. 5767083le, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432.651A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 3297-5
; REFERENCE/DOCKET NUMBER: 3297-5
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURES:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Tri-NH2
; OTHER INFORMATION: /note= "A modified Tri residue: an amine group
; OTHER INFORMATION: replaces a hydroxyl group at the carboxy
; OTHER INFORMATION: terminus."
US-08-432-651A-34

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 FPI 6
   |||
Db 1 FPI 3

US-08-432-651A-34

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGP 3
   |||
Db 1 RGP 3

RESULT 68
US-08-432-651A-44
; Sequence 44, Application US/08432651A
; Patent No. 5767083
; GENERAL INFORMATION:
; APPLICANT: Abajian, Henry B.
; APPLICANT: No. 5767083le, John F.
; APPLICANT: Hlavka, Joseph J.
; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES
; TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lewis F. Gould, Jr.
; STREET: 1700 Market Street, Suite 3232
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432.651A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gould, Jr., Lewis F.
; REGISTRATION NUMBER: 25,057
; REFERENCE/DOCKET NUMBER: 3297-5
; TELEPHONE: (215) 575-6020
; TELEFAX: (215) 575-6015
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURES:
; NAME/KEY: Modified-site
; LOCATION: 5
; OTHER INFORMATION: /label= Tri-NH2
; OTHER INFORMATION: /note= "A modified Tri residue: an amine group
; OTHER INFORMATION: replaces a hydroxyl group at the carboxy
; OTHER INFORMATION: terminus."
US-08-432-651A-44

Query Match 37.5%; Score 3; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PIL 7
   |||
Db 1 PIL 3

RESULT 69
US-08-347-335A-4
; Sequence 4, Application US/08347335A
; Patent No. 5856163
; GENERAL INFORMATION:
; APPLICANT: Hashida, Miyoko
; APPLICANT: Abo, Masarobu
; APPLICANT: Takamura, Yukiko
; APPLICANT: Kirk, Ole
; APPLICANT: Halkier, Torben
; APPLICANT: Pedersen, Sven
; APPLICANT: Patkar, Shamkant A.
; APPLICANT: Hansen, Mogens T.
; TITLE OF INVENTION: NOVEL ENZYMES
```

NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NO. 58561630 No. 5856163disk of No. 5856163th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/347,335A  
FILING DATE: 22-DEC-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Lambiris, Elias J.  
REGISTRATION NUMBER: 33,728  
REFERENCE/DOCKET NUMBER: 3706.204-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-867-0123  
TELEFAX: 212-878-9655  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-347-335A-4

Query Match 37.5%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PFF 5  
|||  
Db 3 PFF 5

RESULT 70  
US-08-640-847C-33  
Sequence 33, Application US/08640847C  
Patent No. 5993865  
GENERAL INFORMATION:  
APPLICANT: BECH, Lene M.  
APPLICANT: SORENSEN, Steen B.  
APPLICANT: VAAG, Pia  
APPLICANT: MULDBJERG, Marianne  
APPLICANT: BEENFELDT, Thorild  
APPLICANT: LEAH, Robert  
APPLICANT: BREDDAM, Klaus  
TITLE OF INVENTION: BEVERAGE AND A METHOD OF PREPARING IT  
NUMBER OF SEQUENCES: 41  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LADAS & PARRY  
STREET: 26 WEST 61 STREET  
CITY: NEW YORK  
STATE: NY  
ZIP: 10023  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/4" Disk 1.44 MB  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: Microsoft Windows for Workgroups 3.11  
SOFTWARE: Wordperfect 8 for Windows  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/640,847C  
FILING DATE: 26-JUN-1996  
CLASSIFICATION: 426  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/DK94/00420

FILING DATE: 08-NOV-1994  
APPLICATION NUMBER: DK001266/93  
FILING DATE: 08-NOV-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: MASS, Clifford J.  
REGISTRATION NUMBER: 30,086  
REFERENCE/DOCKET NUMBER: U-010781-0  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 708-1890  
TELEFAX: (212) 246-8959  
TELEX: 233288  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 Amino Acids  
TYPE: Amino Acids  
TOPOLOGY: Linear  
US-08-640-847C-33

Query Match 37.5%; Score 3; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred.No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGP 3  
|||  
Db 3 RGP 5

RESULT 71  
US-08-962-962C-34  
Sequence 34, Application US/08962962C  
Patent No. 6093797  
GENERAL INFORMATION:  
APPLICANT: Abajian, Henry B.  
APPLICANT: No. 6093797le, John F.  
APPLICANT: Hlavka, Joseph J.  
TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES  
AND THEIR THERAPEUTIC USE AS AN ANTIDEPRESSANT AGENT  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lewis F. Gould, Jr.  
STREET: 1700 Market Street, Suite 3232  
CITY: Philadelphia  
STATE: PA  
COUNTRY: US  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/962,962C  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Gould, Jr., Lewis F.  
REGISTRATION NUMBER: 25,057  
REFERENCE/DOCKET NUMBER: 3297-5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 575-6020  
TELEFAX: (215) 575-6015  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 5  
OTHER INFORMATION: /label= Trp-NH2  
OTHER INFORMATION: /note= "A modified Trp residue: an amine group replaces a



; OTHER INFORMATION: hydroxyl group at the carboxy terminus."  
US-08-962-962C-34

Query Match 37.5%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
DB 1 FPI 3

## RESULT 72

US-08-962-962C-44  
; Sequence 44, Application US/08962962C

; Patent No. 6093797

; GENERAL INFORMATION:

; APPLICANT: Abajian, Henry B.

; APPLICANT: No. 6093797le, John F.

; APPLICANT: Hlavka, Joseph J.

; TITLE OF INVENTION: TRI-, TETRA-, PENTA-, AND POLYPEPTIDES

; TITLE OF INVENTION: AND THEIR THERAPEUTIC USE AS AN ANTIPEPRESSANT AGENT

; NUMBER OF SEQUENCES: 128

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lewis F. Gould, Jr.

; STREET: 1700 Market Street, Suite 3232

; CITY: Philadelphia

; STATE: PA

; COUNTRY: US

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/962,962C

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Gould, Jr., Lewis F.

; REGISTRATION NUMBER: 25,057

; REFERENCE/DOCKET NUMBER: 3297-5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 575-6020

; TELEFAX: (215) 575-6015

; INFORMATION FOR SEQ ID NO: 44:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 5

; OTHER INFORMATION: /label= Trp-NH2

; OTHER INFORMATION: /note= "A modified Trp residue: an amine group replaces a

; OTHER INFORMATION: hydroxyl group at the carboxy terminus."

US-08-962-962C-44

Query Match 37.5%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PIL 7  
DB 1 PIL 3

## RESULT 73

US-09-357-952-84

; Sequence 84, Application US/09357952

; Patent No. 6249904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Who]  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteas  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-84

Query Match 37.5%; Score 3; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6  
DB 3 FPI 5

## RESULT 74

US-09-521-650-84

; Sequence 84, Application US/09521650

; Patent No. 6335429

; GENERAL INFORMATION:

; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong

; APPLICANT: Keana, John F.W.

; APPLICANT: Drewe, John A.

; APPLICANT: Zhang, Han-Zhong

; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and

; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence

; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the

; TITLE OF INVENTION: Use Thereof

; FILE REFERENCE: 1735.0290002

; CURRENT APPLICATION NUMBER: US/09/521,650

; CURRENT FILING DATE: 2000-03-08

; EARLIER APPLICATION NUMBER: 09/168,888

; EARLIER FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,582

; EARLIER FILING DATE: 1997-10-10

; EARLIER APPLICATION NUMBER: US 09/033,661

; EARLIER FILING DATE: 1998-03-03

; NUMBER OF SEQ ID NOS: 142

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 84

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Synthetic

; OTHER INFORMATION: Peptide

US-09-521-650-84

Query Match 37.5%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FPI 6

Db           |||  
              3 FPI 5

RESULT 75  
US-09-168-888-84  
; Sequence 84, Application US/09168888  
; Patent No. 6342611  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290002  
; CURRENT APPLICATION NUMBER: US/09/168,888  
; CURRENT FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 60/061,582  
; EARLIER FILING DATE: 1997-10-10  
; EARLIER APPLICATION NUMBER: US 09/033,661  
; EARLIER FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-168-888-84

Query Match           37.5%; Score 3; DB 4; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches   3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           4 FPI 6  
              |||  
Db           3 FPI 5

Search completed: November 25, 2003, 20:30:05  
Job time : 7.46512 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:28:30 ; Search time 12.3488 Seconds  
(without alignments)  
140.178 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFFNRYQDDHGEELKSL 18

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3883

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

1: Pir1.\*

2: Pir2.\*

3: Pir3.\*

4: Pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3	16.7	7	S45648	Na+-transporting A
2	3	16.7	8	S66296	Na+-transporting A
3	3	16.7	9	B20569	serum amyloid P-co
4	3	16.7	9	PH0108	late G1-69 protein
5	3	16.7	10	XGHUE	erythrocyte membra
6	3	16.7	10	C61440	polygalacturonase
7	3	16.7	11	S65395	chemical-sense-rel
8	3	16.7	11	D45900	complement C3b rec
9	3	16.7	11	S65377	cytochrome-c oxida
10	3	16.7	11	I52708	ELAV-like neuronal
11	3	16.7	12	B58503	outer membrane por
12	3	16.7	12	T46794	hypothetical prote
13	3	16.7	12	S27023	Na+/K+-exchanging
14	3	16.7	13	J02309	hypothetical 1.6K
15	3	16.7	13	J02319	hypothetical 1.6K
16	3	16.7	13	E60396	antigen 7H8/2 - ma
17	3	16.7	13	A23694	myosin heavy chain
18	3	16.7	13	A57789	gallbladder stone
19	3	16.7	13	E53275	Ig kappa-1 chain J
20	3	16.7	14	LFEBWC	trip operon leader
21	3	16.7	14	LFEBWT	trip operon leader
22	3	16.7	14	P50249	porin - rice (stra
23	3	16.7	14	A39239	actin 8 - slime mo
24	3	16.7	14	E61308	hemocyanin chain 3
25	3	16.7	14	S14336	mastoparan B - hor
26	3	16.7	14	P70259	Ig heavy chain CRD
27	3	16.7	15	S49409	H4-transporting tw
28	3	16.7	15	PC2374	unidentified 22k p
29	3	16.7	15	S36897	ribosomal protein

30	15.7	15	2	B56819	PS I complex subun
31	16.7	15	2	P80025	protein QA300026 -
32	16.7	15	2	P80450	23K protein 4307 -
33	16.7	15	2	A60221	apolipoprotein A-I
34	16.7	15	2	A43839	beta-tubulin germ-
35	16.7	15	2	S66215	cartilage oligomer
36	16.7	15	2	P80662	dystrophin-associa
37	16.7	15	2	A31902	bone acidic glycop
38	16.7	15	2	S66443	NAD(P) transhydrog
39	16.7	16	2	S35627	uvax protein - pha
40	16.7	16	2	S29631	beta-glucosidase (
41	16.7	16	2	A47393	neuropeptide calla
42	16.7	16	2	PH1778	T cell receptor al
43	16.7	16	2	S10808	protein kinase C i
44	16.7	16	2	B89821	hypothetical prote
45	16.7	17	1	A05168	conantokin G [vali
46	16.7	17	2	A44896	heat shock protein
47	16.7	18	2	S74195	epoxide hydrolase
48	16.7	18	2	S48863	cyclin C - mouse (
49	16.7	18	2	S46241	NAD(P)H-flavin oxi
50	16.7	18	2	S54272	CTC 75 protein - h
51	16.7	18	2	PH1815	T cell receptor al
52	16.7	18	2	S66627	tau protein - huma
53	16.7	18	2	S78767	ribosomal protein
54	16.7	19	2	S28396	T-complex protein
55	16.7	19	2	C40634	orf21 5' of eryk -
56	16.7	19	2	S43624	cytochrome-c oxida
57	16.7	19	2	A49192	transhyretin - bu
58	16.7	19	2	I52721	gene BMLH1 protein
59	16.7	19	2	S68394	H4-transporting tw
60	16.7	20	2	B60894	crystallin - Pacif
61	16.7	20	2	A33160	H4-transporting tw
62	16.7	20	2	D49164	chromogranin-B - r
63	16.7	20	2	S00492	hemocyanin chain I
64	16.7	20	2	PN0154	groEL-like protein
65	16.7	20	2	I65242	homeotic protein H
66	16.7	20	2	PL0039	outer membrane pro
67	16.7	20	2	S65746	hypothetical prote
68	16.7	20	2	S71017	hypothetical prote
69	16.7	20	2	P50188	superoxide dismuta
70	16.7	20	2	B30208	hypothetical prote
71	16.7	20	2	S38763	S-adenosyl-L-methi
72	16.7	20	2	PC1151	equinotoxin 1C - s
73	16.7	20	2	B34016	tenebrosin B - sea
74	16.7	20	2	S78760	lysosomal protein
75	16.7	20	2	S56005	lysosomal protein
76	16.7	20	2	JP0056	ribosomal protein
77	16.7	20	3	A60898	bursin - chicken
78	11.1	3	3	PT0636	T-cell receptor be
79	11.1	4	2	I40697	biotin A - Citroba
80	11.1	4	2	A61300	22K superhelical D
81	11.1	4	2	S53508	starvation-induced
82	11.1	4	2	I61883	protamine Pl - ora
83	11.1	4	2	PT0645	T-cell receptor be
84	11.1	4	2	PT0677	T-cell receptor be
85	11.1	4	2	S55238	pallidipin - assas
86	11.1	4	2	I37013	protamine Pl - Cer
87	11.1	4	2	I84439	protamine Pl - sav
88	11.1	5	1	H080HA	proctolin - Americ
89	11.1	5	2	A32014	traM protein - Esc
90	11.1	5	2	I39964	ribosomal protein
91	11.1	5	2	I39966	ribosomal protein
92	11.1	5	2	I39965	ribosomal protein
93	11.1	5	2	I40469	dnazX-like protein
94	11.1	5	2	S70615	endo-1,4-beta-xyla
95	11.1	5	2	B45525	actin I - malaria
96	11.1	5	2	A60803	neuropeptide - sea
97	11.1	5	2	A44692	fuligin - giant Af
98	11.1	5	2	A60411	proctolin - Atlant
99	11.1	5	2	S11075	alcohol dehydrogen
100	11.1	5	2	PT0624	T-cell receptor be

## ALIGNMENTS

RESULT 1  
S45648  
Na+-transporting ATP synthase (EC 3.6.1.1-) alpha chain - Acetobacterium woodii (fragment)  
N;Alternate names: ATPase alpha chain  
C;Species: Acetobacterium woodii  
C;Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999  
C;Accession: S45648  
R;Reidlinger, J.; Mueller, V.  
Eur. J. Biochem. 223, 275-283, 1994  
A;Title: Purification of ATP synthase from Acetobacterium woodii and identification as a  
A;Reference number: S45648; MUID:94307271; PMID:8033902  
A;Accession: S45648  
A;Molecule type: protein  
A;Residues: 1-3;4-7 <REI>  
A;Experimental source: DSM 1030  
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEL 14  
|||  
Db 5 EEL 7

RESULT 2  
S66296  
Na+-transporting ATP synthase (EC 3.6.1.1-) chain c - Acetobacterium woodii (fragment)  
N;Alternate names: ATPase chain c  
C;Species: Acetobacterium woodii  
C;Date: 19-Mar-1997 #sequence\_revision 06-Jun-1997 #text\_change 07-May-1999  
C;Accession: S66296  
R;Reidlinger, J.; Mueller, V.  
Eur. J. Biochem. 223, 275-283, 1994  
A;Title: Purification of ATP synthase from Acetobacterium woodii and identification as a  
A;Reference number: S45648; MUID:94307271; PMID:8033902  
A;Accession: S66296  
A;Molecule type: protein  
A;Residues: 1-8 <REI>  
A;Experimental source: DSM 1030  
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15  
|||  
Db 2 EIL 4

RESULT 3  
B20569  
serum amyloid P-component - smooth dogfish (fragment)  
C;Species: Mustelus canis (smooth dogfish)  
C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 18-Jun-1993  
C;Accession: B20569; A05074  
R;Robey, F.A.; Tanaka, T.; Liu, T.Y.  
J. Biol. Chem. 258, 3893-3894, 1983  
A;Title: Isolation and characterization of two major serum proteins from the dogfish, M  
A;Reference number: A92419; MUID:83160932; PMID:6403520  
A;Accession: B20569  
A;Molecule type: protein  
A;Residues: 1-9 <ROB>  
C;Keywords: amyloid

Query Match 16.7%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 5 KSL 7

RESULT 4  
PH0108  
late G1-69 protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH0108  
R;Nikaido, T.; Bradley, D.W.; Pardee, A.B.  
Exp. Cell Res. 192, 102-109, 1991  
A;Title: Molecular cloning of transcripts that accumulate during the late G1 phase in  
A;Reference number: PH0108; MUID:91078351; PMID:1984406  
A;Accession: PH0108  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-9 <NIK>

Query Match 16.7%; Score 3; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 6 GEE 8

RESULT 5  
XGHUE  
erythrocyte membrane glycopeptide - human  
C;Species: Homo sapiens (man)  
C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C;Accession: A03187  
R;Weiss, J.B.; Lote, C.J.; Bobinski, H.  
Nature New Biol. 234, 25-26, 1971  
A;Title: New low molecular weight glycopeptide containing triglycosylcysteine in huma  
A;Reference number: A03187; MUID:72034940; PMID:5286858  
A;Accession: A03187  
A;Molecule type: protein  
A;Residues: 1-10 <WEI>  
C;Comment: The identity of the glycoprotein from which this peptide is derived is unk  
found (see PIR:XGHUEU).  
C;Superfamily: unassigned animal peptides  
C;Keywords: glycoprotein  
F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DHG 11  
|||  
Db 7 DHG 9

RESULT 6  
C61440  
polygalacturonase (EC 3.2.1.15) II b - Aspergillus sp. (fragment)  
C;Species: Aspergillus sp.  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 06-Dec-1996  
C;Accession: C61440  
R;Stratillova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.  
J. Protein Chem. 12, 15-22, 1993  
A;Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and s  
A;Reference number: A61440; MUID:93151362; PMID:8427629  
A;Accession: C61440  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <STR>  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
|||  
Db 6 TFN 8

RESULT 7  
S65395  
Chemical-sense-related lipophilic-ligand-binding protein - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S65395  
R:Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.  
Eur. J. Biochem. 230, 298-308, 1995  
A:Title: A putative lipophilic stimulant carrier protein commonly found in the taste and  
A:Reference number: S65394; MUID:95324537; PMID:7601113  
A:Accession: S65395  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <OZA>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEI 14  
|||  
Db 2 BEI 4

RESULT 8  
D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C:Species: *Mus musculus* (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: D45900  
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.  
J. Immunol. 144, 3591-3591, 1990  
A:Title: The murine complement receptor gene family. IV. Alternative splicing of C-r2 gene  
A:Reference number: A45900; MUID:90229754; PMID:2139460  
A:Accession: D45900  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-11 <KUR>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEI 14  
|||  
Db 3 BEI 5

RESULT 9  
S65377  
cytochrome-c oxidase (BC 1.9.3.1) chain Via-H, cardiac - rat (fragment)  
C:Species: *Rattus norvegicus* (Norway rat)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S65377  
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A:Reference number: S65372; MUID:95324529; PMID:7601105  
A:Accession: S65377  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <SCH>  
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEI 14  
|||  
Db 3 BEI 5

RESULT 9  
S65377  
cytochrome-c oxidase (BC 1.9.3.1) chain Via-H, cardiac - rat (fragment)  
C:Species: *Rattus norvegicus* (Norway rat)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S65377  
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A:Reference number: S65372; MUID:95324529; PMID:7601105  
A:Accession: S65377  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <SCH>  
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
|||  
Db 6 TFN 8

RESULT 7  
S65395  
Chemical-sense-related lipophilic-ligand-binding protein - fruit fly (*Drosophila melanogaster*)  
C:Species: *Drosophila melanogaster*  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
C:Accession: S65395  
R:Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.  
Eur. J. Biochem. 230, 298-308, 1995  
A:Title: A putative lipophilic stimulant carrier protein commonly found in the taste and  
A:Reference number: S65394; MUID:95324537; PMID:7601113  
A:Accession: S65395  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <OZA>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEI 14  
|||  
Db 2 BEI 4

RESULT 8  
D45900  
complement C3b receptor type 2 - mouse (clone 12) (fragment)  
C:Species: *Mus musculus* (house mouse)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: D45900  
R:Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.  
J. Immunol. 144, 3591-3591, 1990  
A:Title: The murine complement receptor gene family. IV. Alternative splicing of C-r2 gene  
A:Reference number: A45900; MUID:90229754; PMID:2139460  
A:Accession: D45900  
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
A:Molecule type: mRNA  
A:Residues: 1-11 <KUR>

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 BEI 14  
|||  
Db 3 BEI 5

RESULT 9  
S65377  
cytochrome-c oxidase (BC 1.9.3.1) chain Via-H, cardiac - rat (fragment)  
C:Species: *Rattus norvegicus* (Norway rat)  
C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 16-Jul-1999  
C:Accession: S65377  
R:Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.  
Eur. J. Biochem. 230, 235-241, 1995  
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term  
A:Reference number: S65372; MUID:95324529; PMID:7601105  
A:Accession: S65377  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <SCH>  
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DHG 11  
|||  
Db 6 DHG 8

RESULT 10  
I52708  
ELAV-like neuronal protein 1, truncated splice form - human  
N:Alternate names: *Drosophila* ELAV(embryonic lethal, abnormal vision)-like 4; Hu anti  
C:Species: *Homo sapiens* (man)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: I52708  
R:Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.  
Cancer Res. 54, 4988-4992, 1994  
A:Title: Molecular analysis of the *Hu*d gene encoding a paraneoplastic encephalomyelit  
A:Reference number: I52708; MUID:94349312; PMID:8069866  
A:Accession: I52708  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-11 <SEK>  
A:Cross-references: GB:S73887; NID:9688242; PIDN:AAI14142.1; PID:94261842  
C:Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I387  
C:Genetics:  
A:Gene: GDB:ELAVL4; HUD; FNM  
A:Cross-references: GDB:141875; OMIM:168360  
A:Map position: lp36-lp36  
A:Map position: lp36-lp36  
C:Keywords: alternative splicing

Query Match 16.7%; Score 3; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16  
|||  
Db 7 ILK 9

RESULT 11  
B58503  
outer membrane porin protein OprD homolog - unidentified bacterium (fragment)  
N:Alternate names: 43K bile stone protein  
C:Species: unidentified bacterium  
C>Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: B58503  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: B58503  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <BIN>  
A:Experimental source: human bile with stones  
A>Note: sequenced along with secondary sequence MXIGVNEXL

Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9  
|||  
Db 3 QDD 5

RESULT 12  
T46794  
hypothetical protein [imported] - *Haloarcula marismortui* (fragment)  
C:Species: *Haloarcula marismortui*

C;Date: 17-Mar-2000 #sequence\_revision 17-Mar-2000 #text\_change 21-Jul-2000  
C;Accession: F46794  
R;Arndt, E.

FEBS Lett. 267, 193-198, 1990  
A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and  
A;Reference number: S10731; MUID:90336772; PMID:2143141  
A;Accession: T46794  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-12 <ARN>  
A;Cross-references: EMBL:X55311; NID:g43610; PIDN:CAA39015.1; PID:g43611

Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 3 GEE 5

## RESULT 13

S27023  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - monarch butterfly (fragment)  
N;Alternate names: Na+/K+-transporting ATPase  
C;Species: Danaus plexippus (monarch butterfly)  
C;Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 19-Apr-2002  
C;Accession: S27023  
R;Holzinger, F.; Frick, C.; Wink, M.  
FEBS Lett. 314, 477-480, 1992  
A;Title: Molecular basis for the insensitivity of the Monarch (Danaus plexippus) to card  
A;Reference number: S27023; MUID:93106209; PMID:1334851  
A;Accession: S27023  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-12 <HOL>  
C;Keywords: hydrolase

Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DDH 10  
|||  
Db 10 DDH 12

## RESULT 14

JQ2309  
hypothetical 1.6K protein - tomato chloroplast (strain Toko)  
C;Species: Chloroplast Lycopersicon esculentum (tomato)  
C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 23-Mar-1995  
C;Accession: JQ2309  
R;Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 81, 13-20, 1991  
A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).  
A;Reference number: JQ2306  
A;Accession: JQ2309  
A;Molecule type: DNA  
A;Residues: 1-13 <KAW>  
A;Experimental source: strain Toko  
C;Genetics:  
A;Genome: chloroplast  
C;Keywords: chloroplast

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6  
|||  
Db 11 NRY 13

## RESULT 15

JQ2319  
hypothetical 1.6K protein - potato chloroplast  
C;Species: chloroplast Solanum tuberosum (potato)  
C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 05-Jan-1996  
C;Accession: JQ2319; JQ2314  
R;Kawagoe, Y.; Kikuta, Y.  
Theor. Appl. Genet. 81, 13-20, 1991  
A;Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).  
A;Reference number: JQ2306  
A;Accession: JQ2319  
A;Molecule type: DNA  
A;Residues: 1-13 <KW1>  
A;Experimental source: cv. W553-4  
A;Accession: JQ2314  
A;Molecule type: DNA  
A;Residues: 1-13 <KW2>  
A;Experimental source: cv. 150  
C;Genetics:  
A;Genome: chloroplast  
C;Keywords: chloroplast

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6  
|||  
Db 11 NRY 13

## RESULT 16

E60396  
antigen 78H/2 - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jun-2000  
C;Accession: E60396  
R;Limpaiboon, T.; Taylor, D.W.; Jones, G.; Geysen, H.M.; Saul, A.  
Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990  
A;Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclon  
A;Reference number: A60396; MUID:91164876; PMID:1706114  
A;Accession: E60396  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-13 <LIM>  
A;Cross-references: GB:M31305

Query Match 16.7%; Score 3; DB 2; Length 13;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17  
|||  
Db 2 LKS 4

## RESULT 17

A23694  
myosin heavy chain, smooth muscle - chicken (fragment)  
C;Species: Gallus gallus (chicken)  
C;Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 07-Feb-1997  
C;Accession: A23694  
R;Cole, D.G.; Yount, R.G.  
J. Biol. Chem. 265, 22537-22546, 1990  
A;Title: Photolabeling of the 6 and 10 S conformations of gizzard myosin with 3'-(2')-  
A;Reference number: A23694; MUID:91093105; PMID:2266144  
A;Accession: A23694  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <COL>  
C;Keywords: smooth muscle

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Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
   |||
Db 11 QDD 13

RESULT 18
A57789
gallbladder stone matrix protein 1, 41K - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
C:Accession: A57789
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, February 1996
A:Description: The proteins of gallbladder stones.
A:Reference number: A57789
A:Accession: A57789
A>Status: Preliminary
A:Molecule type: Protein
A:Residues: 1-13 <BIN>
A:Experimental source: two gallbladder, one bladder, one kidney stone of different patients
A>Note: 9-Leu and 12-Lys were also found

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
   |||
Db 3 QDD 5

RESULT 19
ES3275
Ig kappa-1 chain J5 region (b95 allotype) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 02-May-1994 #sequence_revision 01-Mar-1996 #text_change 20-Sep-1999
C:Accession: ES3275; E20907
R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; MUID:91372868; PMID:1909995
A:Accession: ES3275
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <AYA>
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983
A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
A:Reference number: A20907; MUID:84169523; PMID:6324107
A:Accession: E20907
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <EMO>
C:Comment: This J5 segment may not be functional because of substitutions in the 7 mer
C:Keywords: heterotetramer; immunoglobulin

Query Match          16.7%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
   |||
Db 4 GEE 6

RESULT 20
LFEBWC
trp operon leader peptide - Citrobacter freundii

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C:Species: Citrobacter freundii
C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 13-Nov-1998
C:Accession: A03592
R:Blumenberg, M.; Yanofsky, C.
J. Bacteriol. 152, 57-62, 1982
A:Title: Evolutionary divergence of the Citrobacter freundii tryptophan operon regulatory
A:Reference number: A91792; MUID:83007061; PMID:6749821
A:Accession: A03592
A:Molecule type: DNA
A:Residues: 1-14 <BLU>
C:Genetics:
A:Gene: trpL
C:Function:
A:Description: involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match          16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
   |||
Db 3 ATF 5

RESULT 21
LFEBWT
trp operon leader peptide - Salmonella typhimurium
C:Species: Salmonella typhimurium
C>Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 13-Nov-1998
C:Accession: A03590
R:Lee, F.; Bertrand, K.; Bennett, G.; Yanofsky, C.
J. Mol. Biol. 121, 193-217, 1978
A:Title: Comparison of the nucleotide sequences of the initial transcribed regions of
A:Reference number: A92850; MUID:78196931; PMID:3511195
A:Accession: A03590
A:Molecule type: DNA
A:Residues: 1-14 <LEE>
C:Genetics:
A:Gene: trpL; trpE
C:Function:
A:Description: involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match          16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
   |||
Db 3 ATF 5

RESULT 22
PS0249
porin - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0249
R:Taugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0249
A:Molecule type: protein
A:Residues: 1-14 <TSU>
A:Experimental source: callus

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DDH 10
   |||

```

```

Db          6 DDH 8

RESULT 23
A39239
C:Species: Dictyostelium discoideum (fragment)
C:Date: 20-Sep-1991 #sequence_revision 20-Sep-1991 #text_change 18-Jun-1993
C:Accession: A39239
R;Frankel, S.; Condeelis, J.; Leinwand, L.
J. Biol. Chem. 265, 17980-17987, 1990
A:Title: Expression of actin in Escherichia coli. Aggregation, solubilization, and function
A:Reference number: A39239; MUID:91009269; PMID:2211676
A:Accession: A39239
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <FRA>

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 TFN 4
          |||
Db          8 TFN 10

RESULT 24
E61308
C:Species: Androctonus australis (Sahara scorpion)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: E61308
R;Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
FEBS Lett. 106, 289-291, 1979
A:Title: Structural characterization of seven different subunits in Androctonus australis
A:Reference number: A61308; MUID:80047238; PMID:499512
A:Accession: E61308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <JOL>

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 TFN 4
          |||
Db          8 TFN 10

RESULT 25
S14336
C:Species: Vespa basalis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C:Accession: S14336
R;Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A:Title: Structure and biological activities of a new mastoparan isolated from the venom
A:Reference number: S14336; MUID:91174755; PMID:2006909
A:Accession: S14336
A:Molecule type: protein
A:Residues: 1-14 <HOC>
A:Experimental source: venom
C:Function:
A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal
C:Keywords: amidated carboxyl end; mast cell; venom
F;14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          14 ILK 16
          |||
Db          9 ILK 11

RESULT 26
PT0259
IG heavy chain CRD3 region (clone 2-118C) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0259
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity an
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0259
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match          16.7%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 DHG 11
          |||
Db          12 DHG 14

RESULT 27
S49409
H+-transporting two-sector ATPase (EC 3.6.3.14) chain a - Streptococcus oralis (fragm
C:Species: Streptococcus oralis
C:Date: 29-Nov-1995 #sequence_revision 01-Aug-1997 #text_change 03-Jun-2002
C:Accession: S49409; S38211
R;Penoll, A.; Munoz, R.; Garcia, E.; de la Campa, A.G.
Mol. Microbiol. 12, 587-598, 1994
A:Title: Molecular basis of the optochin-sensitive phenotype of pneumococcus: charact
asee.
A:Reference number: S49398; MUID:95020593; PMID:7934882
A:Accession: S49409
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <PEN>
A:Cross-references: EMBL:226853; NID:g407180; PID:CAA81457.1; PID:g809112
C:Superfamily: H+-transporting ATP synthase protein 6
C:Keywords: ATP biosynthesis; hydrolase; membrane-associated complex

Query Match          16.7%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          11 GEE 13
          |||
Db          13 GEE 15

RESULT 28
PC2374
Unidentified 22K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC2374
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulatio
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2374
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <MAS>

```



Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17  
 |||  
 Db 5 LKS 7

## RESULT 29

S36897  
 ribosomal protein S15 - Mycobacterium bovis (fragment)  
 C:Species: Mycobacterium bovis  
 C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C:Accession: S36897  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis  
 A:Reference number: S36887; MUID:94009653; PMID:8405418  
 A:Accession: S36897  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <OHA>  
 C:Keywords: protein biosynthesis; ribosome

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15  
 |||  
 Db 9 EIL 11

## RESULT 30

E56819  
 PS I complex subunit 8 - cucumber (fragment)  
 C:Species: Cucumis sativus (cucumber)  
 C:Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 05-Jan-1996  
 C:Accession: E56819  
 R:Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.  
 Biochim. Biophys. Acta 1059, 141-148, 1991  
 A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing  
 A:Reference number: A56819; MUID:91355209; PMID:1883835  
 A:Accession: E56819  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <IWA>  
 A:Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9  
 |||  
 Db 12 QDD 14

## RESULT 31

PA0025  
 protein QA300026 - Arabidopsis thaliana (fragment)  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
 C:Accession: PA0025  
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.  
 submitted to JIPID, July 1994  
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis  
 A:Reference number: PA0001  
 A:Accession: PA0025  
 A:Molecule type: protein  
 A:Residues: 1-15 <XAM>

A:Experimental source: leaf

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEI 14  
 |||  
 Db 4 EEI 6

## RESULT 32

PS0450  
 23K protein 4307 - rice (strain Nihonbare) (fragment)  
 C:Species: Oryza sativa (rice)  
 C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995  
 C:Accession: PS0450  
 R:Tsugita, A.; Miyatake, N.  
 submitted to JIPID, April 1993  
 A:Reference number: PS0208  
 A:Accession: PS0450  
 A:Molecule type: protein  
 A:Residues: 1-15 <TSU>  
 A:Experimental source: germ, strain Nihonbare  
 C:Comment: molecular weight 23K, pI 5.3.

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YQD 8  
 |||  
 Db 2 YQD 4

## RESULT 33

A60221  
 apolipoprotein A-I - common carp (fragment)  
 C:Species: Cyprinus carpio (common carp)  
 C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 31-Dec-1993  
 C:Accession: A60221  
 R:Harel, A.; Fainaru, M.; Rubinstein, M.; Tal, N.; Schwartz, M.  
 J. Neurochem. 55, 1237-1243, 1990  
 A:Title: Fish apolipoprotein A-I has heparin binding activity: implication for nerve conduction  
 A:Reference number: A60221; MUID:90376100; PMID:2118944  
 A:Accession: A60221  
 A:Molecule type: protein  
 A:Residues: 1-15 <HAR>  
 A:Note: protein from plasma and from optic nerve yielded the same sequence  
 C:Keywords: lipid binding; lipoprotein

Query Match 16.7%; Score 3; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17  
 |||  
 Db 10 LKS 12

## RESULT 34

A43839  
 beta-tubulin germ-cell isotype - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 11-Apr-1995  
 C:Accession: A43839  
 R:Bieker, J.J.; Yazdani-Buick, M.  
 Differentiation 50, 15-23, 1992  
 A:Title: The multiple beta-tubulin genes of Xenopus: isolation and developmental expression  
 A:Reference number: A43839; MUID:92347627; PMID:1379202  
 A:Accession: A43839  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid

A;Residues: 1-15 <BIE>  
A;Experimental source: oocyte  
A;Note: sequence extracted from NCBI backbone (NCBIP:110252)

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 9 GEE 11

## RESULT 35

S66215  
cartilage oligomeric matrix protein - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)  
C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S66215  
R;Hauser, N.; Paulsson, M.; Kale, A.A.; DiCesare, P.E.  
FEBS Lett. 368, 307-310, 1995  
A;Title: Tendon extracellular matrix contains pentameric thrombospondin-4 (TSP-4).  
A;Reference number: S66214; MUID:95354859; PMID:7628627  
A;Accession: S66215  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <HAI>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 3 FNR 5  
|||  
Db 12 FNR 14

## RESULT 36

PN0662

dystrophin-associated glycoprotein A3a-I - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 07-May-1999  
C;Accession: PN0662  
R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.  
J. Biochem. 114, 634-639, 1993  
A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained  
A;Reference number: PN0662; MUID:94156881; PMID:8113213  
A;Accession: PN0662  
A;Molecule type: protein  
A;Residues: 1-15 <YOS>  
A;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.  
C;Keywords: glycoprotein; skeletal muscle

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 ATF 3  
|||  
Db 3 ATF 5

## RESULT 37

A31902

bone acidic glycoprotein-75 - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 31-Dec-1993  
C;Accession: A31902  
R;Gorski, J.P.; Shimizu, K.  
J. Biol. Chem. 263, 15938-15945, 1988

A;Title: Isolation of new phosphorylated glycoprotein from mineralized phase of bone  
A;Reference number: A31902; MUID:89034045; PMID:2846530  
A;Accession: A31902

A;Molecule type: protein  
A;Residues: 1-15 <GOR>  
A;Note: 14-Glu and 15-Glu were also found  
C;Keywords: glycoprotein

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 5 RYQ 7  
|||  
Db 5 RYQ 7

## RESULT 38

S66443

NAD(P) transhydrogenase (B-specific) (EC 1.6.1.1) - Rhodospirillum rubrum (fragments)  
N;Alternate names: proton-translocating transhydrogenase  
C;Species: Rhodospirillum rubrum

C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 03-Jun-2002  
C;Accession: S66443  
R;Diggle, C.; Cotton, N.P.J.; Grimley, R.L.; Quirk, P.G.; Thomas, C.M.; Jackson, J.B.  
Eur. J. Biochem. 232, 315-326, 1995  
A;Title: Conformational dynamics of a mobile loop in the NAD(H)-binding subunit of pr  
A;Reference number: S66443; MUID:96048062; PMID:7556167  
A;Accession: S66443  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-5;6-10;11-15 <DIG>

Query Match 16.7%; Score 3; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 12 GEE 14

## RESULT 39

S35627

uvx protein - phage T6 (fragment)

C;Species: phage T6  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 08-Oct-1999  
C;Accession: S35627  
R;Winkler, M.; Rueger, W.  
Nucleic Acids Res. 21, 1500, 1993  
A;Title: Cloning and sequencing of the genes of beta-glucosyl-HMC-alpha-glucosyl-tran  
A;Reference number: S35622; MUID:93219141; PMID:8464751  
A;Accession: S35627  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-15 <WIN>

A;Cross-references: EMBL:X68725; NID:G296439; PIDN:CAA48668.1; PID:G296441  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992

Query Match 16.7%; Score 3; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 5.3e+03; Indels 0;  
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 15 LKS 17  
|||  
Db 6 LKS 8

## RESULT 40

S29631

beta-glucosidase (EC 3.2.1.21) - Thermotoga sp. (strain FJSS3-B.1) (fragment)

C;Species: Thermotoga sp.  
A;Variety: FJSS3-B.1  
C;Date: 19-Mar-1997 #sequence\_revision 24-Mar-1999 #text\_change 07-May-1999  
C;Accession: S29631

R;Ruttererith, L.D.; Daniel, R.M.  
 Biochim. Biophys. Acta 1156, 167-172, 1993  
 A;Title: Thermolabile beta-glucosidase and beta-xylosidase from *Thermotoga* sp. strain Fj  
 A;Reference number: S29631; MUID:93152594; PMID:8427876  
 A;Accession: S29631  
 A;Molecule type: protein  
 A;Residues: 1-16 <RUT>  
 A;Experimental source: strain FJSS3-B.1  
 C;Function:  
 A;Description: catalyzes the hydrolysis of terminal, nonreducing 1,4-linked beta-D-glucos  
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 16.7%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15  
 ||||  
 Db 6 EIL 8

RESULT 41  
 A47393  
 neuropeptide callatostatin 1 - bluebottle fly (*Calliphora vomitoria*)  
 N;Contains: neuropeptide callatostatin 2  
 C;Species: *Calliphora vomitoria*  
 C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 20-Aug-1999  
 A;Accession: A47393; B47393; C47393  
 R;Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993  
 A;Title: Callatostatin: neuropeptides from the blowfly *Calliphora vomitoria* with sequen  
 A;Reference number: A47393; MUID:93111980; PMID:8460157  
 A;Accession: A47393  
 A;Molecule type: protein  
 A;Residues: 1-16 <DUV>  
 A;Experimental source: thoracic ganglia, brains, heads  
 A;Note: sequence extracted from NCBI backbone (NCBI:128476)  
 A;Accession: B47393  
 A;Molecule type: protein  
 A;Residues: 3-16 <DU2>  
 A;Experimental source: head  
 A;Note: sequence extracted from NCBI backbone (NCBI:128477)  
 A;Accession: C47393  
 A;Molecule type: protein  
 A;Residues: 1-8 <DU3>  
 A;Experimental source: thoracic ganglia  
 A;Note: sequence extracted from NCBI backbone (NCBI:128478)  
 C;Function:  
 A;Description: inhibits juvenile hormone production  
 C;Keywords: amidated carboxyl end; neuropeptide  
 F;1-16/Product: callatostatin 1 #status experimental <MA1>  
 F;3-16/Product: callatostatin 2 #status experimental <MA2>  
 F;9-16/Product: callatostatin 3 #status experimental <MA3>  
 F;16/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 16.7%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6  
 ||||  
 Db 10 NRY 12

RESULT 42  
 PH1778  
 T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)  
 C;Species: *Homo sapiens* (man)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
 A;Accession: PH1778  
 R;Porcellii, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
 J. Exp. Med. 178, 1-16, 1993  
 A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057  
 A;Accession: PH1778  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-16 <POR>

Query Match 16.7%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
 ||||  
 Db 8 TFN 10

RESULT 43  
 S10808  
 protein kinase C inhibitor KCIP-1 isoform e - sheep (fragment)  
 N;Alternate names: probable lipocortin  
 C;Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)  
 C;Date: 19-Mar-1997 #sequence\_revision 13-Sep-1998 #text\_change 13-Sep-1998  
 A;Accession: S10808  
 R;Toker, A.; Ellis, C.A.; Sellers, L.A.; Aitken, A.  
 Eur. J. Biochem. 191, 421-429, 1990  
 A;Title: Protein kinase C inhibitor proteins. Purification from sheep brain and sequen  
 A;Reference number: S10804; MUID:90345949; PMID:2143472  
 A;Accession: S10808  
 A;Molecule type: protein  
 A;Residues: 1-16 <TOK>  
 A;Experimental source: brain

Query Match 16.7%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9  
 ||||  
 Db 14 QDD 16

RESULT 44  
 B89821  
 hypothetical protein [imported] - *Staphylococcus aureus* (strain N315)  
 C;Species: *Staphylococcus aureus*  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 A;Accession: B89821  
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oc  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.  
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A;Reference number: A89758; MUID:21311952; PMID:11418146  
 A;Accession: B89821  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-16 <KUR>  
 A;Cross-references: GB:BA000018; PID:gl3700427; PIDN:BA041725.1; GSPDB:GN00149  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: SAS015

Query Match 16.7%; Score 3; DB 2; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7  
 ||||  
 Db 8 RYQ 10

RESULT 45  
 A05168

conantokin G [validated] - cone shell (Conus geographus)  
N;Alternate names: conotoxin GV; sleeper peptide  
C;Species: Conus geographus (Geography cone)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 15-Sep-2000  
C;Accession: A05168  
R;McIntosh, J.M.; Oliveira, B.M.; Cruz, L.J.; Gray, W.R.  
J. Biol. Chem. 259, 14343-14346, 1984  
A;Title: gamma-Carboxyglutamate in a neuroactive toxin.  
A;Reference number: A05168; MUID:85054897; PMID:6501296  
A;Accession: A05168  
A;Molecule type: protein  
A;Residues: 1-17 <MCI>  
R;Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.  
submitted to the Brookhaven Protein Data Bank, February 1997  
A;Reference number: A67471; PDB:1AD7  
A;Contents: annotation; conformation by (1)H-NMR, residues 1-17  
R;Rigby, A.C.; Baleja, J.D.; Furie, B.C.; Furie, B.  
Biochemistry 36, 6906-6914, 1997  
A;Title: Three-dimensional structure of a gamma-carboxyglutamic acid-containing conotoxin  
A;Reference number: A58650; MUID:97332451; PMID:9188685  
A;Contents: annotation; conformation by (1)H-NMR  
C;Superfamily: conantokin  
C;Keywords: amidated carboxyl end; carboxyglutamic acid; neurotoxin; venom  
F;3,4,7,10,14/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
F;17/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 16.7%; Score 3; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 GEE 13  
DB 1 GEE 3

RESULT 46  
A44896  
Heat shock protein 18 - Streptomyces albus (fragment)  
C;Species: Streptomyces albus  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 12-Sep-1997  
C;Accession: A44896  
R;Guglielmi, G.; Mazodier, P.; Thompson, C.J.; Davies, J.  
J. Bacteriol. 173, 7374-7381, 1991  
A;Title: A survey of the heat shock response in four Streptomyces species reveals two 94  
A;Reference number: A44896; MUID:52041638; PMID:1682303  
A;Accession: A44896  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-17 <GUG>  
A;Note: sequence extracted from NCBI backbone (NCBIP:65105)  
C;Superfamily: chaperonin groEL

Query Match 16.7%; Score 3; DB 2; Length 17;  
Best Local Similarity 100.0%; Pred. No. 5.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 14 ILK 16  
DB 3 ILK 5

RESULT 47  
S74195  
epoxide hydrolase (EC 3.3.2.3), microsomal - pig (fragment)  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 14-Apr-1998 #sequence\_revision 24-Apr-1998 #text\_change 17-Mar-1999  
C;Accession: S74195  
R;Araya, Z.; Hellman, U.; Hansson, R.  
Eur. J. Biochem. 231, 855-861, 1995  
A;Title: Characterisation of taurochenodeoxycholic acid 6-alpha-hydroxylase from pig liv  
A;Reference number: S66455; MUID:95377322; PMID:7649186  
A;Accession: S74195  
A;Molecule type: protein

A;Residues: 1-18 <ARA>  
A;Experimental source: liver  
C;Superfamily: epoxide hydrolase  
C;Keywords: ether hydrolase

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 EIL 15  
DB 4 EIL 6

RESULT 48  
S48863  
cyclin C - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
C;Accession: S48863  
R;Wu, L.; Hall, F.L.  
submitted to the EMBL Data Library, October 1994  
A;Reference number: S48863  
A;Accession: S48863  
A;Molecule type: mRNA  
A;Residues: 1-18 <WUL>  
A;Cross-references: EMBL:X82403; NID:G563901; PIDN:CAA57797.1; PID:G563902.

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 LKS 17  
DB 5 LKS 7

RESULT 49  
S46241  
NAD(P)H-flavin oxidoreductase (EC 1.-.-.-) - Vibrio fischeri  
C;Species: Vibrio fischeri  
C;Date: 10-Dec-1994 #sequence\_revision 12-May-1995 #text\_change 16-Oct-1998  
C;Accession: S46241  
R;Inouye, S.  
FEBS Lett. 347, 163-168, 1994  
A;Title: NAD(P)H-flavin oxidoreductase from the bioluminescent bacterium, Vibrio fisc  
A;Reference number: S46241; MUID:94307374; PMID:8033996  
A;Accession: S46241  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <IMO>  
C;Keywords: NAD; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 NRY 6  
DB 10 NRY 12

RESULT 50  
S54272  
CTC 75 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 17-Mar-1999  
C;Accession: S54272  
R;Genersch, E.; Eckerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.  
EMBO J. 14, 791-800, 1995  
A;Title: Purification of the sequence-specific transcription factor CTCBF, involved i  
A;Reference number: S54272; MUID:95188883; PMID:7882982  
A;Accession: S54272

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-18 <GEN>

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
|||  
Db 2 TFN 4

## RESULT 51

PH1815  
T cell receptor alpha chain V region (clone 4PBL V alpha 24-7) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH1815  
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J;Exp. Med. 179, 1-16, 1993  
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood  
A;Reference number: PH1754; MUID:93301585; PMID:8391057  
A;Accession: PH1815  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-18 <POR>

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NRY 6  
|||  
Db 7 NRY 9

## RESULT 52

S66627  
tau protein - human (fragments)  
C;Species: Homo sapiens (man)  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S66627  
R;Moreno, F.J.; Medina, M.; Perez, M.; Montejo de Garcini, E.; Avila, J.  
FEBS Lett. 372, 65-68, 1995  
A;Title: Glycogen synthase kinase 3 phosphorylates recombinant human tau protein at serine 262  
A;Reference number: S66627; MUID:96032547; PMID:7556645  
A;Accession: S66627  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8;9-18 <MOR>

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
|||  
Db 4 TFN 6

## RESULT 53

S78767  
ribosomal protein MRP-S29, mitochondrial - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: S78767  
R;Graack, H.R.  
submitted to the Protein Sequence Database, July 1999

A;Reference number: S78760  
A;Accession: S78767  
A;Molecule type: protein

A;Residues: 1-18 <GRA>  
A;Keywords: mitochondrial  
C;Keywords: ribosomal protein MRP-S29 (fragment) #status experimental <MAT>  
F;1-18/Product: ribosomal

Query Match 16.7%; Score 3; DB 2; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5.9e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16  
|||  
Db 6 ILK 8

## RESULT 54

S28396  
T-complex protein 1 - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 04-Sep-1998  
C;Accession: S28396  
R;Frydman, J.; Nimmesgern, E.; Erdjument-Bronage, H.; Wall, J.S.; Tempst, P.; Hartl, F.  
EMBO J. 11, 4767-4778, 1992  
A;Title: Function in protein folding of Tric, a cytosolic ring complex containing TCP.  
A;Reference number: S28395; MUID:9309850; PMID:1361170  
A;Accession: S28396  
A;Molecule type: Protein  
A;Residues: 1-19 <FRY>  
C;Superfamily: molecular chaperone t-complex-type

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9  
|||  
Db 2 QDD 4

## RESULT 55

C40634  
orf21 5' of eryK - Saccharopolyspora erythraea (fragment)  
C;Species: Saccharopolyspora erythraea  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 22-Oct-1999  
C;Accession: C40634  
R;Stassi, D.; Donadio, S.; Staver, M.J.; Katz, L.  
J. Bacteriol. 175, 182-189, 1993  
A;Title: Identification of a Saccharopolyspora erythraea gene required for the final 1  
A;Reference number: A40634; MUID:93106953; PMID:8416893  
A;Accession: C40634  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-19 <STA>  
A;Cross-references: GB:U82823; GB:I05776; NID:G2327012; PIDN:AAC45585.1; PID:G2327021  
A;Note: sequence extracted from NCBI backbone (NCBIN:121243, NCBIPI:121246)

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 11 GEE 13

## RESULT 56

S43624  
cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rainbow trout (fragment)  
C;Species: Oncorhynchus mykiss (rainbow trout)  
C;Date: 20-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 16-Jul-1999  
C;Accession: S43624  
R;Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994  
A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytoch  
A;Reference number: S43624; MUID:94237150; PMID:8181469

A;Accession: S43624  
A;Molecule type: protein  
A;Residues: 1-19 <FR>  
A;Note: the source is designated as *Salmo gairdneri*  
C;Genetics:  
A;Genome: nuclear  
C;Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGE 12  
|||  
Db 3 HGE 5

RESULT 57  
A49192  
transhyretin - bullfrog (fragment)  
N;Alternate names: 3,5,3'-L-triiodothyronine-specific binding protein  
C;Species: *Rana catesbeiana* (bullfrog)  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 28-Apr-1995  
C;Accession: A49192  
R;Yamauchi, K.; Kasahara, T.; Hayashi, H.; Horiuchi, R.  
Endocrinology 132, 2254-2261, 1993  
A;Title: Purification and characterization of a 3,5,3'-L-triiodothyronine-specific binding protein  
A;Reference number: A49192; MUID:93238653; PMID:8477670  
A;Accession: A49192  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-19 <YAM>  
A;Experimental source: tadpole plasma  
A;Note: sequence extracted from NCBI backbone (NCBI:P130235)

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGE 12  
|||  
Db 2 HGE 4

RESULT 58  
I52721  
gene hMLH1 protein - human (fragment)  
C;Species: *Homo sapiens* (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 21-Jul-2000  
C;Accession: I52721  
R;Charbonnier, F.; Martin, C.; Scotte, M.; Sibert, L.; Moreau, V.; Frebourg, T.  
Cancer Res. 55, 1839-1841, 1995  
A;Title: Alternative splicing of MLH1 messenger RNA in human normal cells.  
A;Reference number: I52721; MUID:95246019; PMID:7728749  
A;Accession: I52721  
A;Status: preliminary; translated from GB/EMBL/DBU  
A;Molecule type: mRNA  
A;Residues: 1-19 <RES>  
A;Cross-references: GB:S77856; NID:G998493; PIDN:AA34135.1; PID:G998494  
C;Genetics:  
A;Gene: hMLH1

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YQD 8  
|||  
Db 3 YQD 5

RESULT 59  
S68394  
H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - *Chlamydomonas reinhardtii* (N;Alternate names: ATP synthase chain G  
C;Species: *Chlamydomonas reinhardtii*  
C;Date: 04-Dec-1997 #sequence\_revision 12-Dec-1997 #text\_change 03-Jun-2002  
C;Accession: S68394  
R;Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.  
FEBS Lett. 377, 163-166, 1995  
A;Title: Isolation of CF(0)CF(1) from *Chlamydomonas reinhardtii* cw15 and the N-terminus of the F1-ATPase  
A;Reference number: S68388; MUID:96128220; PMID:8543042  
A;Accession: S68394  
A;Molecule type: protein  
A;Residues: 1-19 <FIE>  
A;Experimental source: strain CW15  
C;Genetics:  
A;Genome: nuclear  
C;Keywords: chloroplast; hydrolase

Query Match 16.7%; Score 3; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 6.1e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
|||  
Db 16 GEE 18

RESULT 60  
E60894  
crystallin - Pacific cuttlefish (fragment)  
C;Species: *Sepia esculenta* (Pacific cuttlefish)  
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 02-Jun-1994  
C;Accession: E60894  
R;Chiou, S.H.  
J. Protein Chem. 7, 527-534, 1988  
A;Title: The protein sequence homology of gamma-crystallins among major vertebrate classes  
A;Reference number: A60894; MUID:89351593; PMID:3255376  
A;Accession: E60894  
A;Molecule type: protein  
A;Residues: 1-20 <CHI>  
C;Superfamily: glutathione transferase  
C;Keywords: eye lens

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EIL 15  
|||  
Db 15 EIL 17

RESULT 61  
A33160  
H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain - rat (fragment)  
C;Species: *Rattus norvegicus* (Norway rat)  
C;Date: 08-Mar-1991 #sequence\_revision 08-Mar-1991 #text\_change 03-Jun-2002  
C;Accession: A33160  
R;Godinot, C.  
submitted to the Protein Sequence Database, February 1991  
A;Reference number: A33160  
A;Accession: A33160  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <GOD>  
C;Superfamily: H+-transporting ATP synthase gamma chain  
C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; mitochondrion;

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17  
|||

Db 10 LKS 12

RESULT 62  
D49164  
Chromogranin-B - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-May-1997  
C:Accession: D49164  
R:Nielsen, E.; Wellinder, B.S.; Madsen, O.D.  
Endocrinology 129, 3147-3156, 1991  
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides  
A:Reference number: A49164; MUID:92063871; PMID:1954895  
A:Accession: D49164  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-20 <NIE>  
A:Note: sequence extracted from NCBI backbone (NCBIP:66368)  
C:Superfamily: chromogranin B precursor

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13  
|||  
Db 17 GEE 19

RESULT 63  
S00492  
hemocyanin chain Ia - Japanese spiny lobster (fragment)  
C:Species: Panulirus japonicus (Japanese spiny lobster)  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 01-Aug-1997  
C:Accession: S00492  
R:Makino, N.; Kimura, S.  
Eur. J. Biochem. 173, 423-430, 1988  
A:Title: Subunits of Panulirus japonicus hemocyanin. 1. Isolation and properties.  
A:Reference number: S00492; MUID:88196131; PMID:3360019  
A:Accession: S00492  
A:Molecule type: protein  
A:Residues: 1-20 <MAK>  
C:Superfamily: hemocyanin  
C:Keywords: copper; hemolymph; hexamer; oxygen carrier

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QDD 9  
|||  
Db 17 QDD 19

RESULT 64  
PN0154  
groEL-like protein - Thermus aquaticus (fragment)  
C:Species: Thermus aquaticus  
C:Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 17-Mar-1999  
C:Accession: PN0154  
R:Mikulik, K.; Benada, O.  
Biochem. Biophys. Res. Commun. 197, 716-721, 1993  
A:Title: GroEL-like protein complex of thermophilic bacterium Thermus aquaticus.  
A:Reference number: PN0154; MUID:94092153; PMID:7903530  
A:Accession: PN0154  
A:Molecule type: protein  
A:Residues: 1-20 <MIK>  
C:Comment: GroEL-like particles are homo-oligomeric complexes of two stacked seven membered rings.  
C:Superfamily: chaperonin groEL  
C:Keywords: molecular chaperone

Query Match 16.7%; Score 3; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16  
|||  
Db 3 ILK 5

RESULT 65  
I65242  
homeotic protein Hox-1 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 15-Oct-1999  
C:Accession: I65242  
R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A:Title: Cloning of rat homeobox genes.  
A:Reference number: I65242; MUID:95217128; PMID:7702549  
A:Accession: I65242  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-20 <RES>  
A:Cross-references: GB:S76293; NID:G913078  
C:Genetics:  
A:Gene: Hox-A; Hox-1  
C:Superfamily: unassigned homeobox proteins; homeobox homology  
C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RYQ 7  
|||  
Db 10 RYQ 12

RESULT 66  
PL0039  
outer membrane protein C class 5 - Neisseria meningitidis (fragment)  
C:Species: Neisseria meningitidis  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 18-Jun-1993  
C:Accession: PL0039  
R:Achtman, M.; Neibert, M.; Crowe, B.A.; Strittmatter, W.; Kusecek, B.; Wayse, E.; Wal  
J. Exp. Med. 168, 507-525, 1988  
A:Title: Purification and characterization of eight class 5 outer membrane protein var  
A:Reference number: PL0038; MUID:88316168; PMID:2457646  
A:Accession: PL0039  
A:Molecule type: protein  
A:Residues: 1-20 <ACH>  
A:Note: residues 17-18 are probably Lys-Ser  
C:Comment: The Neisseria meningitidis class 5 proteins are proposed to correspond to t  
C:Keywords: membrane protein

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17  
|||  
Db 16 LKS 18

RESULT 67  
S65746  
hypothetical protein 2 - Yersinia pseudotuberculosis (fragment)  
C:Species: Yersinia pseudotuberculosis  
C:Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 31-Mar-1997  
C:Accession: S65746  
R:Hobbs, M.; Reeves, P.R.  
Biochim. Biophys. Acta 1245, 273-277, 1995  
A:Title: Genetic organisation and evolution of Yersinia pseudotuberculosis 3,6-dideoxy  
A:Reference number: S65746; MUID:96125720; PMID:8541300

A;Accession: S65746  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-20 <HOB>

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LXS 17  
|||  
Db 11 LXS 13

RESULT 68  
S71017  
hypothetical protein - Streptococcus pneumoniae (fragment)  
C;Species: Streptococcus pneumoniae  
C;Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999  
R;Martin, B.; Sharples, G.J.; Humbert, O.; Lloyd, R.G.; Claverys, J.P.  
Mol. Microbiol. 19, 1035-1045, 1996  
A;Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involved  
A;Reference number: S71015; MUID:96249697; PMID:8830261  
A;Accession: S71017  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-20 <MAR>  
A;Cross-references: EMBL:Z49988  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEI 14  
|||  
Db 8 EEI 10

RESULT 69  
PS0188  
superoxide dismutase (EC 1.15.1.1) (Cu-Zn), chloroplast - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 05-Mar-1993 #sequence\_revision 05-Mar-1993 #text\_change 05-Mar-1999  
A;Accession: PS0188  
R;Kawakami, T.; Tsugita, A.  
submitted to JIPID, June 1991  
A;Reference number: PS0187  
A;Accession: PS0188  
A;Molecule type: protein  
A;Residues: 1-20 <RAW>  
A;Experimental source: leaf  
A;Function:  
A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
C;Keywords: chloroplast; copper; metalloprotein; oxidoreductase; zinc

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16  
|||  
Db 8 ILK 10

RESULT 70  
B30208  
hypothetical protein 1 (cpc-1 5' region) - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 18-Jun-1993  
A;Accession: B30208  
R;Paluh, J.L.; Orbach, M.J.; Legerton, T.L.; Yanofsky, C.

Proc. Natl. Acad. Sci. U.S.A. 85, 3728-3732, 1988  
A;Title: The cross-pathway control gene of Neurospora crassa, cpc-1, encodes a proteol:  
A;Reference number: A30208; MUID:88234499; PMID:2967496  
A;Accession: B30208  
A;Molecule type: DNA  
A;Residues: 1-20 <PAL>  
A;Cross-references: GB:J03262

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 3 KSL 5

RESULT 71  
S38763  
S-adenosyl-L-methionine decarboxylase alpha chain - Acanthamoeba castellanii  
C;Species: Acanthamoeba castellanii  
C;Date: 08-Jun-1994 #sequence\_revision 19-Apr-1996 #text\_change 07-May-1999  
A;Accession: S38763  
R;Hugo, E.R.; Byers, T.J.  
Biochem. J. 295, 203-209, 1993  
A;Title: S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii (Neff): pu:  
A;Reference number: S38763; MUID:94029912; PMID:8216217  
A;Accession: S38763  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <HUG>

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16  
|||  
Db 12 ILK 14

RESULT 72  
PC1151  
equinoxin 1C - sea anemone (Actinia equina) (fragment)  
C;Species: Actinia equina  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
A;Accession: PC1151  
R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.  
Chem. Pharm. Bull. 40, 2873-2875, 1992  
A;Title: Isolation and characterization of equinoxins from the sea anemone Actinia  
A;Reference number: PC1149; MUID:93099631; PMID:1361161  
A;Accession: PC1151  
A;Molecule type: protein  
A;Residues: 1-20 <KOM>  
C;Keywords: toxin

Query Match 16.7%; Score 3; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 6.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFF 4  
|||  
Db 15 TFF 17

RESULT 73  
B34016  
tenebrosin B - sea anemone (Actinia tenebrosa) (fragment)  
C;Species: Actinia tenebrosa  
C;Date: 15-Jun-1990 #sequence\_revision 15-Jun-1990 #text\_change 30-Sep-1993  
A;Accession: B34016  
R;Norton, R.S.; Bobek, G.; Ivanov, J.O.; Thomson, M.; Fiala-Beer, E.; Moritz, R.L.; S  
Toxicol. 28, 29-41, 1990



A:Title: Purification and characterisation of proteins with cardiac stimulatory and haem  
 A:Reference number: A34016; MUID:90232538; PMID:1970442  
 A:Accession: B34016  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-20 <NOR>

Query Match 16.7%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4  
 |||  
 Db 15 TFN 17

## RESULT 74

S78760

ribosomal protein MRP-L4, mitochondrial - bovine (fragments)

C:Species: Bos primigenius taurus (cattle)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: S78760

R:Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78760

A:Molecule type: protein

A:Residues: 1-11;12-20 &lt;GRA&gt;

C:Keywords: mitochondrion

Query Match 16.7%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3  
 |||  
 Db 6 ATF 8

## RESULT 75

S56005

lysosomal protein 22K - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 07-May-1999

C:Accession: S56005

R:Kuwana, I.; Mullock, B.M.; Luzio, J.P.

Biochem. J. 308, 937-946, 1995

A:Title: Identification of a lysosomal protein causing lipid transfer, using a fluoresce

A:Reference number: S56005; MUID:97104296; PMID:8948454

A:Accession: S56005

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-20 &lt;KUN&gt;

Query Match 16.7%; Score 3; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred.No. 6.4e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
 |||  
 Db 16 KSL 18

Search completed: November 25, 2003, 19:36:13  
 Job time : 13.3488 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:17:40 ; Search time 6.38372 Seconds  
(without alignments)  
132.600 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRYQDDHGEEILKSL 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1220

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4	22.2	10	1	TEMK_RANTE
2	3	16.7	9	1	SAMP_MUSCA
3	3	16.7	10	1	GLEM_HUMAN
4	3	16.7	10	1	SPI_HALRO
5	3	16.7	10	1	SYK_CAMUP
6	3	16.7	10	1	URA7_HUMAN
7	3	16.7	13	1	ODPA_CANFA
8	3	16.7	13	1	RS19_ASHYP
9	3	16.7	14	1	LPW_CITFR
10	3	16.7	14	1	LPW_SALTY
11	3	16.7	14	1	MAST_VESBA
12	3	16.7	15	1	AFP3_MALPA
13	3	16.7	15	1	CKX_WHEAT
14	3	16.7	15	1	ITR8_ALBUJU
15	3	16.7	15	1	METK_MAZE
16	3	16.7	15	1	MM01_RAT
17	3	16.7	15	1	PSAO_CUCSA
18	3	16.7	15	1	TRPA_LEUMA
19	3	16.7	16	1	ALL1_CALVO
20	3	16.7	16	1	UVSX_BPT6
21	3	16.7	17	1	GSHX_FINPS
22	3	16.7	19	1	ADC_CLOPA
23	3	16.7	19	1	COX4_ONCMY
24	3	16.7	19	1	DCAM_ACACA
25	3	16.7	19	1	TRPB_KLEAE
26	3	16.7	20	1	AF2L_MALPA
27	3	16.7	20	1	FIBB_FELCA
28	3	16.7	20	1	HCYA_PANJA
29	3	16.7	20	1	M117_BOVIN
30	3	16.7	20	1	SODM_HORVU
31	3	16.7	20	1	TENE_ACTTE
32	2	11.1	5	1	BIOA_CITFR
33	2	11.1	5	1	FARP_ARTTR

34	2	11.1	5	1	PRTC_PERAM
35	2	11.1	5	1	TRM3_ECOLI
36	2	11.1	6	1	UN06_CLOPA
37	2	11.1	7	1	CIA_ENTFA
38	2	11.1	7	1	EIO5_LITRU
39	2	11.1	7	1	FAR1_PROCL
40	2	11.1	7	1	FAR3_HABCO
41	2	11.1	7	1	FAR3_PANRE
42	2	11.1	7	1	UC24_MAZE
43	2	11.1	7	1	LANC_CARUI
44	2	11.1	7	1	UF03_MOUSE
45	2	11.1	8	1	AKH_TABAT
46	2	11.1	8	1	B44K_FORGI
47	2	11.1	8	1	CAD1_ENTFA
48	2	11.1	8	1	FAR4_HOMAM
49	2	11.1	8	1	HTP2_PERAM
50	2	11.1	8	1	LCK1_LEUMA
51	2	11.1	8	1	LCK3_LEUMA
52	2	11.1	8	1	LPMS_STAEP
53	2	11.1	8	1	RS1_ERWCH
54	2	11.1	8	1	RT34_BOVIN
55	2	11.1	8	1	UPAA_HUMAN
56	2	11.1	9	1	AL11_CARMA
57	2	11.1	9	1	ALC_CHIRE
58	2	11.1	9	1	BS43_SERPL
59	2	11.1	9	1	D1_NEPNO
60	2	11.1	9	1	DSIP_RABIT
61	2	11.1	9	1	FAR1_CALVO
62	2	11.1	9	1	FAR2_CALVO
63	2	11.1	9	1	FAR3_CALVO
64	2	11.1	9	1	FAR4_CALVO
65	2	11.1	9	1	FAR5_ASCSU
66	2	11.1	9	1	FAR5_CALVO
67	2	11.1	9	1	FAR5_PENMO
68	2	11.1	9	1	FAR6_CALVO
69	2	11.1	9	1	FAR7_CALVO
70	2	11.1	9	1	FAR7_CALVO
71	2	11.1	9	1	FAR7_CALVO
72	2	11.1	9	1	FARP_CALSI
73	2	11.1	9	1	FARB_CALVO
74	2	11.1	9	1	FIBB_BRYPA
75	2	11.1	9	1	FIBB_MACFU
76	2	11.1	9	1	FIBB_PAPHA
77	2	11.1	9	1	FRLF_SARBU
78	2	11.1	9	1	LITR_PHYRO
79	2	11.1	9	1	LMIP_LOCM1
80	2	11.1	9	1	LPCA_STAUI
81	2	11.1	9	1	MGMT_BOVIN
82	2	11.1	9	1	NEF_HVIZ8
83	2	11.1	9	1	NSK1_SARBU
84	2	11.1	9	1	ORYF_SCYCA
85	2	11.1	9	1	PTSP_BOMMO
86	2	11.1	9	1	RB42_LITRU
87	2	11.1	9	1	TAL1_PICJA
88	2	11.1	9	1	THYF_PIG
89	2	11.1	9	1	UF02_MOUSE
90	2	11.1	9	1	UHA2_HUMAN
91	2	11.1	9	1	ULAH_HUMAN
92	2	11.1	9	1	XYLA_STRSQ
93	2	11.1	10	1	AH3_FRUSE
94	2	11.1	10	1	AKHX_LOCM1
95	2	11.1	10	1	ANGT_CHICK
96	2	11.1	10	1	CA12_LITCI
97	2	11.1	10	1	CAER_LITXA
98	2	11.1	10	1	COXA_ONCMY
99	2	11.1	10	1	COXM_RAT
100	2	11.1	10	1	COXO_RAT

#### ALIGNMENTS

RESULT 1

ID TEMK\_RANTE STANDARD; PRT; 10 AA.  
 AC P56923;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tempurin K.  
 OS Rana temporaria (European common frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OX NCBI\_TaxID=8407;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=97175050; PubMed=5022710;  
 RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,  
 RA Barra D.;  
 RT "temporine, antimicrobial peptides from the European red frog Rana  
 RT temporaria";  
 RL Eur. J. Biochem. 242:788-792(1996).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 CC bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 CC -!- SIMILARITY: Belongs to the brevinin family.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD\_RES 10 10  
 FT SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;  
  
 Query Match 22.2%; Score 4; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 15 LKSL 18  
 DB 6 LKSL 9  
  
 RESULT 2  
 ID SAMP MUSCA STANDARD; PRT; 9 AA.  
 AC P19095;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Serum amyloid P-component (SAP) (Fragment).  
 OS Mustelus canis (Smooth dogfish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
 OC Mustelus.  
 OX NCBI\_TaxID=7812;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83160932; PubMed=6403520;  
 RA Robey F.A., Tanaka T., Liu T.-Y.;  
 RT "Isolation and characterization of two major serum proteins from the  
 RT dogfish, Mustelus canis, C-reactive protein and amyloid P  
 RT component";  
 RL J. Biol. Chem. 258:3889-3894(1983).  
 CC -!- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISC  
 CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
 CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
 CC -!- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.  
 DR PIR; B20569; B20569; Pentaxin.  
 DR InterPro; IPR001759; Pentaxin.  
 DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
 KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
 FT DOMAIN 1 >9  
 FT NON TER 9 9  
 FT SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 16 KSL 18  
 DB 5 KSL 7  
  
 RESULT 3  
 ID GLEM\_HUMAN STANDARD; PRT; 10 AA.  
 AC P02728;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Erythrocyte membrane glycopeptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72034940; PubMed=5286858;  
 RA Weiss J.B., Lote C.J., Bobinski H.;  
 RT "New low molecular weight glycopeptide containing triglycosylcysteine  
 RT in human erythrocyte membrane";  
 RL Nature New Biol. 234:25-26(1971).  
 CC -!- PTM: S-LINKED GLYCAN CONSISTS OF GLC-GLC-GLC TRISACCHARIDE.  
 CC -!- MISCELLANEOUS: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS  
 CC PEPTIDE IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN  
 CC ATTRIBUTED.  
 DR PIR; A03187; XGHUE.  
 KW Glycoprotein; Erythrocyte.  
 FT CARBOHYD 1 1  
 FT SEQUENCE 10 AA; 1049 MW; 239FEAALF5B18 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 9 DHG 11  
 DB 7 DHG 9  
  
 RESULT 4  
 ID SPI\_HALRO STANDARD; PRT; 10 AA.  
 AC Q10997;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Serine proteinase inhibitor (Fragment).  
 OS Halocynthia roretzi (Sea squirt).  
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;  
 OC Stolidobranchia; Pyuridae; Halocynthia.  
 OX NCBI\_TaxID=7729;  
 RN [1]  
 RP SEQUENCE  
 RC TISSUE=Hemolymph;  
 RX MEDLINE=96321313; PubMed=8759295;  
 RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;  
 RT "Purification and characterization of a 58,000-Da proteinase  
 RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia  
 RT roretzi";  
 RL Comp. Biochem. Physiol. 114B:1-9(1996).  
 CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.  
 DR InterPro; IPR000215; Serpin.  
 DR PROSITE; PS00284; SERPIN; PARTIAL.  
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.

```

FT  NON TER      10      10
SQ  SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  11 GEE 13
    |||
Db  5 GEE 7

RESULT 5
SYK CAMUP
ID_ SYK CAMUP      STANDARD;      PRT;      10 AA.
AC  Q46164;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE  (Fragment).
GN  LYSS.
OS  Campylobacter upsaliensis.
OC  Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC  Campylobacteraceae; Campylobacter.
OX  NCBI_TaxID=28080;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 43954;
RX  MEDLINE=97149302; PubMed=8996110;
RA  Bourke B., Rashid S.T., Bingham H.L., Chan V.L.;
RT  "Characterization of Campylobacter upsaliensis fur and its
RT  localization in a highly conserved region of the Campylobacter
RT  genome.";
RL  Gene 183:219-224 (1996).
CC  -!- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) = AMP + diphosphate
CC  + L-lysyl-tRNA(Lys).
CC  -!- COFACTOR: Binds 3 magnesium ions per subunit (By similarity).
CC  -!- SUBUNIT: Homodimer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC  -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CC  -----
DR  EMBL; L77076; AAB41342.1; -.
DR  HAWAP; MF_00252; -.
DR  InterPro; IPR006195; tRNA_ligase_II.
DR  PROSITE; PS50862; AA TRNA LIGASE II; PARTIAL.
KW  Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW  Metal-binding; Magnesium.
FT  NON TER      1
SQ  SEQUENCE 10 AA; 1218 MW; 9CEA46AB13372B05 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  15 LKS 17
    |||
Db  1 LKS 3

RESULT 6
URA7 HUMAN
ID_ URA7 HUMAN      STANDARD;      PRT;      10 AA.
AC  P34990;
DT  01-FEB-1994 (Rel. 28, Created)

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DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Unknown protein from 2D-page of red blood cells (Spot 2D-006HO)
DE  (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Erythrocyte;
RA  Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA  Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Waizer C.,
RA  Balant L., Hochstrasser D.F.;
RL  Submitted (Feb-1994) to the SWISS-PROT data bank.
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 4.77, ITS MW IS: 26 kDa.
CC  SWISS-2DPAGE; P34990; HUMAN.
FT  NON TER      10
SQ  SEQUENCE 10 AA; 1161 MW; F72D82E9C44B1871 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 HGE 12
    |||
Db  3 HGE 5

RESULT 7
ODPA CANFA
ID_ ODPA CANFA      STANDARD;      PRT;      13 AA.
AC  P49823;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Pyruvate dehydrogenase E1 component alpha subunit, somatic form
DE  (EC 1.2.4.1) (PDH-E1 type I) (Fragment).
GN  PDH-E1.
OS  Canis familiaris (Dog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX  NCBI_TaxID=9615;
RN  [1]
RP  SEQUENCE.
RC  TISSUE=Heart;
RX  MEDLINE=98163340; PubMed=9504812;
RA  Dunn M.J., Corbett J.M., Wheeler C.H.;
RT  "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT  dog heart proteins.";
RL  Electrophoresis 18:2795-2802 (1997).
CC  -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC  conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC  multiple copies of three enzymatic components: pyruvate
CC  dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC  lipoamide dehydrogenase (E3).
CC  -!- CATALYTIC ACTIVITY: Pyruvate + lipoamide = S-
CC  acetyldihydrolipoamide + CO(2).
CC  -!- COFACTOR: THIAMINE PYROPHOSPHATE.
CC  -!- ENZYME REGULATION: E1 ACTIVITY IS REGULATED BY PHOSPHORYLATION
CC  (INACTIVATION) AND DEPHOSPHORYLATION (ACTIVATION) OF THE ALPHA
CC  SUBUNIT (BY SIMILARITY).
CC  -!- SUBUNIT: Tetramer of two alpha and two beta subunits.
CC  -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
DR  HSC-2DPAGE; P49823; DOG.
KW  Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate;
KW  Mitochondrion; Phosphorylation.
FT  NON TER      13
SQ  SEQUENCE 13 AA; 1510 MW; C97EEBF844085B19 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATF 3
Db 4 ATF 6

RESULT 8
RS19_ASHYP STANDARD; PRT; 13 AA.
AC Q4452;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (fragment).
GN RPSS OR RPS19.
OS Ash yellow phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35780;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
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or send an email to license@isb-sib.ch).
CC EMBL; L26999; AAA83936.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON TER 1
SQ SEQUENCE 13 AA; 1433 MW; CECA010B84E6305D CRC64;

Query Match 16.7%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 ILK 16
Db 3 ILK 5

RESULT 9
LPW_CITFR STANDARD; PRT; 14 AA.
AC P03056;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE trp operon leader peptide.
GN TRPL.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATF 3
Db 3 ATF 5

RESULT 10
LPW_SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Trp operon leader peptide.
GN TRPL OR TRPEE OR STM722.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=78196931; PubMed=351195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
regions of the tryptophan operons of Escherichia coli and Salmonella
typhimurium.";
RL J. Mol. Biol. 121:193-217(1978).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RN Nature 413:852-856(2001).
CC CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
OF TRYPTOPHAN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; M24960; -. NOT_ANNOTATED_CDS.

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DR EMBL; AE008776; AAL20640.1; -.
DR PIR; A03590; LFEBWT.
DR StyGene; SG10400; trpl.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA; 1635 MW; 49F22A47362248E7 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
Db 3 ATF 5

RESULT 11
MAST_VESBA
ID MAST_VESBA STANDARD; PRT; 14 AA.
AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan B.
OS Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7444;
RN [1]
RP TISSUE=Venom;
RC MEDLINE=91174755; PubMed=2006909;
RA Lo C.-L., Hwang L.-L.;
RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet Vespa basalis.";
RL Biochem. J. 274:453-456(1991).
CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
KW PIR; S14336; S14336.
KW Mast cell degranulation; Amidation.
FT MOD_RES 14
SQ SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;

Query Match      16.7%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17
Db 3 LKS 5

RESULT 12
AFP3_MALPA
ID AFP3_MALPA STANDARD; PRT; 15 AA.
AC P83137;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 3 (CW-3) (Fragment).
OS Malva parviflora (Little mallow) (Cheeseweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
OX NCBI_TaxID=145753;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21193399; PubMed=11302747;
RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
RT "Purification and characterization of three antifungal proteins from
RT cheeseweed (Malva parviflora).";
RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).

CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not P.graminearum.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0007275; P:development; NAS.
KW Fungicide; Antibiotic.
FT NON_TER 15
SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match      16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
Db 7 RYQ 9

RESULT 13
CKX_WHEAT
ID CKX_WHEAT STANDARD; PRT; 15 AA.
AC P58763;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytokinin oxidase (EC 1.4.3.-) (CKO) (CKX) (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=cv. Samantha;
RX MEDLINE=21099312; PubMed=11168382;
RA Galuska P., Frobort I., Sebel M., Sauer P., Jacobsen S., Pec P.;
RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
RT degradation in cereals.";
RL Eur. J. Biochem. 268:450-461(2001).
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
CC substituted adenine derivatives that are plant hormones, where the
CC substituent is an isopentenyl group. Substrate preference is 2-(2-
CC hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
CC zeatin riboside.
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-en-1-yl)adenine + H(2)O +
CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -!- COFACTOR: FAD.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).
CC -!- MISCELLANEOUS: Optimal pH is 6.5.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
KW Oxidoreductase; Flavoprotein; FAD.
FT UNSURE 1
FT UNSURE 13
FT NON_TER 15
SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCDEF CRC64;

Query Match      16.7%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
Db 4 KSL 6

RESULT 14
ITRB_ALBU
ID ITRB_ALBU STANDARD; PRT; 15 AA.
AC P24927;

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DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Trypsin inhibitor B chain (Fragment).  
 OS Albizzia julibrissin (Silk tree).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosoids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizzia.  
 OX NCBI\_TaxID=3813;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Seed;  
 RX MEDLINE=80115605; PubMed=528539;  
 RA Odani S., Ono T., Ikenaka T.;  
 RT "Proteinase inhibitors from a mimosoideae legume, Albizzia  
 RL Julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";  
 RL J. Biochem. 86:1795-1805(1979).  
 CC -!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.  
 CC -!- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A  
 CC -!- DISULFIDE BOND.  
 CC -!- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR  
 CC FAMILY.  
 KW Serine protease inhibitor.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 DDH 10  
 DB 2 DDH 4

RESULT 15  
 METK MAIZE  
 ID NETK\_MAIZE STANDARD; PRT; 15 AA.  
 AC P80616;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Probable S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine  
 DE adenosyltransferase) (AdoMet synthetase) (Spot 178) (Fragment).  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=coleoptile;  
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
 RA Pernollet J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 RT genome analysis program.";  
 RL Theor. Appl. Genet. 93:997-1005(1996).  
 CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM  
 CC METHIONINE AND ATP.  
 CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +  
 CC diphosphate + S-adenosyl-L-methionine.  
 CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and  
 CC 1 potassium ion per subunit (Potential).  
 CC -!- PATHWAY: Activated methyl cycle.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
 CC PROTEIN IS: 5.9. ITS MW IS: 43.3 kDa.  
 CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.  
 DR Maize-2DPAGE; P80616; COLEOPTILE.  
 DR MaizeDB; 123938; -.  
 DR InterPro; IPR002133; S-AdoMet synt.  
 DR Pfam; PF02772; S-AdoMet syntD2; 1.  
 DR PROSITE; PS00376; ADOMET SYNTHETASE 1; PARTIAL.  
 DR PROSITE; PS00377; ADOMET SYNTHETASE 2; PARTIAL.

KW Transferase; One-carbon metabolism; Multigene family; ATP-binding;  
 KW Magnesium; Potassium; Metal-binding.  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1601 MW; 232B07E9AC328D32 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 EBI 14  
 DB 3 EBI 5

RESULT 16  
 MM01 RAT  
 ID MM01\_RAT STANDARD; PRT; 15 AA.  
 AC P81563;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)  
 DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (Fragment).  
 GN MMP1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=96201136; PubMed=8605638;  
 RA Tyagi S.C., Cleutjens J.P.M.;  
 RT "Myocardial collagenase: purification and structural  
 RT characterization";  
 RL Can. J. Cardiol. 12:165-171(1996).  
 CC -!- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN  
 CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY  
 CC PLAY A ROLE IN THE DETRIORATION OF THE HEART WALL EXTRACELLULAR  
 CC MATRIX PROTEINS DURING THE ONSET OF DILATED CARDIOMYOPATHY.  
 CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native  
 CC collagens. Cleavage of the triple helix of collagen at about three-  
 CC quarters of the length of the molecule from the N-terminus, at  
 CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic  
 CC substrates and alpha-macroglobulins at bonds where Pi' is a  
 CC hydrophobic residue.  
 CC -!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.  
 CC -!- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE  
 CC ACTIVATION PEPTIDE.  
 CC -!- PTM: THE N-TERMINAL IS BLOCKED.  
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.  
 KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;  
 KW Extracellular matrix.  
 FT NON TER 1 1  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKS 17  
 DB 3 LKS 5

RESULT 17  
 PS00 CUCSA  
 ID PS00 CUCSA STANDARD; PRT; 15 AA.  
 AC P42052;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Photosystem I reaction centre subunit 8 (Photosystem I 17.5 kDa  
 GN protein) (Fragment).  
 GN PSAM.  
 OS Cucumis sativus (Cucumber).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.  
 OX NCBI\_TaxID=3659;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Cotyledon; PubMed=1883835;  
 RX MEDLINE=91355209; Iwasaki Y., Hibino T., Takabe T.;  
 RA "Characterization of genes that encode subunits of cucumber PS I  
 RT complex by N-terminal sequencing."; (1991).  
 RL Biochim. Biophys. Acta 1059:141-148 (1991).  
 CC -!- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.  
 DR PIR; E56819; E56819.  
 KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid; Membrane.  
 FT NON TER 15 15  
 SQ SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 7 QDD 9  
 Db 12 QDD 14  
  
 RESULT 18  
 TRPA LEUMA  
 ID TRPA LEUMA STANDARD; PRT; 15 AA.  
 AC F81753;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Tachykinin-related peptide 10 (LemRP 10).  
 OS Leucophaea maderae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6983;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Brain;  
 RX MEDLINE=97269266; PubMed=9114447;  
 RA Muren J.E., Naessel D.R.;  
 RT "Seven tachykinin-related peptides isolated from the brain of the  
 RT Madeira cockroach; evidence for tissue-specific expression of  
 RT isoforms."; (1997).  
 RL Peptides 18:7-15 (1997).  
 CC -!- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY  
 CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: BRAIN.  
 CC -!- MASS SPECTROMETRY: MW=1436.0; METHOD=WALDI.  
 CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide.  
 SQ SEQUENCE 15 AA; 1438 MW; 298572F373FA7007 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 ATF 3  
 Db 9 ATF 11  
  
 RESULT 19

ALL1 CALVO  
 ID ALL1 CALVO STANDARD; PRT; 16 AA.  
 AC P41839;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Callatostatin 1 (Leu-callatostatin 1) [Contains: Callatostatin 2 (Leu-  
 DE Callatostatin 2); Callatostatin 3 (Leu-callatostatin 3)].  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain, Head, and Thoracic ganglion;  
 RX MEDLINE=93211980; PubMed=8460157;  
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
 RA Thorpe A.;  
 RT "Callatostatin: neuropeptides from the blowfly Calliphora vomitoria  
 RT with sequence homology to cockroach allatostatins."; (1993).  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460 (1993).  
 RN [2]  
 RP CHARACTERIZATION.  
 RX MEDLINE=94291167; PubMed=8020069;  
 RA Duve H., Thorpe A.;  
 RT "Distribution and functional significance of Leu-callatostatins in  
 RT the blowfly Calliphora vomitoria."; (1994).  
 RL Cell Tissue Res. 276:367-379 (1994).  
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY  
 CC A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE  
 CC INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO  
 CC BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO  
 CC FULFILL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.  
 CC -!- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL  
 CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY  
 CC SYSTEM AND INTESTINE.  
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 DR PIR; A47393; A47393.  
 KW Neuropeptide; Amidation.  
 FT PEPTIDE 1 16 CALLATOSTATIN 1.  
 FT PEPTIDE 3 16 CALLATOSTATIN 2.  
 FT PEPTIDE 9 16 CALLATOSTATIN 3.  
 FT MOD RES 16 16 AMIDATION.  
 SQ SEQUENCE 16 AA; 1907 MW; A435B6C26EC3D09 CRC64;  
  
 Query Match 16.7%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 4 NRY 6  
 Db 10 NRY 12  
  
 RESULT 20  
 UVSX BPT6  
 ID UVSX BPT6 STANDARD; PRT; 16 AA.  
 AC Q06728;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Recombination and repair protein (fragment).  
 GN UVSX.  
 OS Bacteriophage T6.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;  
 OC T4-like viruses.  
 OX NCBI\_TaxID=10666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93219141; PubMed=8464751;  
 RA Winkler M., Rueger W.;  
 RT "Cloning and sequencing of the genes of



RT beta-glucosyl-HMC-alpha-glucosyl-transferases of bacteriophages T2  
 RL and T6";  
 RL Nucleic Acids Res. 21:1500-1500(1993).  
 CC -!- FUNCTION: IMPORTANT IN GENETIC RECOMBINATION, DNA REPAIR, AND  
 CC REPLICATION. POSSESSES PAIRING AND STRAND-TRANSFER ACTIVITY.  
 CC INTERACTS WITH DDA AND GENE 32 PROTEINS.  
 CC -!- SIMILARITY: Belongs to the recA family.  
 CC -----  
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 CC -----  
 CC EMBL; X68725; CAA48668.1; -.  
 DR PIR; S35627; S35627.  
 KW DNA damage; DNA replication; DNA recombination; DNA repair;  
 KW ATP-binding. 16 16  
 FT NON\_TER 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;  
 SQ SEQUENCE 16 AA; 1721 MW; 48164C95D76F3CB4 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKS 17  
 Db 6 LKS 8  
 RESULT 21  
 GSXH\_PINPS STANDARD; PRT; 17 AA.  
 AC P81087;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Glutathione peroxidase homolog (EC 1.1.1.9) (Water stress responsive  
 DE proteins 8 and 9) (Fragment).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=98418576; PubMed=9747804;  
 RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;  
 FT "Water-deficit-responsive proteins in maritime pine.";  
 RL Plant Mol. Biol. 38:587-596(1998).  
 RN [2]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 FT "Separation and characterization of needle and xylem maritime pine  
 FT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- CATALYTIC ACTIVITY: 2 glutathione + H(2)O(2) = oxidized  
 CC glutathione + 2 H(2)O.  
 CC -!- INDUCTION: BY water stress.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 5.6 TO 6.7, ITS MW IS: 20 TO 23 kDa.  
 CC -!- SIMILARITY: Belongs to the glutathione peroxidase family.  
 DR InterPro: IPR000889; Glut\_peroxidase.  
 DR Pfam: PF00255; GSHpx; 1.  
 DR PROSITE: PS00460; GLUTATHIONE\_PEROXID\_1; PARTIAL.  
 DR PROSITE: PS00763; GLUTATHIONE\_PEROXID\_2; 1.  
 KW Peroxidase; Oxidoreductase.  
 FT NON\_TER 1 1

FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1943 MW; 4D245E9B657868C1 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 LKS 15  
 Db 7 LKS 9  
 RESULT 22  
 ADC\_CLOPA STANDARD; PRT; 19 AA.  
 ID ADC\_CLOPA  
 AC P81336;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Acetoacetate decarboxylase (EC 4.1.1.4) (ADC) (AAD) (CP 28/CP 29)  
 DE (Fragment).  
 OS Clostridium pasteurianum.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium  
 OX NCBI\_TaxID=1501;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=W5;  
 RX MEDLINE=98291870; PubMed=9629918;  
 RA Flengsrud R., Skjeldal L.;  
 RT "Two-dimensional gel electrophoresis separation and N-terminal  
 RT sequence analysis of proteins from Clostridium pasteurianum W5.";  
 RL Electrophoresis 19:802-806(1998).  
 CC -!- FUNCTION: Catalyzes the conversion of acetoacetate to acetone and  
 CC carbon dioxide.  
 CC -!- CATALYTIC ACTIVITY: Acetoacetate + H(+) = acetone + CO(2).  
 CC -!- SIMILARITY: Belongs to the ADC family.  
 DR HAMAP; MF\_00597; -; 1.  
 KW Lyase; Decarboxylase.  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2078 MW; 6ACDAA91103AEC31 CRC64;  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKS 17  
 Db 2 LKS 4  
 RESULT 23  
 COX4\_ONCMY STANDARD; PRT; 19 AA.  
 ID COX4\_ONCMY  
 AC P80327;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragments).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Heart;  
 RX MEDLINE=94237150; PubMed=8181469;  
 RA Freund R., Kadenbach B.;  
 FT "Identification of tissue-specific isoforms for subunits Vb and VIIa  
 FT of cytochrome c oxidase isolated from rainbow trout.";  
 RL Eur. J. Biochem. 221:1111-1116(1994).

CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE  
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN  
 CC MITOCHONDRIAL ELECTRON TRANSPORT.  
 CC -!- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE IV FAMILY.  
 DR PIR: S43624; S43624.  
 KW Oxidoreductase; Inner membrane; Mitochondrion.  
 FT NON\_CONS 9 10  
 FT NON\_TER 19 19  
 FT SEQUENCE 19 AA; 1963 MW; 9280E1D8EC77987E CRC64;  
 SQ  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 ILK 12  
 Db 3 HGE 5

RESULT 24  
 DCAM ACACA  
 ID DCAM ACACA STANDARD; PRT; 19 AA.  
 AC P34039.  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE S-adenosylmethionine decarboxylase alpha subunit (EC 4.1.1.50)  
 DE (AdoMetDC) (SamDC) (Fragment).  
 OS Eukaryota; Acanthamoeba; Acanthamoeba.  
 OC Eukaryota; Acanthamoebidae; Acanthamoeba.  
 OX NCBI\_TaxID=5755;  
 RN [1]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RX MEDLINE=94029912; PubMed=8216217;  
 RA HUGO E.R., Byers T.J.;  
 RT "S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii  
 RT (Neff): purification and properties.";  
 RL Biochem. J. 295:203-209(1993).  
 CC -!- FUNCTION: S-ADENOSYLMETHIONINE DECARBOXYLASE IS ESSENTIAL FOR THE  
 CC BIOSYNTHESIS OF SPERMINE AND SPERMIDINE. THE ALPHA SUBUNIT  
 CC CONTAINS THE ACTIVE SITE.  
 CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (S-deoxy-5-  
 CC adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).  
 CC -!- COFACTOR: Pyruvoyl group.  
 CC -!- PATHWAY: DECARBOXYLATION OF S-ADENOSYLMETHIONINE PROVIDES THE  
 CC AMINOPROPYL MOIETY REQUIRED FOR SPERMIDINE AND SPERMINE  
 CC BIOSYNTHESIS FROM PUTRESCINE.  
 CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA CHAINS.  
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED ONLY DURING EXPONENTIAL GROWTH.  
 CC -!- INDUCTION: STIMULATED BY PUTRESCINE. INHIBITED BY AROMATIC  
 CC DIAMIDINES BERENIL, PENTAMIDINE, PROPAMIDINE, HYDROXYSTILBAMIDINE,  
 CC BY ETHIDIUM BROMIDE AND METHYLGLYOXAL.  
 CC -!- SIMILARITY: BELONGS TO THE EUKARYOTIC ADOMETDC FAMILY.  
 DR PIR: S38763; S38763.  
 DR InterPro; IPR001985; SAM decarbox.  
 DR Pfam; PF01536; SAM decarbox; 1.  
 DR PROSITE; PS01336; ADOMETDC; PARTIAL.  
 KW Spermidine biosynthesis; Lyase; Decarboxylase; Pyruvate.  
 FT MOD\_RES 1 1 CONVERTED TO A PYRUVOYL GROUP.  
 FT NON\_TER 19 19  
 FT SEQUENCE 19 AA; 2153 MW; 88B18AD9B6142AEF CRC64;  
 SQ  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 14 ILK 16  
 Db 11 ILK 13

RESULT 25  
 TRPB KLEAE  
 ID TRPB KLEAE STANDARD; PRT; 19 AA.  
 AC P14552;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tryptophan synthase beta chain (EC 4.2.1.20) (Fragment).  
 GN TRPB.  
 GN Klebsiella aerogenes.  
 OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Klebsiella.  
 OX NCBI\_TaxID=28451;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81199002; PubMed=6262736;  
 RA Nichols B.P., Blumenberg M., Yanofsky C.;  
 RT "Comparison of the nucleoside sequence of trpA and sequences  
 RT immediately beyond the trp operon of Klebsiella aerogenes. Salmonella  
 RT typhimurium and Escherichia coli.";  
 RL Nucleic Acids Res. 9:1743-1755(1981).  
 CC -!- FUNCTION: The beta subunit is responsible for the synthesis of L-  
 CC tryptophan from indole and L-serine.  
 CC -!- CATALYTIC ACTIVITY: L-serine + L-(indol-3-yl)glycerol 3-phosphate  
 CC = L-tryptophan + glyceraldehyde 3-phosphate.  
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -!- PATHWAY: Tryptophan biosynthesis; fifth (last) step.  
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By  
 CC similarity).  
 CC -!- SIMILARITY: BELONGS TO THE TRPB FAMILY.  
 CC  
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 CC  
 CC EMBL; V00630; CAA23901.1; -;  
 CC EMBL; J01738; AAA25144.1; -;  
 CC HSSP; P00933; 2TYS.  
 CC HAWAP; MF 00133; -; 1.  
 CC InterPro; IPR006653; Trp synth b rel.  
 CC PROSITE; PS00168; TRP SYNTHASE BETA; PARTIAL.  
 CC Tryptophan biosynthesis; Pyridoxal phosphate; Lyase.  
 CC NON\_TER 1 1  
 CC SEQUENCE 19 AA; 2183 MW; 82864627BF574E2C CRC64;  
 SQ  
 Query Match 16.7%; Score 3; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 14 ILK 16  
 Db 12 ILK 14

RESULT 26  
 AF2L MALPA  
 ID AF2L MALPA STANDARD; PRT; 20 AA.  
 AC P83143;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Antifungal protein 2 large subunit (CW-2) (Fragment).  
 OS Malva parviflora (little mallow) (Cheeseweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids II; Malvales; Malvaceae; Malvoideae; Malva.  
 OX NCBI\_TaxID=145753;  
 RN [1]

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RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=20568734; PubMed=11118343;
RA Wang X., Bunkers G.J.;
RT "Potent heterologous antifungal proteins from cheeseeweed (Malva
RL parviflora).";
RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
CC not F.graminearum.
CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
CC concentration.
CC GO: GO:0003799; F:antifungal peptide activity; IDA.
KW Fungicide; Antibiotic.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2603 MW; 6E766A5E342036DA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RYQ 7
DB 7 RYQ 9

RESULT 27
ID FIBB_FELCA STANDARD; PRT; 20 AA.
AC P14469;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals. ";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 20 FIBRINOPEPTIDE B.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2328 MW; A829E393B8F627D0 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13
DB 8 GEE 10

RESULT 28
ID HCVA_PANJA STANDARD; PRT; 20 AA.
AC P82310;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin subunit 1a (Fragment).
OS Panulirus japonicus (Japanese spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuroidea; Palinuridae; Panulirus.
OX NCBI_TaxID=6736;
RN [1]
RP SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=88196131; PubMed=3360019;
RA Makino N., Kimura S.;
RT "Subunits of Panulirus japonicus hemocyanin. 1. Isolation and
RL properties. ";
RL Eur. J. Biochem. 173:423-430(1988).
CC -!- FUNCTION: Hemocyanins are copper-containing oxygen carriers
CC occurring freely dissolved in the hemolymph of many mollusks and
CC arthropods.
CC -!- SUBUNIT: Composed of 3 major subunits (IB, II and III) and 1 minor
CC subunit (IA) which form homohexamers and heterohexamers. May also
CC form larger structures.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Hemolymph.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
CC PIR; S00492; S00492.
DR InterPro; IPR000896; Hemocyanin.
DR InterPro; IPR002227; Tyrosinase.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
DR PROSITE; PS00497; TYROSINASE_1; PARTIAL.
DR PROSITE; PS00498; TYROSINASE_2; PARTIAL.
KW Transport; Oxygen transport; Copper; Hemolymph.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2154 MW; 313B8E456DDDE09 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9
DB 17 QDD 19

RESULT 29
ID M117_BOVIN STANDARD; PRT; 20 AA.
AC P35451;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 17 kDa milk glycoprotein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk;
RX MEDLINE=93308294; PubMed=8320368;
RA Soerensen E.S., Petersen T.E.;
RT "Purification and characterization of three proteins isolated from
RT the proteose peptone fraction of bovine milk. ";
RL J. Dairy Res. 60:189-197(1993).
CC -!- PTM: N-GLYCOSYLATED.
CC -!- SIMILARITY: TO CAMEL WHEY PROTEIN.
KW Glycoprotein; Milk.
FT NON_TER 1 1
FT NON_TER 20 20

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SQ SEQUENCE 20 AA; 2233 MW; 4CCA589404C62C27 CRC64;
Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILK 16
    |||
DB 16 ILK 18

RESULT 30
SODM HORVU STANDARD; PRT; 20 AA.
AC P28524;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Superoxide dismutase [Mn], mitochondrial (EC 1.15.1.1) (Fragment).
GN SODA.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RC STRAIN=sv. CM 72; TISSUE=Root;
RA Harkman W.J., Tao H.P., Tanaka C.K.;
RT "Germin-like polypeptides increase in barley roots during salt stress.";
RL Plant Physiol. 97:366-374 (1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Manganese (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
CC FAMILY.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR PROSITE; PS00088; SOD MM; PARTIAL.
KW Oxidoreductase; Manganese; Mitochondrion.
FT NON TER 20
SQ SEQUENCE 20 AA; 2152 MW; 7F7CAE8DFF1C9657 CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATF 3
    |||
DB 2 ATF 4

RESULT 31
TENB_ACTTE STANDARD; PRT; 20 AA.
AC P30834;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tenebrosin B (Fragment).
OS Actinia tenebrosa (Australian red waratah sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Actinia.
OX NCBI_TaxID=6105;
RN [1]
RP SEQUENCE.
RX MEDLINE=90232538; PubMed=1970442;
RA Norton R.S., Bobek G., Ivanov J.O., Thomson M., Fiala-Beer E.,
RA Moritz R.L., Simpson R.J.;

SQ SEQUENCE 20 AA; 1960 MW; FA32B426009FF5FA CRC64;

Query Match 16.7%; Score 3; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
    |||
DB 15 TFN 17

RESULT 32
BIOA_CITFR STANDARD; PRT; 5 AA.
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
DE (EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
DE aminotransferase) (Fragment).
GN BIOA.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;
RA Shiuian D., Campbell A.;
RT "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211 (1988).
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC diaminononanoate.
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- PATHWAY: Biotin biosynthesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to class-III of pyridoxal-phosphate-dependent
CC aminotransferases.
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EMBL; M21922; -; NOT_ANNOTATED_CDS.
DR F01; 140697; I40697.
DR InterPro; IPR005814; Aminotrans 3.
DR PROSITE; PS00600; AA_TRANSFER CLASS 3; PARTIAL.
KW Biotin biosynthesis; Transferase; Aminotransferase;
KW Pyridoxal phosphate.
FT NON TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 8 DD 9  
Db 4 DD 5

## RESULT 33

FARP ARTTR STANDARD; PRT; 5 AA.  
-AC P41853;  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE FWRamide-like neuropeptide RYIRP-amide.  
OS Atioposchia triangulata (New Zealand flatworm).  
OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;  
OC Terricola; Geoplanidae; Arthurdendyus.  
ON NCBI\_TaxID=132421;  
RN [1]  
RP SEQUENCE AND SYNTHESIS.  
RX MEDLINE=94211927; PubMed=7909164;  
RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;  
RT "YIRamide: a turbellarian FWRamide-related peptide (FARP).";  
RL Regul. Pept. 50:37-43(1994).  
CC -1- SIMILARITY: BELONGS TO THE FARP (FWRAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 5 5  
SQ SEQUENCE 5 AA; 754 MW; 69D4004B44600000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred.No.1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RY 6  
Db 1 RY 2

## RESULT 34

PRCT PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.  
OS Periplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;  
OC Blattidae; Periplaneta.  
ON NCBI\_TaxID=6978, 6850, 6759;  
RN [1]  
RP SEQUENCE.  
RC SPECIES=P.americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Starratt A.N., Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
in insects.";  
RL Life Sci. 17:1253-1256(1975).  
RN [2]  
RP BIOLOGICAL SOURCE.  
RC SPECIES=P.americana;  
RX MEDLINE=81225865; PubMed=6113690;  
RA O'Shea M., Adams M.E.;  
RT "Pentapeptide (proctolin) associated with an identified neuron.";  
RL Science 213:567-569(1981).  
RN [3]  
RP SEQUENCE.  
RC SPECIES=L.polyphemus;  
RX MEDLINE=90287800; PubMed=2356151;

RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,  
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
RA Shabanowitz J.;  
RT "Identification of proctolin in the central nervous system of the  
RT horseshoe crab, Limulus polyphemus.";  
RL Peptides 11:205-211(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES=C.maenas;  
RX MEDLINE=86232789; PubMed=2872661;  
RA Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
RT pericardial organs of the shore crab, Carcinus maenas.";  
RL Peptides 7:67-72(1986).  
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY.  
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
CC THE CRAB PERICARDIAL ORGANS.  
CR PIR; A01644; HOROHA.  
DR PIR; A60411; A60411.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred.No.1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RY 6  
Db 1 RY 2

## RESULT 35

TRM3\_ECOLI STANDARD; PRT; 5 AA.  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Tram protein (Fragment).  
GN TRAM.  
OS Escherichia coli.  
OC Plasmid IncFII R100.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
ON NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88227859; PubMed=2836369;  
RA Inamoto S., Yoshiooka Y., Ohtsubo E.;  
RT "Identification and characterization of the products from the traJ  
RT and traY genes of plasmid R100.";  
RL J. Bacteriol. 170:2749-2757(1988).  
CC -1- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION  
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- SIMILARITY: BELONGS TO THE TRAM FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license@isb-sib.ch).  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; M20941; -; NOT\_ANNOTATED\_CDS.  
DR PIR; A32014; A32014.  
KW Conjugation; Plasmid; DNA-binding.  
FT NON\_TER 1  
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA4435000000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EE 13  
||  
Db 4 EE 5

RESULT 36  
UN06 CLOPA STANDARD; PRT; 6 AA.  
ID UN06 CLOPA  
AC P81351;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE Unknown protein CP 6 from 2D-page (Fragment).  
OS Clostridium pasteurianum.  
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
OC Clostridium.  
OX NCBI\_TaxID=1501;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=W5;  
RX MEDLINE=96291870; PubMed=9629918;  
RA Flengsrud R., Skjeldal L.;  
RT "Two-dimensional gel electrophoresis separation and N-terminal  
sequence analysis of proteins from Clostridium pasteurianum W5.";  
RL Electrophoresis 19:802-806(1998).  
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
PROTEIN IS: 5.0, ITS MW IS: 75.9 kDa.  
FT NON TER  
PT 6  
SQ SEQUENCE 6 AA; 657 MW; 605B1DCL1A45A8000 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EI 14  
||  
Db 5 EI 6

RESULT 37  
CIA\_ENTFA STANDARD; PRT; 7 AA.  
ID CIA\_ENTFA  
AC F11932;  
DT 01-OCT-1989 (Rel. 12, Created)  
DT 01-OCT-1989 (Rel. 12, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone CAM373 (Clumping-inducing agent) (CIA).  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87005252; PubMed=3093276;  
RA Morie M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,  
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;  
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,  
CAM373.";  
RL FEBS Lett. 206:69-72(1986).  
CC -!- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS  
HARBORING PAM373.  
CC -!- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR  
SPECIFICITY OF PHEROMONES TO PLASMIDS.  
CC -!- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.  
DR PIR; A25269; A25269.  
KW Pheromone.  
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 IL 15  
||  
Db 4 IL 5

RESULT 38  
EI05\_LITRU STANDARD; PRT; 7 AA.  
ID EI05\_LITRU  
AC P82101;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Electrin 5.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amphibian defense peptide; Amidation.  
FT MOD RES  
PT 7  
SQ SEQUENCE 7 AA; 834 MW; 6DD05B076H0B5030 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EI 14  
||  
Db 5 EI 6

RESULT 39  
FARI\_PROCL STANDARD; PRT; 7 AA.  
ID FARI\_PROCL  
AC P38499;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Cardiac excitatory FMRFamide homolog Nrl.  
OS Procambiar clarkii (Red swamp crayfish).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
OC Astacoidea; Cambaridae; Procambiarus.  
OX NCBI\_TaxID=6728;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Pericardial organs;  
RX MEDLINE=93248032; PubMed=8387183;  
RA Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;  
RT "Isolation of two FMRFamide-related peptides from crayfish  
pericardial organs.";  
RL Peptides 14:137-143(1993).  
CC -!- FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS  
CONTRACTIONS OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF  
EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.  
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD RES  
PT 7  
SQ SEQUENCE 7 AA; 966 MW; 69D40729C4540420 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0

QY 4 NR 5  
||  
Db 1 NR 2

RESULT 40  
FAR3\_HAECO  
ID FAR3\_HAECO STANDARD; PRT; 7 AA.  
AC P81258; (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRFamide-like neuropeptide PF3 (KSAYMRF-amide).  
OS Haemochus contortus (Barber pole worm).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.  
OX NCBI\_TaxID=6289;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Neuron;  
RX MEDLINE=99318264; PubMed=10391380;  
RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,  
RA Geary T.G., Shaw C.;  
RT "Structural characterisation and pharmacology of KHEYLRFamide (AF2)  
and KSAYMRFamide (PF3/AF8) from Haemonchus contortus.";  
RL Mol. Biochem. Parasitol. 100:185-194(1999).  
CC -|- FUNCTION: ACTIVE ON NEUROMUSCULATURE.  
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0

QY 16 KS 17  
||  
Db 1 KS 2

RESULT 41  
FAR3\_PANRE  
ID FAR3\_PANRE STANDARD; PRT; 7 AA.  
AC P41874;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE FMRFamide-like neuropeptide PF3 (KSAYMRF-amide).  
OS Panagrellus redivivus.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
OX NCBI\_TaxID=6233;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RX MEDLINE=94235053; PubMed=8179635;  
RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,  
RA Geary T.G., Thim L.;  
RT "KSAYMRFamide: a novel FMRFamide-related heptapeptide from the free-  
living nematode, Panagrellus redivivus, which is myoactive in the  
parasitic nematode, Ascaris suum.";  
RL Biochem. Biophys. Res. Commun. 200:973-980(1994).  
CC -|- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT  
CC MUSCLE TENSION INCREASE.  
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
CC FAMILY.  
DR PIR; PC21132.  
KW Neuropeptide; Amidation.  
FT MOD\_RES 7  
SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

SQ SEQUENCE 7 AA; 902 MW; 69D4068B5DC5B350 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0

QY 16 KS 17  
||  
Db 1 KS 2

RESULT 42  
LANC\_CARUI  
ID LANC\_CARUI STANDARD; PRT; 7 AA.  
AC P36960;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium.  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422(1992).  
CC -|- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).  
CC ACTIVE ON GRAM-POSITIVE BACTERIA.  
KW Antibiotic; Bacteriocin; Lantibiotic.  
FT NON\_TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05; Mismatches 0; Indels 0; Gaps 0;  
Matches 2; Conservative 0

QY 13 EI 14  
||  
Db 3 EI 4

RESULT 43  
UC24\_MAIZE  
ID UC24\_MAIZE STANDARD; PRT; 7 AA.  
AC P80630;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN  
CC PROTEIN IS: 6.0, ITS MW IS: 30.0 kDa.  
DR Maize-2DPAGE; P80630; COLEOPTILE.  
DR MaizeDB; 123956; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

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FT  NON TER      7      7      665 MW; 6DC1B5B33DC1B5D0 CRC64;
SQ  SEQUENCE      7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  16 KS 17
DB  4 KS 5

RESULT 44
UF03_MOUSE
ID  UF03_MOUSE  STANDARD; PRT; 7 AA.
AC  P38641;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  01-FEB-1995 (Rel. 31, Last annotation update)
DE  Unknown protein from 2D-page of fibroblasts (P36) (Fragment).
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE
RC  TISSUE=Fibroblast; PubMed=7523108;
RX  MEDLINE=95009907;
RA  Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT  "Separation and sequencing of familial and novel murine proteins
RT  using preparative two-dimensional gel electrophoresis.";
RL  Electrophoresis 15:735-745(1994).
CC  -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC  PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT  NON TER      7
SQ  SEQUENCE      7 AA; 842 MW; 6AA72B1DD8B1B180 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  12 EE 13
DB  2 EE 3

RESULT 45
AKH_TABAT
ID  AKH_TABAT  STANDARD; PRT; 8 AA.
AC  P14595;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-FEB-1994 (Rel. 28, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)
DE  (DCC I).
OS  Tabanus atratus (Horse fly).
OC  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC  Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC  Tabanus.
OX  NCBI_TaxID=7207;
RN  [1]
RP  SEQUENCE
RC  TISSUE=Corpora cardiaca;
RX  MEDLINE=90046758; PubMed=2813385;
RA  Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA  Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT  "Primary structure of two neuropeptide hormones with adipokinetic and
RT  hypotrehalosemic activity isolated from the corpora cardiaca of horse
RT  flies (Diptera).";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC  -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC  CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC  DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT

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CC  MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC  -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR  PIR; A33995; A33995.
DR  InterPro; IPR002047; AKH.
DR  PROSITE; PS00256; AKH; 1.
KW  Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT  MOD_RES      1      1      PYRROLIDONE CARBOXYLIC ACID.
FT  MOD_RES      8      8      AMIDATION.
SQ  SEQUENCE      8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  2 TF 3
DB  3 TF 4

RESULT 46
B44K_PORGI
ID  B44K_PORGI  STANDARD; PRT; 8 AA.
AC  P81886;
DT  30-MAY-2000 (Rel. 39, Created)
DT  30-MAY-2000 (Rel. 39, Last sequence update)
DT  30-MAY-2000 (Rel. 39, Last annotation update)
DE  44 kDa immunogenic protein (Fragment).
OC  Porphyromonas gingivalis (Bacteroides gingivalis).
OC  Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC  Porphyromonadaceae; Porphyromonas.
OX  NCBI_TaxID=837;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=VPB 3492;
RX  MEDLINE=20198497; PubMed=10731616;
RA  Norris J.M., Love D.N.;
RT  "Serum antibody responses of cats to soluble whole cell antigens of
RT  feline Porphyromonas gingivalis.";
RL  Vet. Microbiol. 73:37-49(2000).
CC  -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
KW  Antigen.
FT  NON TER      8
SQ  SEQUENCE      8 AA; 989 MW; 9554540326CB476D CRC64;

Query Match
Best Local Similarity 11.1%; Score 2; DB 1; Length 8;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  6 YQ 7
DB  3 YQ 4

RESULT 47
CAD1_ENTFA
ID  CAD1_ENTFA  STANDARD; PRT; 8 AA.
AC  P13268;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  01-FEB-1991 (Rel. 17, Last annotation update)
DE  Sex pheromone CAD1.
OS  Enterococcus faecalis (Streptococcus faecalis).
OC  Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX  NCBI_TaxID=1351;
RN  [1]
RP  SEQUENCE
RX  MEDLINE=85051889; PubMed=6437872;
RA  Mori M., Sakagami Y., Narita M., Isogai A., Fujino M., Kitada C.,
RA  Craig R.A., Clewell D.B., Suzuki A.;
RT  "Isolation and structure of the bacterial sex pheromone, CAD1, that
RT  induces plasmid transfer in Streptococcus faecalis.";
RL  FEBS Lett. 178:97-100(1984).
CC  -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE

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CC HEMOLYSIN PLASMAID PADL.
KW Phenomone.
SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SL 18
Db 3 SL 4

RESULT 48
FAR4_HOMAM STANDARD; PRT; 8 AA.
AC P41487;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide 4 (PLI 4) (F1).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RN SEQUENCE.
RC TISSUE=Pericardial organs;
RX MEDLINE=88116164; PubMed=3429714;
RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
RT "Purification and characterization of FMRFamidelike immunoreactive
RT substances from the lobster nervous system: isolation and sequence
RT analysis of two closely related peptides.";
RL J. Comp. Neurol. 266:16-26(1987).
CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
CC NEUROMUSCULAR JUNCTIONS.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1067 MW; DDD40729C4540451 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NR 5
Db 2 NR 3

RESULT 49
HTF2_PERAM STANDARD; PRT; 8 AA.
AC P04549;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrehalosaemic factor II (Neuropeptide M-II) (Periplanetin CC-2)
DE (PeA-CNH-II) (Lep-CC-II) (Hypertrehalosaemic neuropeptide II).
OS Periplaneta americana (American cockroach),
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RN SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,

Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RN SEQUENCE.
RC SPECIES=P. americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RN SEQUENCE.
RC SPECIES=L. decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RN SEQUENCE.
RC SPECIES=B. orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).
CC -1- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TF 3
Db 3 TF 4

RESULT 50
LCK1_LEUMA STANDARD; PRT; 8 AA.
AC P21130;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE Leucokinin I (L-I).
OS Leucophaea maderae (Madeira cockroach),
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RN SEQUENCE AND SYNTHESIS.
RC TISSUE=Head;
RA Holman G.M., Cook B.J., Nachman R.J.;

```

"Isolation, primary structure and synthesis of two neuropeptides from *Leucophaea maderae*: members of a new family of Cephalomyotropins.";  
RT Comp. Biochem. Physiol. 84C:205-211(1986).  
RL !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.  
CC Neuropeptide; Amidation.  
KW MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 893 MW; DC6365B449C866DA CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 FN 4  
DB 4 FN 5  
  
RESULT 51  
LCK3 LEUMA  
ID LCK3 LEUMA STANDARD; PRT; 8 AA.  
AC P21142;  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 01-MAY-1991 (Rel. 18, Last annotation update)  
DE Leucokinin III (L-III).  
OS Leucophaea maderae (Madeira cockroach).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
OC Blaberidae; Leucophaea.  
OX NCBI\_TaxID=6988;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE-Head;  
RA Holman G.W., Cook B.J., Nachman R.J.;  
RT "Primary structure and synthesis of two additional neuropeptides from *Leucophaea maderae*: members of a new family of Cephalomyotropins.";  
RL Comp. Biochem. Physiol. 84C:271-276(1986).  
CC !- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).  
CC !- SIMILARITY: TO THE OTHER LEUCOKININS.  
KW Neuropeptide; Amidation.  
FT MOD RES 8 8 AMIDATION.  
SQ SEQUENCE 8 AA; 910 MW; DC6365B449C866DA CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 FN 4  
DB 4 FN 5  
  
RESULT 52  
LPMS STAPP  
ID LPMS STAPP STANDARD; PRT; 8 AA.  
AC P23211;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-NOV-1991 (Rel. 20, Last sequence update)  
DT 01-MAR-1992 (Rel. 21, Last annotation update)  
DE Probable msrA leader peptide.  
OS Staphylococcus epidermidis.  
OG Plasmid pUL5050.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1282;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=968;  
SQ MEDLINE=91041730; PubMed=2233255;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GE 12  
DB 11

Ross J.I., Eady E.A., Cove J.H., Cunliffe W.J., Baumberg S., Wootton J.C.;  
RT "Inducible erythromycin resistance in staphylococci is encoded by a member of the ATP-binding transport super-gene family.";  
RL Mol. Microbiol. 4:1207-1214(1990).  
CC !- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE PROTEIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X52085; CAA36303.1; -.  
DR PIR; S11157; LFSAME.  
KW Leader peptide; Plasmid.  
SQ SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 15 LK 16  
DB 7 LK 8  
  
RESULT 53  
RS1 ERWCH  
ID RS1 ERWCH STANDARD; PRT; 8 AA.  
AC P37985;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 01-NOV-1995 (Rel. 32, Last annotation update)  
DE 30S ribosomal protein S1 (fragment).  
GN RPSA.  
OS Erwinia chrysanthemi.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Pectobacterium.  
OX NCBI\_TaxID=556;  
RN [1]  
RP SEQUENCE FROM N.A.  
FT STRAIN=3937;  
RC Douillie A., Toussaint A., Faelen M.;  
RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.  
CC !- FUNCTION: BINDS MRNA, THUS FACILITATING RECOGNITION OF THE SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).  
CC !- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X74750; CAA52769.1; -.  
DR PIR; S37141; S37141.  
KW Ribosomal protein; Repeat; RNA-binding.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 8;  
Best Local Similarity 100.0%; Pred.No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 11 GE 12  
DB 11

```
Db          7 GE 8
RESULT 54
RT34_BOVIN
ID RT34_BOVIN STANDARD; PRT; 8 AA.
AC P82929;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) (Fragment).
GN MRP34.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=21276436; PubMed=11279123;
RA Koc E.C., Burkhart W., Blackburn K., Moseley A., Spremulli L.L.;
RT "The small subunit of the mammalian mitochondrial ribosome:
RT identification of the full complement of ribosomal proteins present.";
RL J. Biol. Chem. 276:19363-19374(2001).
CC -!- SUBUNIT: Component of the mitochondrial ribosome small subunit
CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
CC -!- SUBCELLULAR LOCATION: Mitochondrion.
KW Ribosomal protein; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 935 MW; 9639D1A72058637D CRC64;

Query Match          11.1%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 TF 3
Db          6 TF 7

RESULT 55
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 1
FT VARIANT 5 5 F -> P.
FT VARIANT 8 8 /FTid=VAR_000004.
FT NON_TER 8 8
FT NON_TER 8 AA; 909 MW; 86677B59D1A72042 CRC64;
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 TF 3
Db          6 TF 7

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 AT 2
Db          1 AT 2

RESULT 56
AL11_CARMA
ID AL11_CARMA STANDARD; PRT; 9 AA.
AC P81874;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Brachyura; Fortuonoidea; Fortuonidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD_RES 9
FT MOD_RES 9 AMIDATION.
SQ SEQUENCE 9 AA; 927 MW; 832D79DCB46D861 CRC64;

Query Match          11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 AT 2
Db          1 AT 2

RESULT 57
ALC_CHLRE
ID ALC_CHLRE STANDARD; PRT; 9 AA.
AC P82578;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Allantoicase (EC 3.5.3.4) (Allantoate amidohydrolase) (Fragment).
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlamydomonas.
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE
RC STRAIN=6145C;
RX MEDLINE=20318328; PubMed=10860551;
RA Piedras P., Munoz A., Aguilar M., Pineda M.;
RT "Allantoate amidohydrolase (Allantoicase) from Chlamydomonas
RT reinhardtii: its purification and catalytic and molecular
RT characterization.";
RL Arch. Biochem. Biophys. 378:340-348(2000).
CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-
CC ureidoglycolate and (+)-ureidoglycolate to glyoxylate.
CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O = (-)-ureidoglycolate +
CC urea.
CC -!- PATHWAY: Degradation of allantoin (purine catabolism); second
CC step.
CC -!- SUBUNIT: Homohexamer.
```

CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with  
 CC allantate and ureidoglycolate, respectively.  
 CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.  
 KW Hydrolase; Purine metabolism.  
 FT UNSURE 5 5 OR Y.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 943 MW; D934ADD9D6D871F2 CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AT 2  
 Db 7 AT 8  
 RESULT 58  
 BS43 SERPL STANDARD; PRT; 9 AA.  
 ID BS43 SERPL STANDARD; PRT; 9 AA.  
 AC P83375, 2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bacteriocin serracin P 43 kDa subunit (Fragment).  
 OS Serratia plymuthica  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Serratia.  
 OX NCBI\_TaxID=82996;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC STRAIN=J7;  
 RX MEDLINE=22293561; PubMed=12406768;  
 RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,  
 RA Van Beeumen J., Thonart P.;  
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and  
 RT its activity against *Erwinia amylovora*, the fire blight pathogen.";  
 RL Appl. Environ. Microbiol. 68:5704-5710(2002).  
 CC -!- FUNCTION: Major component of a prophage tail sheath (Probable).  
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacterium  
 CC *E. amylovora*.  
 DR InterPro; IPR006498; Tail tube.  
 DR Pfam; PF04985; Phage tube; 1.  
 KW Antibiotic; Bacteriocin.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1095 MW; 1B66D412C871E11FB CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 10 HG 11  
 Db 4 HG 5  
 RESULT 59  
 D1\_NEPNO STANDARD; PRT; 9 AA.  
 ID D1\_NEPNO STANDARD; PRT; 9 AA.  
 AC P24816;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-MAR-1992 (Rel. 21, Last annotation update)  
 DE Gastrin/cholecystokinin-like peptide D1.  
 OS Nephrops norvegicus (Norway lobster).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;  
 OC Nephropoidea; Nephropidae; Nephrops.  
 OX NCBI\_TaxID=6829;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Stomach;  
 RX MEDLINE=92082847; PubMed=1747388;

RA Pavrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;  
 RT "Structure and biological activity of crustacean gastrointestinal  
 RT peptides identified with antibodies to gastrin/cholecystokinin.";  
 RL Biochimie 73:1233-1239(1991).  
 CC -!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.  
 CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.  
 DR PIR; S47432; S47432.  
 KW Hormone.  
 SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 7 QD 8  
 Db 5 QD 6  
 RESULT 60  
 DSIP\_RABIT STANDARD; PRT; 9 AA.  
 ID DSIP\_RABIT STANDARD; PRT; 9 AA.  
 AC P01158;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-OCT-2001 (Rel. 40, Last annotation update)  
 DE Delta sleep-inducing peptide (DSIP).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=77185324; PubMed=862769;  
 RA Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,  
 RA Schoenenberger G.A.;  
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of  
 RT the original and synthetic nonapeptide.";  
 RL Experientia 33:548-552(1977).  
 RN [2]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=79054421; PubMed=568769;  
 RA Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;  
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid  
 RT analysis, sequence, synthesis and activity of the nonapeptide.";  
 RL Pflugers Arch. 376:119-129(1978).  
 RN [3]  
 RP REVIEW.  
 RX MEDLINE=87175129; PubMed=3550726;  
 RA Graf M.V., Kaslin A.J.;  
 RT "Delta-sleep-inducing peptide (DSIP): an update.";  
 RL Peptides 7:1165-1187(1986).  
 CC -!- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF  
 CC RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND  
 CC REDUCED MOTOR ACTIVITIES.  
 CC -!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF  
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC  
 CC STIMULATION OF THE THALAMUS.  
 CC -!- DATABASE: NAME=Protein Spotlight;  
 CC NOTE=Issue 8 of March 2001;  
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".  
 DR PIR; A01422; QDRB.  
 SQ SEQUENCE 9 AA; 849 MW; DDD365BDDAA8787D CRC64;  
 Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 11 GE 12  
 Db 8 GE 9

```

RESULT 61
FAR1 CALVO
ID FAR1 CALVO STANDARD; PRT; 9 AA.
AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A41978; A41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 4 QD 5

RESULT 62
FAR2 CALVO
ID FAR2 CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 4 QD 5

RESULT 63
FAR3 CALVO
ID FAR3 CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; C41978; C41978.
KW Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 4 QD 5

RESULT 64
FAR4 CALVO
ID FAR4 CALVO STANDARD; PRT; 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRFamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

```

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY  
 DR PIR; D41978; D41978.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QD 8  
 ||  
 Db 4 QD 5

## RESULT 65

FAR5 ASCSU  
 ID FAR5 ASCSU STANDARD; PRT; 9 AA.  
 AC P43170;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRFamide-like neuropeptide AF5.  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95380362; PubMed=7651904;  
 RA Cowden C., Stretton A.O.W.;  
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode  
 RT Ascaris suum";  
 RL Peptides 16:491-500 (1995).  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TF 3  
 ||  
 Db 5 TF 6

## RESULT 66

FAR5 CALVO  
 ID FAR5 CALVO STANDARD; PRT; 9 AA.  
 AC P41860;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE CalliFMRFamide 5.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,  
 RA Rehfeld J.F., Thorpe A.;  
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2  
 RT neuropeptides (designated calliFMRFamides) from the blowfly  
 RT Calliphora vomitoria";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY  
 DR PIR; E41978; E41978.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D867 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 QD 8  
 ||  
 Db 4 QD 5

## RESULT 67

FAR5 PENMO  
 ID FAR5 PENMO STANDARD; PRT; 9 AA.  
 AC P83320;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP5 (SMPSLRP-amide).  
 OS Penaeus monodon (Penaeid shrimp).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
 OC Penaeidae; Penaeus.  
 OX NCBI\_TaxID=6687;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RX TISSUE=Eyestalk;  
 RA MEDLINE=21956277; PubMed=11959015;  
 RA Sithigorngul P., Pupuem J., Krungkarn C., Longyant S.,  
 RA Chaivuthangkura P., Sithigorngul W., Petsom A.;  
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk  
 RT of the giant tiger prawn Penaeus monodon";  
 RL Comp. Biochem. Physiol. 131B:325-337 (2002).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY  
 KW Neuropeptide; Amidation.  
 FT MOD RES 9  
 SQ SEQUENCE 9 AA; 1106 MW; B6B07340735A766 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SL 18  
 ||  
 Db 4 SL 5

## RESULT 68

FAR6 CALVO  
 ID FAR6 CALVO STANDARD; PRT; 9 AA.  
 AC P41861;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE CalliFMRFamide 6.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92196111; PubMed=1549595;  
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

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RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; F41978; F41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1058 MW; 96D10699CAB6D865 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 4 QD 5

RESULT 69
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC F41862;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRFamide 7.
OS Calliphora vomitoria (Blue blowfly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; G41978; G41978.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1081 MW; E1D10699CAB6D86A CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 4 QD 5

RESULT 70
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC F41865;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRFamide 10.
OS Calliphora vomitoria (Blue blowfly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
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RN SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A44787; A44787.
KW Neuropeptide; Amidation.
FT MOD RES 9
FT UNSURE 1 1
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
Db 3 NR 4

RESULT 71
FARP CALVO
ID FARP CALVO STANDARD; PRT; 9 AA.
AC F41868;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CallifMRFamide 13.
OS Calliphora vomitoria (Blue blowfly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated callifMRFamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -|- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; D44787; D44787.
KW Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 1028 MW; 22D10699C87AB6D8 CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QD 8
Db 3 QD 4

RESULT 72
FARP CALSI
ID FARP CALSI STANDARD; PRT; 9 AA.
AC P38495;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
```

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DE FWRamide-like neuropeptide.
OS Callinectes sapidus (Blue crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Callinectes.
OX NCBI_TaxID=6763;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270479; PubMed=1815216;
RA Krajniak K.G.;
RT "The identification and structure-activity relations of a
RT cardioactive FWRamide-related peptide from the blue crab Callinectes
RT sapidus."
RL Peptides 12:1295-1302(1991).
CC -!- FUNCTION: CARDIOACTIVE PEPTIDE.
CC -!- FAMILY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION
SQ SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NR 5
DB 3 NR 4

RESULT 73
FIBB_ERYPA
ID FIBB_ERYPA STANDARD; PRT; 9 AA.
AC P19346;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Erythrocybus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR FIR; D24180; D24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE5B9C735BB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EE 13
DB 2 EE 3

RESULT 74
FIBB_MACFU
ID FIBB_MACFU STANDARD; PRT; 9 AA.
AC P19345;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Macaca fuscata fuscata (Japanese macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9543;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocybus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons."
RL J. Biochem. 97:1487-1492(1985).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR FIR; C24180; C24180.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1038 MW; 69FE5B9C735BB1B CRC64;

Query Match 11.1%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EE 13
DB 2 EE 3

RESULT 75
FIBB_PAPHA
ID FIBB_PAPHA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
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RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,  
RT and Theropithecus gelada): their amino acid sequences and  
RT evolutionary rates and a molecular phylogeny for the baboons.";  
RL J. Biochem. 94:1973-1978(1983).  
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT  
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET  
CC AGGREGATION.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY  
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA  
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES  
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.  
DR PIR; E28854; E28854.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma. FIBRINOPEPTIDE B.  
FT PEPTIDE 1 9  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1057 MW; DDFE71E9C7287B06 CRC64;  
  
Query Match 11.1%; Score 2; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 10 HG 11  
Db 7 HG 8

Search completed: November 25, 2003, 19:28:26  
Job time : 7.45515 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:25:50 ; Search time 33.8023 Seconds  
(without alignments)  
137.415 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRQDDHGEELKSL 18

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6968

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database :

SPTREMBL.23.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	22.2	18	2 Q9R4V9	Q9R4V9 campylobact
2	4	22.2	20	2 Q9R4L7	Q9R4L7 leuconostoc
3	4	22.2	20	6 Q9TR34	Q9TR34 oviz aries
4	4	22.2	20	6 Q9TR33	Q9TR33 canis famill
5	4	22.2	20	10 Q9S8X5	Q9S8X5 Glycine max
6	4	22.2	20	13 Q9PRN6	Q9PRN6 scyllorhinu
7	4	22.2	20	15 Q993P2	Q993P2 human immun
8	4	22.2	20	15 Q993Q0	Q993Q0 human immun
9	4	22.2	20	15 Q993Q4	Q993Q4 human immun
10	4	22.2	20	15 Q993P4	Q993P4 human immun
11	4	22.2	20	15 Q993N6	Q993N6 human immun
12	4	22.2	20	15 Q993P8	Q993P8 human immun
13	4	22.2	20	15 Q993N8	Q993N8 human immun
14	4	22.2	20	15 Q993Q6	Q993Q6 human immun
15	3	16.7	7	4 Q15897	Q15897 homo sapien
16	3	16.7	8	2 Q51594	Q51594 escherichia

17	3	16.7	8	2	Q8GL21	Q8GL21 borrelia bu
18	3	16.7	8	4	Q15895	Q15895 homo sapien
19	3	16.7	8	8	P93963	P93963 psathyrosta
20	3	16.7	8	8	P92384	P92384 hordeum mur
21	3	16.7	8	8	P93973	P93973 eremopyrum
22	3	16.7	8	8	P92215	P92215 amblyopyrum
23	3	16.7	8	8	P93957	P93957 festucopsis
24	3	16.7	8	8	P92222	P92222 bromus iner
25	3	16.7	8	8	P92388	P92388 henrardia p
26	3	16.7	8	8	P92441	P92441 thinopyrum
27	3	16.7	8	8	P92404	P92404 lophopyrum
28	3	16.7	8	8	P93961	P93961 psathyrosta
29	3	16.7	8	8	P93970	P93970 eremopyrum
30	3	16.7	8	8	P93955	P93955 festucopsis
31	3	16.7	8	8	P93965	P93965 secale stri
32	3	16.7	8	8	P92394	P92394 hordeum vul
33	3	16.7	8	8	P92382	P92382 hordeum bra
34	3	16.7	8	8	P93966	P93966 aegilops sp
35	3	16.7	8	8	P92227	P92227 crithopsis
36	3	16.7	8	8	P92373	P92373 haynaldia v
37	3	16.7	8	8	P92211	P92211 agropyron c
38	3	16.7	8	8	P92428	P92428 peridictyon
39	3	16.7	8	8	P92386	P92386 hordeum mar
40	3	16.7	8	8	P93959	P93959 hordeum ere
41	3	16.7	8	8	P93985	P93985 aegilops co
42	3	16.7	8	8	P92443	P92443 taeniatheir
43	3	16.7	8	8	P92391	P92391 heteranthel
44	3	16.7	8	8	P93981	P93981 crithodium
45	3	16.7	8	8	P93992	P93992 australopyr
46	3	16.7	8	8	P92426	P92426 pseudoroegn
47	3	16.7	8	8	P92431	P92431 aegilops ta
48	3	16.7	8	8	P92422	P92422 psathyrosta
49	3	16.7	8	10	Q40530	Q40530 nicotiana t
50	3	16.7	8	11	Q9ERD2	Q9ERD2 mus musculu
51	3	16.7	8	13	Q90ZV5	Q90ZV5 fulica leuc
52	3	16.7	9	2	Q8GL31	Q8GL31 borrelia bu
53	3	16.7	9	12	Q9IBY9	Q9IBY9 kaposi's sa
54	3	16.7	10	8	Q8W7U4	Q8W7U4 anolis nite
55	3	16.7	10	11	Q63056	Q63056 rattus norv
56	3	16.7	10	11	Q8VII8	Q8VII8 mus musculu
57	3	16.7	10	11	Q9JLI5	Q9JLI5 mus musculu
58	3	16.7	11	2	Q9L4F7	Q9L4F7 bacillus ce
59	3	16.7	11	2	Q8618	Q8618 prochloroco
60	3	16.7	11	2	Q8GL19	Q8GL19 borrelia bu
61	3	16.7	11	4	Q16234	Q16234 homo sapien
62	3	16.7	11	10	Q8RV30	Q8RV30 zea mays (m
63	3	16.7	11	12	Q8JS92	Q8JS92 hepatitis b
64	3	16.7	12	2	Q93A08	Q93A08 thiobacillu
65	3	16.7	12	2	Q93U04	Q93U04 escherichia
66	3	16.7	12	2	Q9L4M9	Q9L4M9 streptococc
67	3	16.7	12	2	Q47251	Q47251 escherichia
68	3	16.7	12	6	Q9TRU1	Q9TRU1 bos taurus
69	3	16.7	12	8	P82164	P82164 spinacia ol
70	3	16.7	12	11	Q62966	Q62966 rattus norv
71	3	16.7	12	12	Q84268	Q84268 human papil
72	3	16.7	13	2	Q9R3R6	Q9R3R6 prochloroco
73	3	16.7	13	4	Q9UDE0	Q9UDE0 homo sapien
74	3	16.7	13	5	Q812E2	Q812E2 plasmodium
75	3	16.7	13	10	Q945C1	Q945C1 cryptothecodi
76	3	16.7	13	13	Q86129	Q86129 vesicular s
77	3	16.7	14	2	Q9R5I7	Q9R5I7 escherichia
78	3	16.7	14	2	Q9LCS1	Q9LCS1 bacillus su
79	3	16.7	14	2	Q44847	Q44847 borrelia bu
80	3	16.7	14	10	P82341	P82341 pisum sativ
81	3	16.7	15	2	Q9R5H5	Q9R5H5 rhodospiril
82	3	16.7	15	2	Q9R543	Q9R543 mycobacteri
83	3	16.7	15	3	Q9UR90	Q9UR90 saccharomyc
84	3	16.7	15	4	Q16297	Q16297 homo sapien
85	3	16.7	15	4	Q9UC22	Q9UC22 homo sapien
86	3	16.7	15	5	Q9TWF3	Q9TWF3 dictyosteli
87	3	16.7	15	6	P82207	P82207 bombyx mori
88	3	16.7	15	6	Q9TRT6	Q9TRT6 sus scrofa
89	3	16.7	15	6	Q9N0G0	Q9N0G0 canis famil

Q9R4V9 3 16.7 15 6 Q9R54 Q9R54 ovis aries  
 91 3 16.7 15 6 P82665 P82665 bos taurus  
 92 3 16.7 15 6 Q8H279 Q8H279 bos taurus  
 93 3 16.7 15 8 Q8WK21 Q8WK21 bolidomonas  
 94 3 16.7 15 11 Q8CJ29 Q8CJ29 mus musculus  
 95 3 16.7 15 12 Q88954 Q88954 vaccinia vi  
 96 3 16.7 15 13 Q9PRZ9 Q9PRZ9 micropogoni  
 97 3 16.7 16 2 Q9R4J0 Q9R4J0 arthrobaacte  
 98 3 16.7 16 2 O54357 O54357 bacillus am  
 99 3 16.7 16 2 Q937K1 Q937K1 escherichia  
 100 3 16.7 16 2 Q8VLX6 Q8VLX6 thermus the

## ALIGNMENTS

RESULT 1  
 Q9R4V9 PRELIMINARY; PRT; 18 AA.  
 ID Q9R4V9  
 AC Q9R4V9  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)  
 DE 10 kDa heat shock- and alkaline PH-induced protein (Fragment).  
 OS Campylobacter jejuni.  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Campylobacteraceae; Campylobacter.  
 OX NCBI\_TaxID=197;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95012609; PubMed=7927682;  
 RA Wu Y.L., Lee L.H., Rollins D.M., Ching W.M.;  
 RT "Heat shock- and alkaline pH-induced proteins of Campylobacter jejuni:  
 RT characterization and immunological properties.";  
 RL Infect. Immun. 62:4256-4260(1994).  
 SQ SEQUENCE 18 AA; 2056 MW; 9E4FED7BB4DA76C4 CRC64;

Query Match 22.2%; Score 4; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13  
 Db 14 HGEE 17

RESULT 2  
 Q9R4L7 PRELIMINARY; PRT; 20 AA.  
 ID Q9R4L7  
 AC Q9R4L7  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
 DE Dextranucrase (EC 2.4.1.5) (Fragment).  
 OS Leuconostoc mesenteroides.  
 OC Bacteria; Firmicutes; Lactobacilliales; Leuconostoc.  
 OX NCBI\_TaxID=1245;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95306915; PubMed=7540436;  
 RA Funane K., Yamada M., Shiraishi M., Takahara H., Yamamoto N.,  
 RA Ichishima E., Kobayashi M.;  
 RT "Aggregated form of dextranucrases from Leuconostoc mesenteroides  
 RT NRRL B-512F and its constitutive mutant.";  
 RL Biosci. Biotechnol. Biochem. 59:776-780(1995).  
 DR InterPro: IPR003318; Glyco\_hydro.70.  
 DR Pfam: PF02324; Glyco\_hydro.70; 1\_  
 SQ SEQUENCE 20 AA; 2356 MW; 701179A7AC89957F CRC64;

Query Match 22.2%; Score 4; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YQDD 9  
 Db 12 YQDD 15

RESULT 3  
 Q9TR34 PRELIMINARY; PRT; 20 AA.  
 ID Q9TR34  
 AC Q9TR34  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE Cytochrome C oxidase subunit VIA-L (Fragment).  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_TaxID=9940;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96092035; PubMed=8529022;  
 RA Linder D., Freund R., Kadenbach B.;  
 RT "Species-specific expression of cytochrome c oxidase isozymes.";  
 RL Comp. Biochem. Physiol. 112B:461-469(1995).  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2079 MW; 97E5DDCAB5076C26 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13  
 Db 5 HGEE 8

RESULT 4  
 Q9TR33 PRELIMINARY; PRT; 20 AA.  
 ID Q9TR33  
 AC Q9TR33  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 DE Cytochrome C oxidase subunit VIA-L (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96092035; PubMed=8529022;  
 RA Linder D., Freund R., Kadenbach B.;  
 RT "Species-specific expression of cytochrome c oxidase isozymes.";  
 RL Comp. Biochem. Physiol. 112B:461-469(1995).  
 FT NON\_TER 1  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2109 MW; 97E5C71075076C26 CRC64;

Query Match 22.2%; Score 4; DB 6; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13  
 Db 5 HGEE 8

RESULT 5  
 Q9S8X5 PRELIMINARY; PRT; 20 AA.  
 ID Q9S8X5  
 AC Q9S8X5  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Vegetative storage protein 94 peptide 2, VSP94=LIPXYGENASE  
 DE (Fragment).  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eursoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92361246; PubMed=1822994;  
 RA Tranbarger T.J., Franceschi V.R., Hildebrand D.F., Grimes H.D.;  
 RT "The soybean 94-kilodalton vegetative storage protein is a  
 RT lipoxigenase that is localized in paraveinal mesophyll cell  
 RT vacuoles."  
 RL Plant Cell 3:973-987(1991).  
 FT NON\_TER 1  
 FT NON\_TER 20  
 FT NON\_TER 20  
 SQ SEQUENCE 20 AA; 2330 MW; B889AB684EA09968 CRC64;  
 Query Match 22.2%; Score 4; DB 10; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db ||||  
 6 LKSL 9  
 RESULT 6  
 Q9PRN6 PRELIMINARY; PRT; 20 AA.  
 AC Q9PRN6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Urotensin I homolog.  
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;  
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;  
 OC Scyliorhinidae; Scyliorhinus.  
 OX NCBI\_TaxID=7830;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96051495; PubMed=8536945;  
 RA Waugh D., Anderson G., Armour K.J., Balment R.J., Hazon N.,  
 RA Conlon J.M.;  
 RT "A peptide from the caudal neurosecretory system of the dogfish  
 RT Scyliorhinus canicula that is structurally related to urotensin I."  
 RL Gen. Comp. Endocrinol. 99:333-339(1995).  
 SQ SEQUENCE 20 AA; 2305 MW; 77A92D52817E97B7 CRC64;  
 Query Match 22.2%; Score 4; DB 13; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TFNR 5  
 Db ||||  
 11 TFNR 14  
 RESULT 7  
 Q993P2 PRELIMINARY; PRT; 20 AA.  
 AC Q993P2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag protein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retroviridae; Lentivirus.

OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRB670;  
 RX MEDLINE=21136890; PubMed=11238855;  
 RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
 RT to Viral Infectivity, Replication, and Protein Maturation of  
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."  
 RL J. Virol. 75:3291-3300(2001).  
 DR EMBL; AF316847; AAK21098.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2167 MW; B9EBC80E8A2AE340 CRC64;  
 Query Match 22.2%; Score 4; DB 15; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db ||||  
 9 LKSL 12  
 RESULT 8  
 Q993Q0 PRELIMINARY; PRT; 20 AA.  
 AC Q993Q0;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag protein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PR-RTB497;  
 RX MEDLINE=21136890; PubMed=11238855;  
 RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;  
 RT "Individual Contributions of Mutant Protease and Reverse Transcriptase  
 RT to Viral Infectivity, Replication, and Protein Maturation of  
 RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1."  
 RL J. Virol. 75:3291-3300(2001).  
 DR EMBL; AF316843; AAK21090.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 1  
 SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;  
 Query Match 22.2%; Score 4; DB 15; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db ||||  
 9 LKSL 12  
 RESULT 9  
 Q993Q4 PRELIMINARY; PRT; 20 AA.  
 AC Q993Q4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Gag protein (Fragment).  
 GN GAG.  
 OS Human immunodeficiency virus 1.  
 OS Viruses; Retroviridae; Lentivirus.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PRB497;  
 RX MEDLINE=21136890; PubMed=11238855;

```

RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
RT to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316840; AAK21086.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 10
Q993P4 PRELIMINARY; PRT; 20 AA.
ID Q993P4
AC Q993P4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
DE GAG.
GN Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PR-BTB670;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
RT to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316846; AAK21096.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 11
Q993N6 PRELIMINARY; PRT; 20 AA.
ID Q993N6
AC Q993N6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
DE GAG.
GN Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PR-BTB670;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
RT to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).

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DR EMBL; AF316851; AAK21104.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 12
Q993P8 PRELIMINARY; PRT; 20 AA.
ID Q993P8
AC Q993P8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
DE GAG.
GN Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PR-RTB497;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
RT to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316844; AAK21092.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 9 LKSL 12

RESULT 13
Q993N8 PRELIMINARY; PRT; 20 AA.
ID Q993N8
AC Q993N8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
DE GAG.
GN Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxID=11676;
OX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=PR-RTB670;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
RT to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316850; AAK21102.1; -.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80E8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 9 LKSL 12

RESULT 14
Q99306 PRELIMINARY; PRT; 20 AA.
AC Q99306;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRB497;
RX MEDLINE=21136890; PubMed=11238855;
RA Bleiber G., Munoz M., Ciuffi A., Meylan P., Telenti A.;
RT "Individual Contributions of Mutant Protease and Reverse Transcriptase
to Viral Infectivity, Replication, and Protein Maturation of
RT Antiretroviral Drug-Resistant Human Immunodeficiency Virus Type 1.";
RL J. Virol. 75:3291-3300(2001).
DR EMBL; AF316839; AAK21084.1; -.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2194 MW; B9EBC80B8A3B1340 CRC64;

Query Match 22.2%; Score 4; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18
Db 9 LKSL 12

RESULT 15
Q15897 PRELIMINARY; PRT; 7 AA.
AC Q15897;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XPeAlla) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32077; AAA73887.1; -.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 814 MW; 572B1DD3372046B0 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 3 ILK 5

RESULT 16
Q51594 PRELIMINARY; PRT; 8 AA.
AC Q51594;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE CopB protein (Fragment).
OS Escherichia coli.
OG Plasmid ColV2-K34.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86223772; PubMed=2423502;
RA Weber P.C., Falchaudhuri S.;
RT "Incompatibility repressor in a repA-like replicon of the IncFI
RT plasmid ColV2-K34.";
RL J. Bacteriol. 166:1106-1112(1986).
DR EMBL; M13472; AAA23194.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 998 MW; 0F37205AA73416D7 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 6 ILK 8

RESULT 17
Q8GL21 PRELIMINARY; PRT; 8 AA.
AC Q8GL21;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid group cp32-8.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sh-2-82;
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142094; AAN17903.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1042 MW; 1437244337204373 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 3 ILK 5

RESULT 18
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Q15895 ID Q15895 PRELIMINARY; PRT; 8 AA.  
AC Q15895;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE (Clone XP6A10A) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC TISSUE=Placenta;  
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,  
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,  
RA Caskey C.T.H.;  
RT "Isolation of chromosome-specific genes by reciprocal probing of  
RT arrayed cDNAs and cosmid libraries."  
RL Hum. Mol. Genet. 0:0-0(1995).  
DR EMBL; L32075; AAA73885.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;  
Query Match 16.7%; Score 3; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
Db ||||  
1 KSL 7  
RESULT 19  
P93963 ID P93963 PRELIMINARY; PRT; 8 AA.  
AC P93963;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Psathyrostachys stoloniformis.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Psathyrostachys.  
OX NCBI\_TaxID=58873;  
RN [1]  
RC SEQUENCE FROM N.A.  
RA STRAIN=H9182; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77754; CAB01341.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
Db ||||  
1 KSL 3  
RESULT 20  
P92384 ID P92384 PRELIMINARY; PRT; 8 AA.  
AC P92384;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum murinum subsp. glaucum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=98113;  
RN [1]  
RC SEQUENCE FROM N.A.  
RA STRAIN=H801; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77762; CAB01365.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
Db ||||  
1 KSL 3  
RESULT 21  
P93973 ID P93973 PRELIMINARY; PRT; 8 AA.  
AC P93973;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Eremopyrum distans.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Eremopyrum.  
OX NCBI\_TaxID=58936;  
RN [1]  
RC SEQUENCE FROM N.A.  
RA STRAIN=H5552; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77745; CAB01314.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
Db ||||  
1 KSL 3  
RESULT 22  
P92384 ID P92384 PRELIMINARY; PRT; 8 AA.  
AC P92384;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum murinum subsp. glaucum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=98113;  
RN [1]  
RC SEQUENCE FROM N.A.  
RA STRAIN=H801; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
RT sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77762; CAB01365.1; -.  
FT NON TER 1 1  
FT NON TER 8 8  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
Db ||||  
1 KSL 3

P92215  
ID P92215 PRELIMINARY; PRT; 8 AA.  
AC P92215;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Amblyopyrum muticum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Amblyopyrum.  
OX NCBI\_TaxID=4595;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5572; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77756; CAB01347.1; -.  
DR Chloroplast.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
DB 1 KSL 3

RESULT 23  
P93957  
ID P93957 PRELIMINARY; PRT; 8 AA.  
AC P93957;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Festucopsis serpentina.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Festucopsis.  
OX NCBI\_TaxID=72456;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6511; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z79501; CAB01777.1; -.  
DR Chloroplast.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
DB 1 KSL 3

RESULT 24  
P92222  
ID P92222 PRELIMINARY; PRT; 8 AA.  
AC P92222;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Bromus inermis (Smooth brome grass).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Broneae; Bromus.  
OX NCBI\_TaxID=15371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OSA414; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77759; CAB01356.1; -.  
DR Chloroplast.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
DB 1 KSL 3

RESULT 25  
P92388  
ID P92388 PRELIMINARY; PRT; 8 AA.  
AC P92388;  
DT 01-MAY-1997 (TREMBlrel. 03, Created)  
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Henrardia persica.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Henrardia.  
OX NCBI\_TaxID=37678;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5556; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G.; Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
RL EMBL; Z77748; CAB01323.1; -.  
DR Chloroplast.  
KW NON\_TER  
FT NON\_TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;  
Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 KSL 18  
DB 1 KSL 3



## RESULT 26

P92441 ID P92441 PRELIMINARY; PRT; 8 AA.  
 AC P92441; 1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Thinopyrum bessarabicum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Thinopyrum.  
 OX NCBI\_TaxID=4601;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6725; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77769; CAB01386.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 ||||  
 Db 1 KSL 3

## RESULT 27

P92404 ID P92404 PRELIMINARY; PRT; 8 AA.  
 AC P92404; 1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Lophopyrum elongatum (Tall wheatgrass) (Argopyrum elongatum).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Lophopyrum.  
 OX NCBI\_TaxID=4588;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6692; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77743; CAB01308.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 ||||  
 Db 1 KSL 3

## RESULT 28

P93961 ID P93961 PRELIMINARY; PRT; 8 AA.  
 AC P93961; 1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Psathyrostachys rupestris.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Psathyrostachys.  
 OX NCBI\_TaxID=58938;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H6703; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77755; CAB01344.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 ||||  
 Db 1 KSL 3

## RESULT 29

P93970 ID P93970 PRELIMINARY; PRT; 8 AA.  
 AC P93970; 1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Eremopyrum triticeum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Eremopyrum.  
 OX NCBI\_TaxID=58937;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5553; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77746; CAB01315.1; -.  
 KW Chloroplast.  
 FT NON TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 ||||  
 Db 1 KSL 3

Db 1 KSL 3

## RESULT 30

P93955  
ID P93955 PRELIMINARY; PRT; 8 AA.  
AC P93955;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Festuopsis festuoides.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Festuopsis.  
OX NCBI\_TaxID=72455;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6731; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77770; CAB01389.1; -.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 31

P93965  
ID P93965 PRELIMINARY; PRT; 8 AA.  
AC P93965;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Secale strictum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Secale.  
OX NCBI\_TaxID=58866;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4342; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77765; CAB01373.1; -.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18

Db 1 KSL 3

## RESULT 32

P92394  
ID P92394 PRELIMINARY; PRT; 8 AA.  
AC P92394;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum vulgare (Barley).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H3139; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77764; CAB01371.1; -.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 33

P92382  
ID P92382 PRELIMINARY; PRT; 8 AA.  
AC P92382;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum brachyantherum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=52712;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77761; CAB01362.1; -.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
 |||  
 Db 1 KSL 3

## RESULT 34

P93966 PRELIMINARY; PRT; 8 AA.  
 AC P93966;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Aegilops speltoides (Goat grass).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Aegilops.  
 OX NCBI\_TaxID=4573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4523; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77766; CAB01377.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
 |||  
 Db 1 KSL 3

## RESULT 35

P92227 PRELIMINARY; PRT; 8 AA.  
 AC P92227;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Crithopsis delileana.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Crithopsis.  
 OX NCBI\_TaxID=37674;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4558; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77751; CAB01332.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
 |||  
 Db 1 KSL 3

## RESULT 36

P92373 PRELIMINARY; PRT; 8 AA.  
 AC P92373;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Haynaldia villosa.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Haynaldia.  
 OX NCBI\_TaxID=40247;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5561; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77741; CAB01302.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
 |||  
 Db 1 KSL 3

## RESULT 37

P92211 PRELIMINARY; PRT; 8 AA.  
 AC P92211;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE PetD protein (Fragment).  
 GN PETD.  
 OS Agropyron cristatum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
 OC Triticeae; Agropyron.  
 OX NCBI\_TaxID=4593;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H4349; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G., Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 sequence data.";  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77771; CAB01392.1; -.  
 KW Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 1 KSL 3

## RESULT 38

P92428 ID P92428 PRELIMINARY; PRT; 8 AA.  
AC P92428;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Peridictyon sanctum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Peridictyon.  
OX NCBI\_TaxID=37683;  
RN [1]\_\_TaxID=37683;  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5575; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77749; CAB01326.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 1 KSL 3

## RESULT 39

P92386 ID P92386 PRELIMINARY; PRT; 8 AA.  
AC P92386;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum marinum subsp. gussoneanum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=98114;  
RN [1]\_\_TaxID=98114;  
RP SEQUENCE FROM N.A.  
RC STRAIN=H299; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77763; CAB01368.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 884 MW; 1EDAE8773AE735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 1 KSL 3

## RESULT 40

P93959 ID P93959 PRELIMINARY; PRT; 8 AA.  
AC P93959;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Hordeum erectifolium.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=58926;  
RN [1]\_\_TaxID=58926;  
RP SEQUENCE FROM N.A.  
RC STRAIN=H1150; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z79500; CAB01776.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;

Best Local Similarity 100.0%; Pred. No. 8.3e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
|||  
Db 1 KSL 3

## RESULT 41

P93985 ID P93985 PRELIMINARY; PRT; 8 AA.  
AC P93985;  
DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Aegilops comosa.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Aegilops.  
OX NCBI\_TaxID=4485;  
RN [1]\_\_TaxID=4485;  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6673; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77742; CAB01305.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 42

P92443 ID P92443 PRELIMINARY; PRT; 8 AA.  
AC P92443; 1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Tseniatherum caput-medusae (Medusahead).  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Teneiatherum.  
OX NCBI\_TaxID=37687;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H10254; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."; Evol. 7:217-230(1997).  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77760; CAB01359.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 43

P92391 ID P92391 PRELIMINARY; PRT; 8 AA.  
AC P92391; 1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Heteranthelium pilliferum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Heteranthelium.  
OX NCBI\_TaxID=37679;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5557; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."; Evol. 7:217-230(1997).  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77750; CAB01329.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 44

P93981 ID P93981 PRELIMINARY; PRT; 8 AA.  
AC P93981; 1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Crithodium monocoecum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Crithodium.  
OX NCBI\_TaxID=72428;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4547; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."; Evol. 7:217-230(1997).  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77757; CAB01350.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18  
Db 1 KSL 3

## RESULT 45

P93992 ID P93992 PRELIMINARY; PRT; 8 AA.  
AC P93992; 1997 (TrEMBLrel. 03, Created)  
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PetD protein (Fragment).  
GN PETD.  
OS Austroalopurum velutinum.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Austroalopurum.  
OX NCBI\_TaxID=58935;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6724; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data."; Evol. 7:217-230(1997).  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77768; CAB01383.1; -.  
KW Chloroplast.  
FT NON TER 1  
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

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SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;
Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 46
P92426 PRELIMINARY; PRT; 8 AA.
ID P92426;
AC P92426;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Pseudoroegneria.
OX NCBI_TaxID=4604;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H9082; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77744; CAB01311.1; -.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 47
P92431 PRELIMINARY; PRT; 8 AA.
ID P92431;
AC P92431;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PetD protein (Fragment).
GN PETD.
OS Aegilops tauschii (Aegilops squarrosa).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H6668; TISSUE=Leaf;
RX MEDLINE=97271648; PubMed=9126564;
RA Petersen G.; Seberg O.;
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA
sequence data.";
RL Mol. Phylogenet. Evol. 7:217-230(1997).
DR EMBL; Z77758; CAB01353.1; -.
KW Chloroplast.

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FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 48
P92422 PRELIMINARY; PRT; 8 AA.
ID P92422;
AC P92422; P92420;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE Chloroplast rpoA gene (Fragment).
GN PETD.
OS Feathyrostachys fragilis.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Psathyrostachys.
OX NCBI_TaxID=37729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H4372, and H917; TISSUE=Leaf;
RA Petersen G.; Seberg O.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z77753; CAB01338.1; -.
DR EMBL; Z77752; CAB01335.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 878 MW; 1EC7287731A735B3 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 1 KSL 3

RESULT 49
Q40530 PRELIMINARY; PRT; 8 AA.
ID Q40530;
AC Q40530;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE P20 n with a leader peptide.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089808; PubMed=3540612;
RA Herman L.M.F.; Montagu M.C.V.; Depicker A.G.;
RT "Isolation of tobacco DNA segments with plant promoter activity.";
RL Mol. Cell. Biol. 6:4486-4492(1986).
DR EMBL; M14685; AAA34090.1; -.
SQ SEQUENCE 8 AA; 1103 MW; E257205B19C9C9C6 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 13 EIL 15

Db 5 EIL 7

## RESULT 50

ID Q9ERD2 PRELIMINARY; PRT; 8 AA.

AC Q9ERD2;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE Galactose-1-phosphate uridylyl transferase (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/D3;

RA Leslie N.D., Bai S.;

RT "Functional analysis of the mouse galactose-1-phosphate uridylyl

RT transferase (GALT) promoter."

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF314226; AAG31161.1; -.

KW Transferase.

FT NON TER

SQ SEQUENCE 8 AA; 854 MW; ECBDC409D1ADDD6 CRC64;

## Query Match

Best Local Similarity 16.7%; Score 3; DB 11; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATF 3

Db 3 ATF 5

## RESULT 51

ID Q90ZV5 PRELIMINARY; PRT; 8 AA.

AC Q90ZV5;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Adenylate kinase (Fragment).

OS Fulica leucoptera.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.

OX NCBI\_TaxID=156758;

RN [1]

RP SEQUENCE FROM N.A.

RA Shapiro L.H., Dumbacher J.P.;

RT "Adenylate kinase intron 5: a new nuclear locus for avian

RT systematics."

RL Auk 118:248-255(2001).

DR EMBL; AF307898; AAK43537.1; -.

KW Kinase.

FT NON TER

SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

## Query Match

Best Local Similarity 16.7%; Score 3; DB 13; Length 8;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13

Db 2 GEE 4

## RESULT 52

Q8GLJ1

ID Q8GLJ1

AC Q8GLJ1;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE PF-50 protein (Fragment).

GN PF-50.

OS Borrelia burgdorferi (Lyme disease spirochete).

OG Plasmid group cp32-1.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.

OX NCBI\_TaxID=139;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Sh-2-82;

RA Stevenson B., Miller J.C.;

RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32

RT prophages: conservation amidst diversity."

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY142089; AAN17869.1; -.

KW Plasmid.

FT NON TER

SQ SEQUENCE 9 AA; 1206 MW; 5A4A244337204373 CRC64;

## Query Match

Best Local Similarity 16.7%; Score 3; DB 2; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16

Db 4 ILK 6

## RESULT 53

Q9IBY9

ID Q9IBY9

AC Q9IBY9;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

DE ORF 10-like protein (Fragment).

OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Gammaherpesvirinae; Rhadinovirus.

OX NCBI\_TaxID=37296;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=KS187;

RX MEDLINE=20240083; PubMed=10775636;

RA Schultz E.R., Rankin G.W. Jr., Blanc M.P., Raden B.W., Tsai C.C.,

RA Rose T.M.;

RT "Characterization of two divergent lineages of macaque rhadinoviruses

RT related to Kaposi's sarcoma-associated herpesvirus."

J. Virol. 74:4919-4928(2000).

DR EMBL; AF005477; AAF78829.1; -.

FT NON TER

SQ SEQUENCE 9 AA; 1053 MW; CD1959D1ADDB01B6 CRC64;

## Query Match

Best Local Similarity 16.7%; Score 3; DB 12; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATF 3

Db 5 ATF 7

## RESULT 54

Q8W7U4

ID Q8W7U4

AC Q8W7U4;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

```
DE Cytochrome oxidase subunit 1 (Fragment).
GN COL.
OS Anolis mitens.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
OX NCBI_TaxID=174262;
RN [1]
SEQUENCE FROM N.A.
RA Glor R.E., Vitt L.J., Larson A.;
RP Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF337800; AAL72083.1; -.
DR EMBL; AF337801; AAL72085.1; -.
KW Mitochondrion.
FT NON TER 10
SQ SEQUENCE 10 AA; 1349 MW; C9348E29D3640449 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 FNR 5
DB 3 FNR 5

RESULT 55
Q63056 PRELIMINARY; PRT; 10 AA.
ID O63056 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Rat asialoglycoprotein receptor (ASGP) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=87026895; PubMed=2945599;
RX Watts C.;
RA "Isolation and expression of cDNA clones for a rat liver
RT asialoglycoprotein receptor.";
RL Biosci. Rep. 6:527-534(1986).
DR EMBL; M21739; AAA40763.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1312 MW; 56ADE0CAB6C5AA3 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YOD 8
DB 5 YOD 7

RESULT 56
Q8VIL8 PRELIMINARY; PRT; 10 AA.
ID Q8VIL8 (TEMBLrel. 20, Created)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Immediate early gene protein Homer1A (Fragment).
OS Mus musculus (Mouse).
OG HOMER1.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
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RN [1]
SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Bottai D., Guzowski J.F., Schwarz M.K., Kang S.H., Xiao B.,
RA Lanahan A., Worley P.F., Seeburg P.H.;
RT "Synaptic Activity-Induced Conversion of Intronic to Exonic Sequence
in Homer1 Immediate Early Gene Expression.";
RL J. Neurosci. 0:0-0(2002).
DR EMBL; AF425674; AAL34511.1; -.
DR MGD; MGI:1347345; Homer1.
FT NON TER 1
SQ SEQUENCE 10 AA; 1187 MW; CD7A2B905DC5B449 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TFN 4
DB 2 TFN 4

RESULT 57
Q9JLI5 PRELIMINARY; PRT; 10 AA.
ID Q9JLI5 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
DE Melanocortin type 1 receptor MC1R (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RC MEDLINE=20090876; PubMed=10623832;
RX Adachi S., Morii E., Kim D.-k., Oginhara H., Jippo T., Ito A., Lee Y.M.,
RA Kitamura Y.;
RT "Involvement of mi-transcription factor in expression of alpha-
RT melanocyte-stimulating hormone receptor in cultured mast cells of
RT mice.";
RL J. Immunol. 164:855-860(2000).
DR EMBL; AFI76016; AAF37323.1; -.
KW Receptor.
FT NON TER 10
SQ SEQUENCE 10 AA; 1148 MW; 95B58A26C76B06C1 CRC64;

Query Match 16.7%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KSL 18
DB 8 KSL 10

RESULT 58
Q9L4F7 PRELIMINARY; PRT; 11 AA.
ID Q9L4F7 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
DE (Fragment).
OG PLCA.
OC Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
SEQUENCE FROM N.A.
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RC STRAIN=ATCC 14579 type strain;
RX MEDLINE=2005637; PubMed=10589720;
RA Okstad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
RT "Sequence analysis of three Bacillus cereus loci under PicR-regulated
RL genes encoding degradative enzymes and enterotoxin.";
RL Microbiology 145:3129-3138(1999).
DR EMBL; AJ243711; CAB69804.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 7 ILK 9

RESULT 59
Q9S618 ID Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PPTD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220.
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RL sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070132; AAD20740.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 3 ILK 5

RESULT 60
Q8GL19 ID Q8GL19 PRELIMINARY; PRT; 11 AA.
AC Q8GL19;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE PF-50 protein (Fragment).
GN PF-50.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RA Stevenson B., Miller J.C.;
RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RL prophages: conservation amidst diversity.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY142096; AAN17880.1; -.
KW Plasmid.

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FT NON TER 1 1
SQ SEQUENCE 11 AA; 1366 MW; 4E441D5337204373 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 6 ILK 8

RESULT 61
Q16234 ID Q16234 PRELIMINARY; PRT; 11 AA.
AC Q16234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Hud protein (Fragment).
GN HUD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349312; PubMed=8069866;
RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;
RT "Molecular analysis of the HUD gene encoding a paraneoplastic
RL encephalomyelitis antigen in human lung cancer cell lines.";
RL Cancer Res. 54:4988-4992(1994).
DR EMBL; S73887; AAD14142.1; -.
FT NON TER 11
SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 16.7%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 ILK 16
Db 7 ILK 9

RESULT 62
Q8RV30 ID Q8RV30 PRELIMINARY; PRT; 11 AA.
AC Q8RV30;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Methionine adenosyltransferase 1-like protein (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Various strains;
RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
RA Morgante M., Rafalski J.A.;
RT "SNP frequency, haplotype structure and linkage disequilibrium in
RL elite maize inbred lines.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486085; AAL85893.1; -.
DR EMBL; AF486086; AAL85894.1; -.
DR EMBL; AF486087; AAL85895.1; -.
DR EMBL; AF486088; AAL85896.1; -.
DR EMBL; AF486089; AAL85897.1; -.
DR EMBL; AF486090; AAL85898.1; -.
DR EMBL; AF486091; AAL85899.1; -.

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DR EMBL; AF486092; AAL85900.1; -  
DR EMBL; AF486093; AAL85901.1; -  
DR EMBL; AF486094; AAL85902.1; -  
DR EMBL; AF486095; AAL85903.1; -  
DR EMBL; AF486096; AAL85904.1; -  
DR EMBL; AF486097; AAL85905.1; -  
DR EMBL; AF486098; AAL85906.1; -  
DR EMBL; AF486099; AAL85907.1; -  
DR EMBL; AF486100; AAL85908.1; -  
DR EMBL; AF486101; AAL85909.1; -  
DR EMBL; AF486102; AAL85910.1; -  
DR EMBL; AF486104; AAL85911.1; -  
DR EMBL; AF486105; AAL85912.1; -  
DR EMBL; AF486106; AAL85913.1; -  
DR EMBL; AF486107; AAL85914.1; -  
DR EMBL; AF486108; AAL85915.1; -  
DR EMBL; AF486109; AAL85916.1; -  
DR EMBL; AF486110; AAL85917.1; -  
DR EMBL; AF486111; AAL85918.1; -  
DR EMBL; AF486112; AAL85919.1; -  
DR EMBL; AF486113; AAL85920.1; -  
DR EMBL; AF486114; AAL85921.1; -  
DR EMBL; AF486115; AAL85922.1; -  
DR EMBL; AF486116; AAL85923.1; -  
DR EMBL; AF486117; AAL85924.1; -  
DR EMBL; AF486118; AAL85925.1; -  
KW Transferase.  
FT NON\_TER 1  
SQ SEQUENCE 11 AA; 1183 MW; 448D42ED3B05B337 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKS 17  
Db 4 LKS 6

## RESULT 63

Q8JS92  
ID Q8JS92 PRELIMINARY; PRT; 11 AA.  
AC Q8JS92;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE X protein (Fragment).  
OS Hepatitis B virus  
OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.  
OX NCBI\_TaxID=10407;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=34;  
RX PubMed=12185284;  
RA Hou J., Lin Y., Waters J., Wang Z., Min J., Liao H., Jiang J.,  
RA Chen J., Luo K., Karayannis P.;  
RT "Detection and significance of a G1862T variant of hepatitis B virus  
RT in Chinese patients with fulminant hepatitis.";  
RL J. Gen. Virol. 83:2291-2298(2002).  
DR EMBL; AF495695; AAM34089.1; -  
FT NON\_TER 1  
SQ SEQUENCE 11 AA; 1315 MW; DC70528AB5B73412 CRC64;

Query Match 16.7%; Score 3; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
Db 1 GEE 3

## RESULT 64

Q8JS92

Q93A08  
ID Q93A08 PRELIMINARY; PRT; 12 AA.  
AC Q93A08;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ResB protein (Fragment).  
GN ResB.  
OS Thiobacillus ferrooxidans.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.  
OX NCBI\_TaxID=920;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC33020;  
RA Levan G., Bruscella P., Guacanano M., Inostroza C., Jedlicki E.,  
RA Bonhefoy V., Holmes D.S.;  
RT "Characterization of the pet and res operons of Acidithiobacillus  
RT ferrooxidans";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ413194; CAC88360.1; -  
FT NON\_TER 1  
SQ SEQUENCE 12 AA; 1405 MW; 886AB7DF1E13240A CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QDD 9  
Db 3 QDD 5

RESULT 65  
Q93U04  
ID Q93U04 PRELIMINARY; PRT; 12 AA.  
AC Q93U04;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Orf.  
OS Escherichia coli O157:H7.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=83334;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Miyamoto T., Ichioke N., Sasaki C., Kobayashi H., Honjoh K., Iio M.,  
RA Hatano S.;  
RT "PCR assay using primers amplify the DNA region specific to  
RT Escherichia coli O157:H7.";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB061018; BAB47188.1; -  
SQ SEQUENCE 12 AA; 1422 MW; 04CF73E560D559C0 CRC64;  
  
Query Match 16.7%; Score 3; DB 2; Length 12;  
Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEE 13  
Db 10 GEE 12

RESULT 66  
Q914M9  
ID Q914M9 PRELIMINARY; PRT; 12 AA.  
AC Q914M9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE Guanosine bipyrophosphate synthetase, putative (Fragment).  
GN REL.  
OS Streptococcus equisimilis.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 RX NCBI\_TaxID=119602;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=H46A;  
 RX MEDLINE=20123454; PubMed=10660058;  
 RA Geyer A., Schmidt K.H.;  
 RT "Genetic organisation of the M protein region in human isolates of  
 RT group C and G streptococci: two types of multigene regulator-Like  
 RT (mgrC) regions.";  
 RL Mol. Gen. Genet. 262:965-974(2000).  
 DR EMBL; AJ133440; CAB70616.1; -.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1334 MW; 0A82EC4258A72440 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEE 13  
 Db 9 GEE 11

## RESULT 67

Q47251 ID Q47251 PRELIMINARY; PRT; 12 AA.  
 AC Q47251;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)  
 DE HEMC protein (Fragment).  
 GN HEMC.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=562;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=K12;  
 RX MEDLINE=88096587; PubMed=3320969;  
 RA Jordan P.M., Mgebe B.I.A., Alwan A.F., Thomas S.D.;  
 RT "Nucleotide sequence of hemD, the second gene in the hem operon of  
 RT Escherichia coli K-12.";  
 RL Nucleic Acids Res. 15:10583-10583(1987).  
 DR EMBL; Y00883; CAA68775.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1375 MW; 5D2DE8339BA045B3 CRC64;

Query Match 16.7%; Score 3; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKS 17  
 Db 4 LKS 6

## RESULT 68

Q9TRU1 ID Q9TRU1 PRELIMINARY; PRT; 12 AA.  
 AC Q9TRU1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE 43 kDa CYANOGEN bromide fragment PEAK 7 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;

RN SEQUENCE.  
 RX MEDLINE=92132498; PubMed=1734497;  
 RA Velby O.P., Sletten K., Husby G., Nordstoga K.;  
 RT "Amino acid sequence analyses of non-AA proteins from amyloid fibrils  
 RT of bovine kidney.";  
 RL Scand. J. Immunol. 35:63-69(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1257 MW; 0D5C94FDE9B76AA4 CRC64;

Query Match 16.7%; Score 3; DB 6; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFN 4  
 Db 3 TFN 5

## RESULT 69

P82164 ID P82164 PRELIMINARY; PRT; 12 AA.  
 AC P82164;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S14 beta (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OC NCBI\_TaxID=3562;  
 [1]  
 RN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.  
 RC STRAIN=CV. ALVARO; TISSUE=Leaf;  
 RX MEDLINE=20435797; PubMed=10874039;  
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 RT the small subunit of an organelle ribosome (chloroplast).";  
 J. Biol. Chem. 37:28455-28465(2000).  
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -1- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN P.I. S14 ALPHA  
 CC FORM IS THE LEAST BASIC FORM.  
 CC -1- MASS SPECTROMETRY: MW=11745.9; METHOD=ELECTROSPRAY.  
 CC -1- MASS SPECTROMETRY: MW=11947; METHOD=MALDI.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.  
 CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro; IPR001209; Ribosomal\_S14.  
 DR InterPro; IPR001648; Ribosomal\_S18.  
 DR Pfam; PF00253; Ribosomal\_S14; PARTIAL.  
 DR PROSITE; PS00057; RIBOSOMAL\_S18; PARTIAL.  
 KW Ribosomal protein; Chloroplast; rRNA-binding.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1513 MW; 5E84D3F10116D057 CRC64;

Query Match 16.7%; Score 3; DB 8; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 Db 3 KSL 5

## RESULT 70

Q62966 ID Q62966 PRELIMINARY; PRT; 12 AA.  
 AC Q62966;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Interstitial collagenase (Fragment).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=96408720; PubMed=8813727;  
 RA Rajakumar R.A., Quinn C.O.;  
 RT "Parathyroid hormone induction of rat interstitial collagenase mRNA in  
 RT osteosarcoma cells is mediated through an AP-1-binding site.";  
 RL Mol. Endocrinol. 10:867-878(1996).  
 DR EMBL; U53605; AAB47407.1; -.  
 KW Collagen.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1432 MW; 148A4DFE8ADD720 CRC64;  
 Query Match 16.7%; Score 3; DB 11; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATF 3  
 Db ||||  
 7 ATF 9  
 RESULT 71  
 Q84268  
 ID Q84268 PRELIMINARY; PRT; 12 AA.  
 AC Q84268;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE E1 ORF (Fragment).  
 OS Human papillomavirus.  
 OS Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89095007; PubMed=2536104;  
 RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;  
 RT "Presence of Caenated Human Papillomavirus Type 16 Episomes in a  
 RT Cervical Carcinoma Cell Line";  
 RL J. Virol. 63:782-789(1989).  
 DR EMBL; M24215; AAA46945.1; -.  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1178 MW; 993F1F424D51A861 CRC64;  
 Query Match 16.7%; Score 3; DB 12; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GEE 13  
 Db ||||  
 9 GEE 11  
 RESULT 72  
 Q9R3R6  
 ID Q9R3R6 PRELIMINARY; PRT; 13 AA.  
 AC Q9R3R6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Cytochrome B6/F complex subunit IV (Fragment).  
 GN PETD.  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.

OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 RT sorted from the Sargasso Sea and Gulf Stream.";  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070222; AAD23275.1; -.  
 DR EMBL; AF070221; AAD23273.1; -.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1522 MW; 4CDE4CC38013B763 CRC64;  
 Query Match 16.7%; Score 3; DB 2; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 14 ILK 16  
 Db ||||  
 3 ILK 5  
 RESULT 73  
 Q9UDE0  
 ID Q9UDE0 PRELIMINARY; PRT; 13 AA.  
 AC Q9UDE0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Aggrecan core protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92235266; PubMed=1569188;  
 RA Sandy J.D., Flannery C.R., Neame P.J., Lohmander L.S.;  
 RL J. Clin. Invest. 89:1512-1516(1992).  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1407 MW; 3A1B032DD2751B18 CRC64;  
 Query Match 16.7%; Score 3; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GEE 13  
 Db ||||  
 6 GEE 8  
 RESULT 74  
 Q812E2  
 ID Q812E2 PRELIMINARY; PRT; 13 AA.  
 AC Q812E2;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 GN PPA0655W.  
 OS Plasmodium falciparum (isolate 3D7).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 NCBI\_TaxID=36329;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22255708; PubMed=12368867;  
 RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,  
 RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,  
 RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,  
 RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,  
 RA Cronin A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,  
 RA Felwell T., Gobie A., Goodhead I., Gwilliam R., Hamlin N., Hance Z.,  
 RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,

RA Humphray S., Jagels K., James K.D., Johnson D., Kerhornou A.,  
 RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,  
 RA Line A., Maddison M., Mclean J., Mooney P., Moule S., Murphy L.,  
 RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,  
 RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,  
 RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,  
 RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,  
 RA Sulston J.E., Craig A., Newbold C., Barrell B.G;  
 RT "Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";  
 RL Nature 419:527-531(2002).  
 DR EMBL; AL031744; CAD48947.1; --  
 KW Hypothetical protein.  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1619 MW; 50E352E2F7FED1A7 CRC64;

Query Match 16.7%; Score 3; DB 5; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EIL 15  
 |||  
 Db 4 EIL 6

## RESULT 75

Q945C1  
 ID Q945C1 PRELIMINARY; PRT; 13 AA.  
 AC Q945C1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Dip5 protein (Fragment).  
 OS Cryptocodium cohnii (Dinoflagellate).  
 CC Eukaryota; Alveolata; Dinophyceae; Gonyaulacales; Cryptecodiniaceae;  
 CC Cryptecodinium.  
 OX NCBI\_TaxID=2856;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21428164; PubMed=11545436;  
 RA Guillebaud D., Derelle E., Bhaud Y., Moreau H.;  
 RT "Role of nuclear WW domains and proline-rich proteins in  
 RT dinoflagellate transcription.";  
 RL Protist 152:127-138(2001).  
 DR EMBL; AF417570; AAL15908.1; --  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1225 MW; 322FA05EE70CB327 CRC64;

Query Match 16.7%; Score 3; DB 10; Length 13;  
 Best Local Similarity 100.0%; Pred.No. 1.2e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 KSL 18  
 |||  
 Db 7 KSL 9

Search completed: November 25, 2003, 19:34:12  
 Job time : 35.8023 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 25, 2003, 18:16:09 ; Search time 45.9419 Seconds  
(without alignments)  
62.189 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFFNYQDDHGSEILKSL 18

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 399878

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : A\_Geneseq\_19Jun03.\*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*
- 9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*
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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*
- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	22	Colostrin derixe
2	18	100.0	18	22	Colostrin peptid
3	18	100.0	18	22	Colostrin peptid
4	18	100.0	18	22	Ewe colostrin pe
5	18	100.0	18	22	Colostrin consti
6	18	100.0	18	23	Colostrin consti
7	18	100.0	18	23	Neural cell regula
8	18	100.0	19	22	Ewe colostrin pe
9	6	33.3	11	22	Rat SNS1 ion chann

83 HIV A01 super moti  
 84 HIV A03 super moti  
 85 HIV A24 super moti  
 86 HIV A24 super moti  
 87 HIV B07 super moti  
 88 HIV B07 super moti  
 89 HIV B07 super moti  
 90 HIV B07 super moti  
 91 HIV B62 super moti  
 92 HIV B62 super moti  
 93 HIV A03 motif gag  
 94 HIV A03 motif gag  
 95 HIV A03 motif gag  
 96 HIV A03 motif pol  
 97 HIV A11 motif pol  
 98 Schizophrenia-Asso  
 99 Schizophrenia-Asso  
 100 Human HLA-A1 bindi

## ALIGNMENTS

RESULT 1  
 AAB72275  
 ID AAB72275 standard; peptide; 18 AA.  
 AC AAB72275;  
 DT 14-MAY-2001 (first entry)  
 XX  
 DE Colostrinin derived cytokine inducing peptide SEQ ID 30.  
 XX  
 KW Colostrinin; immune response; cytokine; blood cell proliferation;  
 KW central nervous system disorder; neurological disorder; mental disorder;  
 KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;  
 KW neurosis; infection.  
 OS Synthetic.  
 XX  
 XX WO200111937-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 17-AUG-2000; 2000WO-US22818.  
 XX  
 XX 17-AUG-1999; 99US-0149311.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX (REGG-) REGEN THERAPEUTICS PLC.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I, Georgiades J;  
 XX WPI; 2001-202804/20.  
 XX  
 XX Inducing a cytokine and modulating an immune response, useful for  
 XX treating central nervous system diseases and bacterial and viral  
 XX infections, comprises administering colostrinin as an immunological  
 XX regulator -  
 XX  
 XX Claim 1; Page 34; 50pp; English.  
 XX  
 XX Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 XX a proline rich polypeptide aggregate contained in colostrum. The  
 XX peptides have immune response modulatory activity, and are capable of  
 XX inducing cytokines. Colostrinin and its derived peptides are useful for  
 XX inducing cytokine production, for modulating an immunological response  
 XX and for inducing blood cell proliferation. The peptides are useful in the  
 XX treatment of disorders of the central nervous system, neurological  
 XX disorders, mental disorders, dementia, neurodegenerative diseases,  
 XX Alzheimer's disease, motor neuron disease, psychosis, neurosis, chronic  
 XX disorders of the immune system, bacterial and viral infections and  
 XX acquired immunological deficiencies.

XX SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATFNRYQDDHGEBILKSL 18  
 |||||  
 DB 1 ATFNRYQDDHGEBILKSL 18  
 |||||  
 RESULT 2  
 AAB72528  
 ID AAB72528 standard; Peptide; 18 AA.  
 XX  
 AC AAB72528;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #29.  
 XX  
 KW Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200112650-A2.  
 XX  
 XX 22-FEB-2001.  
 XX  
 XX 17-AUG-2000; 2000WO-US22665.  
 XX  
 XX 17-AUG-1999; 99US-0149310.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 XX WPI; 2001-218342/22.  
 XX  
 XX Modulating oxidative stress level in a cell, involves contacting the  
 XX cell with an oxidative stress regulator selected from colostrinin, its  
 XX constituent peptide, analog or their combinations -  
 XX  
 XX Claim 6; Page 26; 48pp; English.  
 XX  
 XX The present invention relates to a method for modulating the oxidative  
 XX stress level in a cell or a patient, comprising contacting the cell with,  
 XX or administering to the patient, an oxidative stress regulator selected  
 XX from colostrinin, or its constituent peptide (e.g. the present peptide),  
 XX to change the level of an oxidizing species in the cell. The method can  
 XX be used to treat oxidative damage to skin, by decreasing or preventing an  
 XX increase in the level of damage to a biomolecule of the patient.  
 XX  
 XX SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATFNRYQDDHGEBILKSL 18  
 |||||  
 DB 1 ATFNRYQDDHGEBILKSL 18  
 |||||  
 RESULT 3  
 AAB72560  
 ID AAB72560 standard; Peptide; 18 AA.  
 XX  
 AC AAB72560;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX

DE Colostrinin peptide #29.  
 XX Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KW colostrinum.  
 XX Unidentified.  
 OS  
 XX  
 PN WO200112651-A2.  
 XX  
 XX 22-FEB-2001.  
 PD  
 XX 17-AUG-2000; 2000WO-US22774.  
 PF  
 XX 17-AUG-1999; 99US-0149633.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Boldogh I;  
 PI  
 XX WPI; 2001-226545/23.  
 DR  
 XX Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 PT  
 XX Claim 6; Page 22; 35pp; English.  
 PS  
 XX The present invention relates to a method for promoting neural cell  
 XX differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 CC  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATFNRYQDDHGGEILKSL 18  
 |||||  
 Db 1 ATFNRYQDDHGGEILKSL 18  
 |||||  
 RESULT 4  
 AAB59340  
 ID AAB59340 standard; Peptide; 18 AA.  
 AC  
 AC AAB59340;  
 XX  
 XX 21-MAR-2001 (first entry)  
 DT  
 XX Ewe colostrinin peptide fragment D-1.  
 DE  
 XX Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;  
 KW central nervous system disorder; dietary supplement; beta-amyloid plaque.  
 XX  
 XX Ovis sp.  
 OS  
 XX WO2000075173-A2.  
 PN  
 XX 14-DEC-2000.  
 PD  
 XX 02-JUN-2000; 2000WO-GB02128.  
 PF  
 XX 02-JUN-1999; 99GB-0012852.  
 PR  
 XX (REG- ) REGEN THERAPEUTICS PLC.  
 PA  
 XX Georgiades JA;  
 PI  
 XX WPI; 2001-071058/08.  
 DR  
 XX Peptides having an N-terminal amino acid sequence isolated from  
 PT

PT colostrinin for treating e.g. disorders of the central nervous system  
 PT and immune system, viral and bacterial infections, and diseases  
 XX characterized by amyloid plaques -  
 XX Claim 7; Page 27; 63pp; English.  
 PS  
 XX The present invention provides the sequences of a number of peptides  
 CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide  
 CC fragment of colostrum. These peptides can be used in the treatment of  
 CC central nervous system disorders such as senile dementia, Parkinson's  
 CC disease, Alzheimer's disease, psychosis and neurosis, immune system  
 CC disorders such as bacterial and viral infections, to improve the  
 CC development of a child's immune system, as a dietary supplement, and to  
 CC promote the dissolution of beta-amyloid plaques.  
 XX  
 SQ Sequence 18 AA;  
 Query Match 100.0%; Score 18; DB 22; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ATFNRYQDDHGGEILKSL 18  
 |||||  
 Db 1 ATFNRYQDDHGGEILKSL 18  
 |||||  
 RESULT 5  
 AAE20257  
 ID AAE20257 standard; peptide; 18 AA.  
 XX  
 AC AAE20257;  
 XX  
 XX 18-JUN-2002 (first entry)  
 DT  
 XX Colostrinin constituent peptide #29.  
 DE  
 XX Blood cell regulator; colostrinin; constituent peptide; oxidative stress;  
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;  
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;  
 KW transplantation; implantation; dermatological; vulneryary.  
 XX  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 18  
 FT /note= "Optionally C-terminal amide"  
 FT  
 XX WO200213850-A1.  
 PN  
 XX 21-FEB-2002.  
 PD  
 XX 17-AUG-2000; 2000WO-US22776.  
 PF  
 XX 17-AUG-2000; 2000WO-US22776.  
 PR  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Stanton GJ, Hughes TK, Boldogh I;  
 PI  
 XX WPI; 2002-269151/31.  
 DR  
 XX Composition useful for the modulation of blood cell proliferation in a  
 PT patient comprises a blood cell regulator selected from colostrinin, its  
 PT constituent peptide and/or analog -  
 PT  
 XX Claim 6; Page 26; 51pp; English.  
 PS  
 XX The invention relates to a composition which comprises a blood cell  
 CC regulator selected from colostrinin, its constituent peptide and/or  
 CC analogue. The invention is used for modulating the oxidative stress  
 CC level in a cell e.g. mammalian or human cell present in a cell culture,  
 CC tissue, organ, or organism; or for treating oxidative damage to the skin  
 CC of a patient e.g. animal or human; to modulate oxidative stress during/



CC after a premature birth or normal birth, preventing/delaying aging in a  
 CC patient, enhancing wound healing, and the reduction of side effects of  
 CC cosmetic procedures. The method changes the level of an oxidising species  
 CC in the cell, such as decreases or prevents increase in the level of  
 CC damage to a biomolecule of the patient selected from DNA, protein and/or  
 CC lipid, compared to the same conditions when the oxidative stress  
 CC regulator is not present. The modulation of oxidative stress results in  
 CC enhanced repair, regeneration, and replacement of cells, tissues and  
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and  
 CC external organs), as well as enhanced preservation of such organs for  
 CC transplantation, implantation, or scientific research. The present  
 CC sequence is a colostrinin constituent peptide.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATFNRYQDDHGEEILKSL 18  
 |||||  
 Db 1 ATFNRYQDDHGEEILKSL 18

# RESULT 6

AA051064  
 ID AA051064 standard; Peptide; 18 AA.

XX AC AA051064;

XX DT 30-MAY-2002 (first entry)

XX DE Colostrinin constituent peptide (annexin amino acids 203-220).

XX KW Colostrinin; colostrum; immunomodulator; cardiovascular;

XX KW blood cell regulator; cytokine inducer; annexin; human.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amidation"

XX PN WO200213849-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22775.

XX PR 17-AUG-2000; 2000WO-US22775.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PA (REGG-) REGEN THERAPEUTICS PLC.

XX PI Stanton GU, Hughes TK, Boldogh I, Georgiades J;

XX DR WPI; 2002-269150/31.

XX PT Modulation of blood cell proliferation in a patient involves use of  
 PT blood cell regulator selected from colostrinin, its constituent peptide  
 PT and/or analogue -

XX PS Claim 1; Page 34; 54pp; English.

XX CC The present sequence is that of a colostrinin constituent peptide  
 CC that is used as an immunological regulator and as a blood cell  
 CC regulator in claimed methods of the invention. It is classified  
 CC as having an annexin precursor, and corresponds to annexin amino  
 CC acids 203-220. Methods are claimed for: inducing a cytokine in a  
 CC cell by contact with an immunological regulator, where the cell is  
 CC present in a cell culture, a tissue, an organ or an organism, and  
 CC the cell is mammalian, including human; modulating an immune  
 CC response in a cell by contact with the immunological regulator

CC under conditions effective to induce a cytokine; modulating an  
 CC immune response in a patient by administering an immunological  
 CC regulator under conditions effective to induce a cytokine, where  
 CC the immunological regulator is administered topically or as part  
 CC of a dietary supplement, and where the immune response is specific  
 CC or non specific, an interferon response or an antibody response;  
 CC modulating blood cell proliferation by contacting blood cells with  
 CC a blood cell regulator, where the blood cells are present in a cell  
 CC culture or an organism, are mammalian or human, and where the blood  
 CC cells are increased in number or differentiated; and a method for  
 CC modulating blood cell proliferation in a patient. A claimed  
 CC cytokine-inducing composition comprises a pharmaceutical carrier  
 CC and an active agent as the present peptide.

XX SQ Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-12; Indels 0; Gaps 0;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATFNRYQDDHGEEILKSL 18  
 |||||  
 Db 1 ATFNRYQDDHGEEILKSL 18

# RESULT 7

AA014606

ID AA014606 standard; peptide; 18 AA.

XX AC AA014606;

XX DT 27-MAY-2002 (first entry)

XX DE Neural cell regulatory colostrinin peptide 29.

XX KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

XX KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

XX KW neural cell treatment.

XX OS Unidentified.

XX FH Key Location/Qualifiers

FT Modified-site 18 /note= "Optional C-terminal amide"

XX PN WO200213851-A1.

XX PD 21-FEB-2002.

XX PF 17-AUG-2000; 2000WO-US22777.

XX PR 17-AUG-2000; 2000WO-US22777.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Boldogh I, Stanton JG, Hughes TK;

XX DR WPI; 2002-269152/31.

XX PT Promoting cell differentiation in a patient involves use of blood cell  
 PT regulator selected from colostrinin, its constituent peptide and/or  
 PT analog -

XX PS Claim 7; Page 22; 37pp; English.

XX CC The invention comprises a method for promoting cell differentiation (e.g.  
 CC neural cell differentiation). The method involves contacting cells with a  
 CC neural cell regulator (i.e. a colostrinin peptide) in order to change the  
 CC cells in morphology to form neural cells. Colostrinin is a proline-rich  
 CC polypeptide aggregate that is present in colostrum. The method of the  
 CC invention is useful for promoting the differentiation of cells and for  
 CC treating damaged neural cells in a patient. The present amino acid  
 CC sequence represents a specifically claimed colostrinin peptide used in

CC the method of the invention.

XX Sequence 18 AA;

Query Match 100.0%; Score 18; DB 23; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.7e-12;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFNRYQDDHGEILKSL 18

Db 1 ATFNRYQDDHGEILKSL 18

RESULT 8

AAB59357

ID AAB59357 standard; Peptide; 19 AA.

XX AC

XX AAB59357;

XX DT

XX 21-MAR-2001 (first entry)

XX DE

XX Ewe colostrin peptide fragment derived sequence #17.

XX KW

XX Sheep; colostrin; proline rich polypeptide; colostrum; immune disorder;

XX KW

XX central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX OS

XX Ovis sp.

XX PN

XX WO200075173-A2.

XX PD

XX 14-DEC-2000.

XX PF

XX 02-JUN-2000; 2000WO-GE02128.

XX PR

XX 02-JUN-1999; 99GB-0012852.

XX PA

XX (REG- ) REGEN THERAPEUTICS PLC.

XX PI

XX Georgiades JA;

XX DR

XX WPI; 2001-071058/08.

XX PT

XX Peptides having an N-terminal amino acid sequence isolated from

XX colostrin for treating e.g. disorders of the central nervous system

XX and immune system, viral and bacterial infections, and diseases

XX characterized by amyloid plaques -

XX PS

XX Claim 8; Page 27; 63pp; English.

XX CC

XX The present invention provides the sequences of a number of peptides found in ewe's colostrin. Colostrin is the proline-rich polypeptide fragment of colostrum. These peptides can be used in the treatment of central nervous system disorders such as senile dementia, Parkinson's disease, Alzheimer's disease, psychosis and neurosis, immune system disorders such as bacterial and viral infections, to improve the development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

XX SQ

Sequence 19 AA;

Query Match

Best Local Similarity 100.0%; Score 18; DB 22; Length 19;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFNRYQDDHGEILKSL 18

Db 2 ATFNRYQDDHGEILKSL 19

RESULT 9

AAG65972

ID AAG65972 standard; peptide; 11 AA.

XX

AC AAG65972;

XX DT

XX 11-FEB-2002 (first entry)

XX DE

XX Rat SNS1 ion channel protein mutant 2 (A1560E).

XX KW

XX Ion channel protein; gating; sensory neurone specific protein; SNS; analgesic; antiinflammatory; immunosuppressive; rat; mutant.

XX OS

XX Rattus sp.

XX PN

XX WO200168681-A2.

XX PD

XX 20-SEP-2001.

XX PF

XX 14-MAR-2001; 2001WO-GB01108.

XX PR

XX 14-MAR-2000; 2000GB-0006024.

XX PA

XX (GLAX ) GLAXO GROUP LTD.

XX PI

XX Aitken AJ, Chen MX, Gladwell ZM, Powell AJ, Tate SN;

XX DR

XX WPI; 2001-590038/66.

XX DR

XX N-PSDB; A167050.

XX PT

XX Altered ion channel protein useful for screening modulators that are useful in the manufacture of a medicament for the treatment of pain, inflammation and hypersensitivity, has acquired sensitivity to gating agent -

XX PS

XX Disclosure; Fig 3; 64pp; English.

XX CC

XX The invention provides an altered ion channel protein having acquired sensitivity to a gating agent. The altered ion channel protein can be expressed by standard recombinant methodology. The altered ion channel protein can be derived from a rat, mouse or human unaltered, gating agent insensitive ion channel proteins. The altered protein is useful in screening assay for the identification of modulators capable of modulating an unaltered gating agent insensitive ion channel protein. The modulator identified by the assay is preferably an antagonist of the altered protein, which is useful in the manufacture of a medicament for the treatment of pain, inflammation or hypersensitivity, and for treating a mammalian patient, particularly human. The present sequence represents a mutant fragment of the rat sensory neurone specific (SNS) 1 protein.

XX SQ

Sequence 11 AA;

Query Match

Best Local Similarity 33.3%; Score 6; DB 22; Length 11;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILKSL 18

Db 6 EILKSL 11

RESULT 10

ABJ04200

ID ABJ04200 standard; Peptide; 18 AA.

XX AC

XX ABJ04200;

XX DT

XX 24-OCT-2002 (first entry)

XX DE

XX Kinase-associated signal transduction modulating peptide 33.

XX KW

XX Kinase-associated signal transduction; diabetes; cancer; obesity; restenosis; bone healing; alopecia; osteoporosis;

XX KW

XX neurodegenerative disease; autoimmune disease; inflammation;

XX KW

XX atherosclerosis; skin disorder; central nervous system disease;

XX KW

XX inflammatory disorder; autoimmune disease; cardiovascular disease.

OS Unidentified.  
 XX WO200248336-A2.  
 XX  
 PD 20-JUN-2002.  
 XX  
 XX 11-DEC-2001; 2001WO-US47443.  
 XX  
 XX 11-DEC-2000; 2000US-0734520.  
 XX  
 XX (CHIL-) CHILDRENS MEDICAL CENT.  
 PA (YISS ) YISSUM RES & DEV CO.  
 XX  
 XX Ben-sasson S;  
 XX  
 XX WPI; 2002-583508/62.  
 XX  
 PT Identifying compounds for modulating kinase-associated signal  
 PT transduction and treating cancer, by synthesizing compounds having  
 PT short sequences identical to native sequences appearing in specific  
 PT region of a kinase -  
 XX  
 XX Claim 36; Fig 1; 143pp; English.  
 XX  
 CC The invention comprises a method for identifying compounds for the  
 CC modulation of kinase-associated signal transduction. The invention also  
 CC comprises a number of peptides which modulate kinase-associated signal  
 CC transduction. The method of the invention is useful for identifying  
 CC compounds for the modulation of kinase-associated signal transduction.  
 CC The kinase-associated signal transduction modulating peptides of the  
 CC invention are useful for treating: diabetes; cancer; obesity;  
 CC bone healing; alopecia; osteoporosis; neurodegenerative disease;  
 CC autoimmune disease; inflammation; restenosis; atherosclerosis; skin  
 CC disorders; central nervous system disease; inflammatory disorders;  
 CC autoimmune diseases; and cardiovascular diseases. The peptides ABU04168 -  
 CC ABU04300 represent the kinase-associated signal transduction modulating  
 CC peptides of the invention.  
 XX  
 XX Sequence 18 AA;  
 XX  
 Query Match 33.3%; Score 6; DB 23; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 EILKSL 18  
 Db 2 EILKSL 7  
 |||||  
 |||||  
 RESULT 11  
 ABUS4247  
 ID ABUS4247 standard; Peptide; 18 AA.  
 XX  
 XX ABUS4247;  
 AC  
 DT 06-MAR-2003 (first entry)  
 XX  
 DE Jak2 protein kinase A-region peptide.  
 XX  
 KW Kinase; A-region; PKA; PKA-Calpha; signal transduction; inhibitor;  
 KW stimulator; proliferation; differentiation; oncogenesis; cancer;  
 KW arteriosclerosis; psoriasis; septic shock; therapeutic; diabetes;  
 KW obesity; restenosis; tissue remodeling; bone healing; alopecia; scarring;  
 KW osteoporosis; neurodegenerative disease; autoimmune disease;  
 KW inflammation; atherosclerosis; skin disorder; central nervous system;  
 KW cardiovascular disease; dermatological; neuroprotective;  
 KW immunosuppressive.  
 XX  
 OS Unidentified.  
 OS Synthetic.  
 XX  
 XX US2002137141-A1.  
 XX

PD 26-SEP-2002.  
 XX  
 XX 11-DEC-2001; 2001US-0012034.  
 XX  
 PR 11-DEC-2000; 2000US-0734520.  
 XX  
 XX (CHIL-) CHILDRENS MEDICAL CENT.  
 PA Ben-sasson S;  
 XX  
 XX WPI; 2003-110601/10.  
 DR  
 XX  
 XX Identifying candidate compounds for the modulation of kinase-associated  
 PT signal transduction, useful for treating diabetes, cancer, obesity,  
 PT osteoporosis, autoimmune disorders, atherosclerosis and cardiovascular  
 PT diseases -  
 XX  
 XX Claim 36; Fig 1; 79pp; English.  
 XX  
 CC The invention discloses compounds, or variants of them, and methods for  
 CC identifying and synthesizing the candidate compounds which comprise a  
 CC peptide region in the protein kinase A-region (PKA). This region is  
 CC determined by aligning catalytic subunits of the kinase and PKA-Calpha  
 CC and determining the sequence of the kinase corresponding to positions  
 CC 92-109 of PKA-Calpha. The capacity of the compound to modulate the signal  
 CC transduction associated with the kinase (as a kinase inhibitor or  
 CC stimulator) is then determined. Protein kinases mediate signal  
 CC transduction in a wide variety of cellular events, such as cell  
 CC proliferation, differentiation, oncogenesis and immune/inflammatory  
 CC responses. Enhanced stimulation can lead to proliferative diseases, such  
 CC as cancer, arteriosclerosis, psoriasis and septic shock. The methods and  
 CC compositions are useful for detecting A-region ligands and for treating a  
 CC disease where a therapeutically beneficial effect may be evident by the  
 CC modulation of a signal transduction associated with a kinase, where the  
 CC kinase from which the A-region is determined is the kinase associated  
 CC with the signal transduction, and where the disease is diabetes, cancer,  
 CC obesity, restenosis, tissue remodeling including improved bone healing,  
 CC prevention of alopecia, reduced scarring, osteoporosis, neurodegenerative  
 CC disease, autoimmune disease, inflammation, atherosclerosis, skin  
 CC disorders, diseases of the central nervous system and cardiovascular  
 CC diseases. The sequences presented in ABUS4215-ABUS4336 are the A-region  
 CC peptides disclosed in the invention which are N-myristylated and  
 CC C-amidated.  
 XX  
 XX Sequence 18 AA;  
 XX  
 Query Match 33.3%; Score 6; DB 24; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 13 EILKSL 18  
 Db 2 EILKSL 7  
 |||||  
 |||||  
 RESULT 12  
 ABP59049  
 ID ABP59049 standard; Peptide; 17 AA.  
 XX  
 XX ABP59049;  
 AC  
 XX 20-FEB-2003 (first entry)  
 DT  
 XX Chlamydia trachomatis peptide epitope #90.  
 DE  
 XX Antibacterial; secreted protein; intracellular bacterium.  
 KW  
 XX Chlamydia trachomatis.  
 OS  
 XX WO200282091-A2.  
 XX  
 XX 17-OCT-2002.  
 PD  
 XX

PF 09-APR-2002; 2002WO-DK00234.  
 XX  
 PR 09-APR-2001; 2001DK-0000581.  
 PR 09-APR-2001; 2001US-282513P.  
 XX  
 PA (SHAW/) SHAW A C.  
 PA (VAND/) VANDAHN B B.  
 XX  
 PI Shaw AC, Vandahl BB;  
 XX  
 DR WPI; 2003-058585/05.  
 XX  
 PT Identifying intracellular bacterial proteins by labeling proteins in  
 PT the presence of a eukaryotic protein synthesis inhibitor, performing  
 PT electrophoresis, autoradiography and comparing profiles to an  
 PT infected-cell lysate profile -  
 XX  
 XX Disclosure; Page 20; 179pp; English.  
 PS  
 CC The present invention relates to a method (M1) for identifying secreted  
 CC intracellular bacterial proteins (BP). M1 comprises: (a) selectively  
 CC visualising BP by pulse labelling in the presence of an inhibitor of  
 CC eukaryotic protein synthesis followed by 2D electrophoresis and  
 CC autoradiography; (b) comparing protein profiles (PP) of purified bacteria  
 CC to PP of total lysate (TL) of infected cells; and (c) identifying protein  
 CC spots present in differential images from gels loaded with TL. The  
 CC present sequence is one such bacterial peptide epitope which was  
 CC identified by the method of the invention.  
 XX  
 XX Sequence 17 AA;  
 SQ  
 Query Match 27.8%; Score 5; DB 24; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GEEIL 15  
 DB 10 GEEIL 14  
 DE  
 DE Amino acid sequence of SP-22 derived peptide.  
 DE  
 KW Fertility-associated protein; SP-22; SP-16; testis;  
 KW testicular sperm; sperm membrane; fertility; testicular toxicant;  
 KW epididymal toxicant; vaccine; infertile.  
 XX  
 OS Rattus sp.  
 XX  
 XX WO9954354-A1.  
 XX  
 XX 28-OCT-1999.  
 XX  
 XX 15-APR-1999; 99WO-US08282.  
 XX  
 XX 23-APR-1998; 98US-0082753.  
 XX  
 XX (USSI ) US ENVIRONMENTAL PROTECTION AGENCY.  
 PA Klinefelter G;  
 XX  
 XX WPI; 2000-013227/01.  
 XX  
 XX New isolated fertility-associated protein, SP22, used to develop  
 PT products for affecting or testing male fertility, e.g. for use as  
 PT contraceptives or fertility enhancers -

XX Claim 4; Page 45; 67pp; English.  
 XX  
 CC AAY43755-58 represent peptides derived from a fertility-associated  
 CC protein, SP-22. SP22-A, SP-22B and SP-22C are an alternatively spliced  
 CC versions of SP-22. The SP-22 protein was originally designated SP-16. The  
 CC SP-22 protein is synthesised in the testis and can be recovered from  
 CC testicular sperm before they enter the epididymis. SP-22 is an integral  
 CC component of the sperm membrane, and is a component of ejaculated sperm  
 CC from other species including bull, stallion and human. It is highly  
 CC correlated with fertility following exposure to testicular toxicants as  
 CC well as epididymal toxicants. The SP22 is significantly correlated with  
 CC fertility and predictive of fertility. The products can be used to screen  
 CC for disruptors of fertility. The SP22, SP22A and SP22B or functional  
 CC derivatives can be used to improve fertility in a male animal by  
 CC addition to a semen sample or subset of sperm of the animal. They can  
 CC also be used in vaccines for rendering an animal infertile. An antibody  
 CC or targeted molecular antagonist to SP22A or SP22B or functional  
 CC derivative can be used for temporarily rendering a female animal  
 CC infertile by administering the protein vaginally.  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 22.2%; Score 4; DB 21; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 EILK 16  
 DB 1 EILK 4  
 DE  
 DE AAW90997 standard; Protein; 5 AA.  
 XX  
 AC AAW90997;  
 XX  
 DT 21-JUL-2000 (first entry)  
 DE  
 DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan protein fragment.  
 XX  
 KW Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;  
 KW transgenic plant; flavor; perfume; packaging material; papermaking;  
 KW ultra-violet light adsorber; starch; textile; wetting agent.  
 XX  
 OS Neisseria denitrificans.  
 XX  
 XX WO200022140-A1.  
 XX  
 XX 20-APR-2000.  
 XX  
 XX 08-OCT-1999; 99WO-EP07562.  
 XX  
 XX 09-OCT-1998; 98DE-1046635.  
 XX  
 XX 27-MAY-1999; 99DE-1024342.  
 XX  
 XX (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.  
 XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 XX Buettcher V, Quanz M;  
 XX  
 XX WPI; 2000-317992/27.  
 XX  
 XX New nucleic acid encoding a branching enzyme, useful for in vitro  
 PT synthesis of branched glucans and to prepare transgenic plants  
 PT producing modified starch -  
 XX  
 XX Disclosure; Page 108; 115pp; German.  
 XX  
 XX This invention describes a novel nucleic acid (I) isolated from  
 CC Neisseria which encodes a branching enzyme (II). (I) is used for  
 CC recombinant production of (II) subsequently used in the in vitro

CC production of alpha-1,6-branched alpha-1,4-glucans. It is also used to  
 CC prepare transgenic plants that produce starches with modified properties.  
 CC (iii) are used as binders for tablets, carriers for pharmaceuticals,  
 CC flavors and perfumes and powdered additives, packaging materials,  
 CC ultra-violet light adsorbers in sunscreens and also for any of the usual  
 CC applications of starch in foods, papermaking, as textile size, in soil  
 CC stabilization, as wetting agent for agricultural chemicals, as polymer  
 CC additives etc. Fragments of (i) are useful as PCR primers and antisense  
 CC molecules or ribozymes for inhibiting expression of (i), and the  
 CC regulatory region of (ii) can be used to control expression of  
 CC heterologous sequences in host cells. (i) provides an inexpensive method  
 CC for producing alpha-1,6-branched alpha-1,4-glucans (iii), producing  
 CC products that can be tailored for particular applications, particularly  
 CC by controlling the degree of branching. Starch from transgenic plants  
 CC has increased gel strength; reduced phosphate content; reduced peak  
 CC viscosity; lower pasting temperature and granule size and/or altered  
 CC sidechain distribution. This sequence represents an alpha-1,6-branched  
 CC alpha-1,4-glucan protein fragment isolated from *Neisseria denitrificans*  
 CC which is described in the method of the invention.

XX SQ Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DDHG 11  
 Db 1 DDHG 4

RESULT 15  
 AAY92081  
 ID AAY92081 standard; Peptide; 5 AA.

XX AC AAY92081;

XX DT 01-AUG-2000 (first entry)

XX DE C-terminal peptide of recombinant human DKR-3 expressed in *E. coli*.

XX DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
 KW growth factor; cytostatic; sonic hedgehog; tissue differentiation;  
 KW bacterial expression.

XX OS Synthetic.

XX PN WO200018914-A2.

XX PD 06-APR-2000.

XX PF 17-SEP-1999; 99WO-US21647.

XX PR 25-SEP-1998; 98US-0161241.

XX PA (AMGE-) AMGEN INC.

XX PI Bass MB, Sullivan JK, Theill LE, Wang D;

XX WPI; 2000-293153/25.

XX New nucleic acid molecule encoding a biologically active DKR  
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
 PT stem cell tumors

XX Example 9; Page 78; 143pp; English.

CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified  
 CC in *Xenopus* and mouse, purportedly an antagonist of wnt-8 signaling.  
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.  
 CC Dkk-1 is also involved in morphogenesis in the developing embryo, and  
 CC therefore a growth factor, by inference DKR polypeptides are also  
 CC growth-factors. The DKR polypeptides are useful for treating cancer,

CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt  
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
 CC They can also be used to enhance tissue differentiation, such as bone  
 CC formation and hematopoietic cell formation.

XX SQ Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14  
 Db 2 GEEI 5

RESULT 16

AAY92083

ID AAY92083 standard; Peptide; 5 AA.

XX AC AAY92083;

XX DT 01-AUG-2000 (first entry)

XX DE C-terminal peptide of recombinant human DKR-3 expressed in *E. coli*.

XX DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
 KW growth factor; cytostatic; sonic hedgehog; tissue differentiation;  
 KW bacterial expression.

XX OS Synthetic.

XX PN WO200018914-A2.

XX PD 06-APR-2000.

XX PF 17-SEP-1999; 99WO-US21647.

XX PR 25-SEP-1998; 98US-0161241.

XX PA (AMGE-) AMGEN INC.

XX PI Bass MB, Sullivan JK, Theill LE, Wang D;

XX WPI; 2000-293153/25.

XX New nucleic acid molecule encoding a biologically active DKR  
 PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
 PT stem cell tumors

XX Example 9; Page 79; 143pp; English.

CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified  
 CC in *Xenopus* and mouse, purportedly an antagonist of wnt-8 signaling.  
 CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.  
 CC Dkk-1 is also involved in morphogenesis in the developing embryo, and  
 CC therefore a growth factor, by inference DKR polypeptides are also  
 CC growth factors. The DKR polypeptides are useful for treating cancer,  
 CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt  
 CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
 CC They can also be used to enhance tissue differentiation, such as bone  
 CC formation and hematopoietic cell formation.

XX SQ Sequence 5 AA;

Query Match 22.2%; Score 4; DB 21; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14  
 Db 2 GEEI 5

RESULT 17  
ID AAY92085  
AC AAY92085 standard; Peptide; 5 AA.  
XX  
AC AAY92085;  
XX  
DT 01-AUG-2000 (first entry)  
XX  
DE C-terminal peptide of recombinant human DKR-3-42-350.  
XX  
KW DKR-3; dkk-1; dickkopf-1; antagonist; wnt-8 signaling; morphogenesis;  
KW growth factor; cytoskeletal; sonic hedgehog; tissue differentiation;  
KW bacterial expression.  
XX  
OS Synthetic.  
XX  
FN WO200018914-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 17-SEP-1999; 99WO-US21647.  
XX  
PR 25-SEP-1998; 98US-0161241.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Bass MB, Sullivan JK, Theill LE, Wang D;  
XX  
DR WPI; 2000-293153/25.  
XX  
CC New nucleic acid molecule encoding a biologically active DKR  
PT polypeptide, useful in treatment of cancer, e.g. mammary tumors and  
PT stem cell tumors  
XX  
PS Example 9; Page 79; 143pp; English.  
XX  
CC DKR-1 is a human ortholog of dkk-1 (dickkopf-1), a novel gene identified  
CC in Xenopus and mouse, purportedly an antagonist of wnt-8 signaling.  
CC DKR-2, -3 and -4 are each related to DKR-1 by their cysteine pattern.  
CC Dkk-1 is also involved in morphogenesis in the developing embryo, and  
CC therefore a growth factor, by inference DKR polypeptides are also  
CC growth factors. The DKR polypeptides are useful for treating cancer,  
CC e.g. mammary tumors, stem cell tumors, or other cancers in which the wnt  
CC and/or sonic hedgehog (shh) signal transduction pathways are activated.  
CC They can also be used to enhance tissue differentiation, such as bone  
CC formation and hematopoietic cell formation.  
XX  
SQ Sequence 5 AA;  
Query Match 22.2%; Score 4; DB 21; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 GEEI 14  
Db |||||  
2 GEEI 5  
RESULT 18  
ID AAB55641  
XX AAB55641 standard; Peptide; 5 AA.  
XX  
AC AAB55641;  
XX  
DT 07-MAR-2001 (first entry)  
XX  
DE Monocyte surface receptor PDZ domain sequence #12.  
XX  
KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;  
KW allergy; asthma; multiple sclerosis; cancer; infection.  
XX  
OS Synthetic.

XX WO200069896-A2.  
XX  
PD 23-NOV-2000.  
XX  
PF 12-MAY-2000; 2000WO-US13161.  
XX  
PR 14-MAY-1999; 99US-0134114.  
PR 14-MAY-1999; 99US-0134117.  
PR 14-MAY-1999; 99US-0134118.  
PR 21-OCT-1999; 99US-0160860.  
PR 29-OCT-1999; 99US-0162498.  
PR 13-DEC-1999; 99US-0170453.  
PR 14-JAN-2000; 2000US-0176195.  
PR 14-FEB-2000; 2000US-0182296.  
PR 11-APR-2000; 2000US-0196460.  
PR 11-APR-2000; 2000US-0196527.  
XX  
PA (ARBO-) ARBOR VITA CORP.  
XX  
PI Lu PS;  
XX  
DR WPI; 2001-080245/09.  
XX  
CC Modulating a biological function of an endothelial cell or  
PT hematopoietic cell, useful for treating autoimmune diseases and  
PT infectious diseases, by administering an antagonist that inhibits  
PT binding between a PDZ protein and a PL protein -  
XX  
PS Disclosure; Page 87-94; 141pp; English.  
XX  
CC The present invention relates to a new method for modulating a  
CC biological function of an endothelial cell or hematopoietic cell. The  
CC method involves introducing into a cell, an antagonist that inhibits  
CC binding between a PDZ protein and a PL protein. The inhibitor is used  
CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune  
CC disease. It may also be used to prevent transplantation rejection of  
CC a solid organ transplant. The method may also be used in the treatment  
CC of inflammation, allergy, inflammatory bowel diseases, ulcerative  
CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune  
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,  
CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
CC graft rejection, transplantation rejection), atherosclerosis, cancers,  
CC infectious diseases, ischemia, vasculitis and Crohn's disease.  
XX  
SQ Sequence 5 AA;  
Query Match 22.2%; Score 4; DB 22; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 LKSL 18  
Db |||||  
1 LKSL 4  
RESULT 19  
ID AAB57488  
XX AAB57488 standard; Peptide; 5 AA.  
XX  
AC AAB57488;  
XX  
DT 12-MAR-2001 (first entry)  
XX  
DE CD61 C-terminal core sequence #2.  
XX  
KW Endothelial cell; hematopoietic cell; PDZ domain protein;  
KW PL domain protein; leukocyte activation; T cell surface receptor;  
KW synapse formation; transmembrane neurotransmitter receptor;  
KW autoimmune disease; transplantation rejection; inflammation; allergy;  
KW inflammatory bowel disease; ulcerative colitis; psoriasis;  
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
KW ischaemia; vasculitis; Crohn's disease.

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XX OS Homo sapiens.
XX KW WO200069997-A2.
XX XX
XX PD 23-NOV-2000.
XX PF 12-MAY-2000; 2000WO-US13166.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX PI Lu PS;
XX XX
XX XX WPI; 2001-025003/03.
XX DR
XX PT New inhibitors of binding of a PDZ protein and PL protein for
XX PT inhibiting T cell-mediated response by hematopoietic cells, or for
XX PT treating diseases characterized by inflammatory and humoral immune
XX PT responses, e.g. inflammation, cancer
XX XX
XX PS Disclosure; Page 90; 139pp; English.
XX CC
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 15 LKSL 18
XX |||||
XX Db 1 LKSL 4
XX
XX RESULT 20
XX AAB57898
XX ID AAB57898 standard; Peptide; 5 AA.
XX AC AAB57898;
XX XX
XX DT 12-MAR-2001 (first entry)
XX XX

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```

DE CD61 C-terminal core sequence #2.
XX Endothelial cell; hematopoietic cell; PDZ domain protein;
XX PL domain protein; leukocyte activation; T cell surface receptor;
XX synapse formation; transmembrane neurotransmitter receptor;
XX autoimmune disease; transplantation rejection; inflammation; allergy;
XX inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
XX asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
XX ischaemia; vasculitis; Crohn's disease.
XX
XX OS Homo sapiens.
XX XX
XX PN WO200069998-A2.
XX XX
XX PD 23-NOV-2000.
XX PF
XX PF 12-MAY-2000; 2000WO-US13205.
XX PR 14-MAY-1999; 99US-0134114.
XX PR 14-MAY-1999; 99US-0134117.
XX PR 14-MAY-1999; 99US-0134118.
XX PR 21-OCT-1999; 99US-0160860.
XX PR 29-OCT-1999; 99US-0162498.
XX PR 13-DEC-1999; 99US-0170453.
XX PR 14-JAN-2000; 2000US-0176195.
XX PR 14-FEB-2000; 2000US-0182296.
XX PR 11-APR-2000; 2000US-0196460.
XX PR 11-APR-2000; 2000US-0196527.
XX PA (ARBO-) ARBOR VITA CORP.
XX XX
XX PI Lu PS;
XX XX
XX DR WPI; 2001-061214/07.
XX CC
XX CC Modulating a biological function of a hematopoietic cell for treating
XX CC an allergic response, or diseases mediated by immune system cells, or
XX CC comprises introducing into the cell a PDZ-PL interaction enhancer or
XX CC inhibitor -
XX XX
XX PS Disclosure; Page 93; 143pp; English.
XX CC
XX CC The present invention relates to a method for modulating a biological
XX CC function of an endothelial cell or hematopoietic cell, comprises
XX CC introducing into a cell an antagonist that inhibits binding between a
XX CC PDZ domain protein and a PL domain protein to result in inhibition of
XX CC leukocyte activation. The present sequence is a core sequence of a PL
XX CC domain protein (a T cell surface receptor). PDZ domains of proteins are
XX CC named after three prototypical proteins: PSD95, Drosophila large disc
XX CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved
XX CC in synapse formation by organising transmembrane neurotransmitter
XX CC receptors through intracellular interactions. The inhibitors identified
XX CC by the present invention can be used to treat a disease mediated by
XX CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy
XX CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,
XX CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple
XX CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,
XX CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.
XX CC viral infection), ischaemia, vasculitis and Crohn's disease. The
XX CC inhibitors can also be used to prevent transplantation rejection of a
XX CC solid organ transplant.
XX XX
XX SQ Sequence 5 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 5;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 15 LKSL 18
XX |||||
XX Db 1 LKSL 4
XX
XX RESULT 20
XX AAB57898
XX ID AAB57898 standard; Peptide; 5 AA.
XX AC AAB57898;
XX XX
XX DT 12-MAR-2001 (first entry)
XX XX

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RESULT 21  
ABJ05120  
ID ABJ05120 standard; Peptide; 5 AA.  
XX AC ABJ05120;  
XX DT 07-NOV-2002 (first entry)  
XX DE T-cell surface receptor C-terminal core peptide SEQ ID No 115.  
XX KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
KW inflammatory; humoral immune response; inflammation; C-terminal core;  
KW T-cell surface receptor.  
XX OS Unidentified.  
XX PN WO200231512-A2.  
XX PD 18-APR-2002.  
XX PF 11-OCT-2001; 2001WO-US32150.  
XX PR 13-OCT-2000; 2000US-0688017.  
XX PA (ARBO-) ARBOR VITA CORP.  
XX PI Rabinowitz JD, Lu PS, Schweizer J;  
XX WPI; 2002-416878/44.  
XX DR Assays for determining the affinity of binding between a PDZ domain and  
XX a ligand, and determining the Ki of an inhibitor of the binding,  
XX PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
XX domain -  
XX PS Disclosure; Page 114; 164pp; English.  
XX CC The invention relates to methods and reagents for determining the  
XX apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
XX invention also relates to methods and reagents for determining the Ki of  
XX an inhibitor of binding between a PDZ domain and a ligand, identifying an  
XX agent that enhances binding of a PDZ domain and a ligand, and determining  
XX the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
XX determining the ligand bound with an immobilised polypeptide comprising a  
XX PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
XX an inhibitor) of interaction between PDZ and PL is useful for treating a  
XX disease characterised by leukocyte activation, e.g., an autoimmune  
XX disease that is characterised by inflammatory or humoral immune response,  
XX and for reducing inflammation in a subject. This sequence represents a T-  
XX cell surface receptor C-terminal core peptide relating to the PDZ  
XX containing proteins of the invention.  
XX SQ Sequence 5 AA;  
XX Query Match 22.2%; Score 4; DB 23; Length 5;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 15 LKSL 18  
XX Db 1 LKSL 4  
XX RESULT 22  
XX ABP63413  
XX ID ABP63413 standard; Peptide; 5 AA.  
XX AC ABP63413;  
XX DT 28-OCT-2002 (first entry)  
XX

DE XX Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:115.  
KW KW Molecular interaction; haematopoietic cell; immune response; T cell;  
KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;  
KW anticancer; antipeptidic; dermatological; antiasthmatic; cytostatic;  
KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
KW angiogenesis-dependent disorder; infectious disease.  
OS Homo sapiens.  
OS Synthetic.  
XX WO200242422-A2.  
XX PN 30-MAY-2002.  
XX PD 09-NOV-2001; 2001WO-US44138.  
XX PF 11-NOV-2000; 2000US-0710059.  
XX PR 24-NOV-2000; 2000US-0721915.  
XX FR 24-NOV-2000; 2000US-0722069.  
XX PR 28-NOV-2000; 2000US-0724553.  
XX PA (ARBO-) ARBOR VITA CORP.  
XX PI Lu P, Rabinowitz JD, Schweizer J;  
XX WPI; 2002-608221/65.  
XX DR Modulating the biological function of an endothelial cell or  
XX haematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
XX the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
XX ligand protein in the cell -  
XX PS Disclosure; Page 132; 207pp; English.  
XX CC The present invention describes a method (M1) for modulating a biological  
XX function of an endothelial cell or haematopoietic cell. M1 comprises  
XX introducing into the cell, an agent that inhibits binding of a PDZ  
XX (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)  
XX protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
XX biological function. Also described is a method (M2) for determining  
XX whether a test compound is an inhibitor of binding between a PDZ protein  
XX and a PL protein. M1 is used for modulating a biological function of an  
XX endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
XX inflammatory or humoral immune response, or an autoimmune disease. An  
XX inhibitor (I) is useful for treating a disease characterised by leukocyte  
XX activation, where the disease is characterised by an inflammatory or  
XX humoral immune response, e.g., an autoimmune disease. The compounds  
XX e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
XX symptoms of) a variety of diseases and conditions characterised by  
XX inflammatory and humoral immune responses e.g., inflammation, allergy,  
XX inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
XX psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
XX diseases such as asthma, allergic rhinitis, transplantation rejection  
XX (cardiac, kidney, lung, liver, small bowel, pancreas, cadaver,  
XX autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
XX angiogenesis-dependent disorders, infectious diseases and ischaemia.  
XX ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
XX in the exemplification of the present invention.  
XX SQ Sequence 5 AA;  
XX Query Match 22.2%; Score 4; DB 23; Length 5;  
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX Qy 15 LKSL 18



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Db      1 LKSL 4
|||||
RESULT 23
AAY21763
ID AAY21763 standard; peptide; 6 AA.
XX
AC AAY21763;
XX
XX 10-SEP-1999 (first entry)
XX
DE Conserved peptide sequence of Cpp32 (caspase-3).
XX
KW Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
KW autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
KW tumour cell; myocardial infarction; human.
XX
OS Homo sapiens.
XX
XX WO9935277-A2.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-US00632.
XX
XX 09-JAN-1998; 98US-0070987.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 1999-419353/35.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used
XX for screening and identifying inhibitors or enhancers for treating
XX cancer or autoimmune disease
XX
XX Disclosure; Fig 6; 74pp; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins
XX after Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAY21734 -AAY21795 represent conserved peptide sequences in various
XX caspases.
XX
XX Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 HGEE 13
XX |||||
XX Db 3 HGEE 6
XX
XX RESULT 24
XX AAY21768
XX ID AAY21768 standard; peptide; 6 AA.
XX
XX AC AAY21768;
XX
XX

```

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DT 10-SEP-1999 (first entry)
XX Conserved peptide sequence of CED3.
XX
XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
XX tumour cell; myocardial infarction; human.
XX
XX Homo sapiens.
XX
XX WO9935277-A2.
XX
XX 15-JUL-1999.
XX
XX 11-JAN-1999; 99WO-US00632.
XX
XX 09-JAN-1998; 98US-0070987.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemri ES;
XX
XX WPI; 1999-419353/35.
XX
XX New isolated nucleic acid molecule encoding a rev-caspase - used
XX for screening and identifying inhibitors or enhancers for treating
XX cancer or autoimmune disease
XX
XX Disclosure; Fig 6; 74pp; English.
XX
XX The invention relates to nucleic acid molecules encoding rev-caspases.
XX Rev-caspases are cysteine proteases that specifically cleave proteins
XX after Asp residues and is expressed as a zymogen, in which the small
XX subunit is N-terminal to a large subunit. A gene delivery vehicle
XX comprising a rev-caspase coding sequence is useful for the treatment of
XX cancer, where the gene delivery vehicle is internalised by tumour cells.
XX The gene delivery vehicle can also be used to treat autoimmune diseases.
XX Cells transfected with a rev-caspase expressing vector can be used in
XX identification of inhibitors or enhancers of caspase-mediated apoptosis.
XX In vitro translated rev-caspase can be used to identify an inhibitor or
XX enhancer of caspase processing activity. Caspase inhibitors are useful
XX for treating neurodegenerative diseases as well as for inhibiting
XX apoptosis in the heart following myocardial infarction. Sequences
XX AAY21734 -AAY21795 represent conserved peptide sequences in various
XX caspases.
XX
XX Sequence 6 AA;
XX
XX Query Match 22.2%; Score 4; DB 20; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 10 HGEE 13
XX |||||
XX Db 3 HGEE 6
XX
XX RESULT 25
XX AAY21752
XX ID AAY21752 standard; peptide; 6 AA.
XX
XX AC AAY21752;
XX
XX 10-SEP-1999 (first entry)
XX
XX Conserved peptide sequence of Mch3 (caspase-7).
XX
XX Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy;
XX autoimmune disease; caspase-mediated apoptosis; neurodegenerative;
XX tumour cell; myocardial infarction; human.
XX
XX Homo sapiens.
XX

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PN WO9935277-A2.  
 XX 15-JUL-1999.  
 XX  
 PF 11-JAN-1999; 99WO-US00632.  
 XX  
 PR 09-JAN-1998; 98US-0070987.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Alnemri ES;  
 XX  
 XX WPI; 1999-419353/35.  
 XX  
 XX New isolated nucleic acid molecule encoding a rev-caspase - used  
 PT for screening and identifying inhibitors or enhancers for treating  
 PT cancer or autoimmune disease  
 XX  
 PS Disclosure; Fig 6; 74pp; English.  
 XX  
 XX The invention relates to nucleic acid molecules encoding rev-caspases.  
 CC Rev-caspases are cysteine proteases that specifically cleave proteins  
 CC after Asp residues and is expressed as a zymogen, in which the small  
 CC subunit is N-terminal to a large subunit. A gene delivery vehicle  
 CC comprising a rev-caspase coding sequence is useful for the treatment of  
 CC cancer, where the gene delivery vehicle is internalised by tumour cells.  
 CC The gene delivery vehicle can also be used to treat autoimmune diseases.  
 CC Cells transfected with a rev-caspase expressing vector can be used in  
 CC identification of inhibitors or enhancers of caspase-mediated apoptosis.  
 CC In vitro translated rev-caspase can be used to identify an inhibitor or  
 CC enhancer of caspase processing activity. Caspase inhibitors are useful  
 CC for treating neurodegenerative diseases as well as for inhibiting  
 CC apoptosis in the heart following myocardial infarction. Sequences  
 CC AA21734 -AA21795 represent conserved peptide sequences in various  
 CC caspases.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 20; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 10 HGE 13  
 DB |||||  
 3 HGE 6  
 RESULT 26  
 AA08967  
 ID AA08967 standard; peptide; 6 AA.  
 XX  
 AC AA08967;  
 XX  
 DT 15-NOV-2001 (first entry)  
 XX  
 DE Mammalian ced-3 homologue 3 (Mch3) peptide fragment #2.  
 XX  
 KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer;  
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;  
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;  
 KW cytoskeletal; Parkinson's disease; immunomodulator; antimicrobial;  
 KW viral infection; cell death-mediated disease; neuroprotective.  
 XX  
 OS Unidentified.  
 XX  
 PN US6271361-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 25-FEB-1999; 99US-0257218.  
 XX  
 PR 29-MAY-1997; 97US-0865579.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Alnemri ES, Fernandes-alnemri T, Litwack G;  
 XX WPI; 2001-528686/58.  
 XX  
 XX New apoptotic genes and their apoptotic protease products, useful for  
 PT modulating apoptosis for the therapeutic treatment of human diseases,  
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's  
 PT disease -

PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Alnemri ES, Fernandes-alnemri T, Litwack G;  
 XX WPI; 2001-528686/58.  
 XX  
 DR  
 XX  
 XX New apoptotic genes and their apoptotic protease products, useful for  
 PT modulating apoptosis for the therapeutic treatment of human diseases,  
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's  
 PT disease -  
 XX  
 XX Disclosure; Column 35; 36pp; English.  
 XX  
 CC The invention relates to an isolated gene encoding apoptotic protease,  
 CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the  
 CC aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and  
 CC protein sequences are useful for modulating apoptosis for the  
 CC therapeutic treatment of human diseases. Mch6 sequences are useful  
 CC for upregulating apoptosis (e.g. for treating cancers, autoimmune  
 CC disease or viral infections) or downregulating apoptosis (e.g. for  
 CC treating Alzheimer's disease, Parkinson's disease or cerebellar  
 CC degeneration). The Mch6 sequence is useful for diagnosing, treating  
 CC or reducing the severity of cell death-mediated diseases, as well as  
 CC other diseases mediated by either increased or decreased programmed  
 CC cell death. The present amino acid sequence is Mch3 peptide fragment.  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 10 HGE 13  
 DB |||||  
 3 HGE 6  
 RESULT 27  
 AA08978  
 ID AA08978 standard; peptide; 6 AA.  
 XX  
 AC AA08978;  
 XX  
 DT 15-NOV-2001 (first entry)  
 XX  
 DE CPP32 peptide fragment #2.  
 XX  
 KW Apoptotic protease; mammalian ced-3 homologue 6; Mch6; cancer; CPP32;  
 KW aspartate-specific cysteine protease; ASCP; apoptosis; therapy;  
 KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;  
 KW cytoskeletal; Parkinson's disease; immunomodulator; antimicrobial;  
 KW viral infection; cell death-mediated disease; neuroprotective.  
 XX  
 OS Unidentified.  
 XX  
 PN US6271361-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 25-FEB-1999; 99US-0257218.  
 XX  
 PR 29-MAY-1997; 97US-0865579.  
 XX  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Alnemri ES, Fernandes-alnemri T, Litwack G;  
 XX WPI; 2001-528686/58.  
 XX  
 XX New apoptotic genes and their apoptotic protease products, useful for  
 PT modulating apoptosis for the therapeutic treatment of human diseases,  
 PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's  
 PT disease -

XX Disclosure; Column 39; 36pp; English.

PS The invention relates to an isolated gene encoding apoptic protease,

XX mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the

CC aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and

CC protein sequences are useful for modulating apoptosis for the

CC therapeutic treatment of human diseases. Mch6 sequences are useful

CC for upregulating apoptosis (e.g. for treating cancers, autoimmune

CC disease or viral infections) or downregulating apoptosis (e.g. for

CC treating Alzheimer's disease, Parkinson's disease or cerebellar

CC degeneration). The Mch6 sequence is useful for diagnosing, treating

CC or reducing the severity of cell death-mediated diseases, as well as

CC other diseases mediated by either increased or decreased programmed

CC cell death. The present amino acid sequence is a fragment of CPP32

CC peptide which cleaves Mch6.

XX Sequence 6 AA;

SQ Query Match 22.2%; Score 4; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13

Db ||||

3 HGEE 6

RESULT 28

AAE08983

ID AAE08983 standard; peptide; 6 AA.

XX AAE08983;

XX 15-NOV-2001 (first entry)

DT CED-3 peptide fragment #2.

XX Apoptic protease; mammalian ced-3 homologue 6; Mch6; cancer; CED-3;

XX aspartate-specific cysteine protease; ASCP; apoptosis; therapy;

KW autoimmune disease; cerebellar degeneration; Alzheimer's disease;

KW cytostatic; Parkinson's disease; immunomodulator; antimicrobial;

KW viral infection; cell death-mediated disease; neuroprotective.

XX Unidentified.

XX US6271361-B1.

PN 07-AUG-2001.

PD 25-FEB-1999; 99US-0257218.

PF 29-MAY-1997; 97US-0865579.

PR (UJBE-) UNIV JEFFERSON THOMAS.

PA Alnemri ES, Fernandes-alnemri T, Litwack G;

PI WPI; 2001-528686/58.

XX New apoptotic genes and their apoptotic protease products, useful for

PT modulating apoptosis for the therapeutic treatment of human diseases,

PT e.g. cancers, autoimmune disease, Alzheimer's disease or Parkinson's

PT disease -

XX Disclosure; Column 41; 36pp; English.

PS The invention relates to an isolated gene encoding apoptic protease,

CC mammalian ced-3 homologue 6 (Mch6). Mch6 is a member of the

CC aspartate-specific cysteine protease (ASCP) family. Mch6 DNA and

CC protein sequences are useful for modulating apoptosis for the

CC therapeutic treatment of human diseases. Mch6 sequences are useful

CC for upregulating apoptosis (e.g. for treating cancers, autoimmune

CC disease or viral infections) or downregulating apoptosis (e.g. for

CC treating Alzheimer's disease, Parkinson's disease or cerebellar

CC degeneration). The Mch6 sequence is useful for diagnosing, treating

CC or reducing the severity of cell death-mediated diseases, as well as

CC other diseases mediated by either increased or decreased programmed

CC cell death. The present amino acid sequence is CED-3 peptide fragment.

XX Sequence 6 AA;

SQ Query Match 22.2%; Score 4; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13

Db ||||

3 HGEE 6

RESULT 29

AAE5642

ID AAE5642 standard; Peptide; 6 AA.

XX AAE5642;

XX 07-MAR-2001 (first entry)

DT Monocyte surface receptor PDZ domain sequence #13.

XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;

KW allergy; asthma; multiple sclerosis; cancer; infection.

XX Synthetic.

XX WO200069896-A2.

PN 23-NOV-2000.

PD 12-MAY-2000; 2000WO-US13161.

PF 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

PA Lu PS;

PI WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or

PT hematopoietic cell, useful for treating autoimmune diseases and

PT infectious diseases, by administering an antagonist that inhibits

PT binding between a PDZ protein and a PL protein -

XX Disclosure; Page 87-94; 141pp; English.

PS The present invention relates to a new method for modulating a

CC biological function of an endothelial cell or hematopoietic cell. The

CC method involves introducing into a cell, an antagonist that inhibits

CC binding between a PDZ protein and a PL protein. The inhibitor is used

CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune

CC disease. It may also be used to prevent transplantation rejection of

CC a solid organ transplant. The method may also be used in the treatment

CC of inflammation, allergy, inflammatory bowel diseases, ulcerative

CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune

CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,

CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
 CC graft rejection, transplantation rejection, atherosclerosis, cancers,  
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 2 LKSL 5

RESULT 30  
 AAB57489  
 ID AAB57489 standard; Peptide; 6 AA.

AC AAB57489;

XX 12-MAR-2001 (first entry)

DE CD61 C-terminal core sequence #3.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX WO200069897-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13166.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

XX 29-OCT-1999; 99US-0162498.

XX 13-DEC-1999; 99US-0170453.

XX 14-JAN-2000; 2000US-0176195.

XX 14-FEB-2000; 2000US-0182296.

XX 11-APR-2000; 2000US-0196460.

XX 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for  
 PT inhibiting T cell-mediated response by hematopoietic cells, or for  
 PT treating diseases characterized by inflammatory and humoral immune  
 PT responses, e.g. inflammation, cancer -  
 XX Disclosure; Page 90; 139pp; English.

XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved

CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 2 LKSL 5

RESULT 31

AAB57899

ID AAB57899 standard; Peptide; 6 AA.

XX AAB57899;

XX 12-MAR-2001 (first entry)

XX CD61 C-terminal core sequence #3.

XX Endothelial cell; haematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX WO200069898-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13205.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

XX 29-OCT-1999; 99US-0162498.

XX 13-DEC-1999; 99US-0170453.

XX 14-JAN-2000; 2000US-0176195.

XX 14-FEB-2000; 2000US-0182296.

XX 11-APR-2000; 2000US-0196460.

XX 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

XX Lu PS;

XX WPI; 2001-061214/07.

XX Modulating a biological function of a hematopoietic cell for treating  
 PT an allergic response, or diseases mediated by immune system cells, or  
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
 PT inhibitor -  
 XX Disclosure; Page 93; 143pp; English.

XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 22; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
 ||||  
 Db 2 LKSL 5

RESULT 32  
 ABJ05121  
 ID ABJ05121 standard; Peptide; 6 AA.  
 AC ABJ05121;  
 XX  
 DT 07-NOV-2002 (first entry)  
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 116.  
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;  
 KW T-cell surface receptor.

OS Unidentified.  
 XX  
 FN WO200231512-A2.  
 XX  
 PD 18-APR-2002.

PF 11-OCT-2001; 2001WO-US32150.  
 XX  
 PR 13-OCT-2000; 2000US-0688017.  
 XX  
 PA (ARBO-) ARBOR VITA CORP.

PI Rabinowitz JD, Lu PS, Schweizer J;  
 XX  
 DR WPI; 2002-416878/44.

PT Assays for determining the affinity of binding between a PDZ domain and  
 PT a ligand, and determining the Ki of an inhibitor of the binding,  
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 PT domain -

PS Disclosure; Page 114; 164pp; English.

XX The invention relates to methods and reagents for determining the  
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The

CC invention also relates to methods and reagents for determining the Ki of  
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 CC agent that enhances binding of a PDZ domain and a ligand, and determining  
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 CC determining the ligand bound with an immobilised polypeptide comprising a  
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a  
 CC disease characterised by leukocyte activation, e.g., an autoimmune  
 CC disease that is characterised by inflammatory or humoral immune response,  
 CC and for reducing inflammation in a subject. This sequence represents a T-  
 CC cell surface receptor C-terminal core peptide relating to the PDZ  
 CC containing proteins of the invention.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
 ||||  
 Db 2 LKSL 5

RESULT 33  
 ABP63414  
 ID ABP63414 standard; Peptide; 6 AA.

AC ABP63414;

XX  
 DT 28-OCT-2002 (first entry)

DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID No:116.

KW Molecular interaction; haematopoietic cell; immune response; T cell;  
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
 KW immunosuppressive; antiinflammatory; anti-allergic; antiatherosclerotic;  
 KW antiulcer; antipsoriatic; dermatological; antiasthmatic; cytostatic;  
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
 KW angiogenesis-dependent disorder; infectious disease.

OS Homo sapiens.  
 OS Synthetic.

FN WO200242422-A2.

XX  
 PD 30-MAY-2002.

PF 09-NOV-2001; 2001WO-US44138.

XX 11-NOV-2000; 2000US-0710059.

PR 24-NOV-2000; 2000US-0721915.

PR 24-NOV-2000; 2000US-0722069.

XX 28-NOV-2000; 2000US-0724553.

PA (ARBO-) ARBOR VITA CORP.

PI Lu P, Rabinowitz JD, Schweizer J;

XX WPI; 2002-608221/65.

PT Modulating the biological function of an endothelial cell or  
 PT haematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
 PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
 PT ligand protein in the cell -

PS Disclosure; Page 132; 207pp; English.

XX

CC The present invention describes a method (M1) for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell. M1 comprises  
 CC introducing into the cell, an agent that inhibits binding of a PDZ  
 CC (PS995, Drosophila large disc protein, and Zonula Occludin 1 protein)  
 CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
 CC biological function. Also described is a method (M2) for determining  
 CC whether a test compound is an inhibitor of binding between a PDZ protein  
 CC and a PL protein. M1 is used for modulating a biological function of an  
 CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
 CC inflammatory or humoral immune response, or an autoimmune disease. An  
 CC inhibitor (I) is useful for treating a disease characterised by leukocyte  
 CC activation, where the disease is characterised by an inflammatory or  
 CC humoral immune response, e.g., an autoimmune disease. The compounds  
 CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
 CC symptoms of) a variety of diseases and conditions characterised by  
 CC inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
 CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
 CC diseases such as asthma, allergic rhinitis, transplantation rejection  
 CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
 CC autologous, bone marrow xenotransplantation), atherosclerosis, cancers,  
 CC angiogenesis-dependent disorders, infectious diseases and ischaemia.  
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 DB 2 LKSL 5

RESULT 34

ABJ01256  
 ID ABJ01256 standard; Peptide; 6 AA.

XX AC ABJ01256;

XX DT 18-SEP-2002 (first entry)

XX DE Human caspase conserved region SEQ ID NO: 72.

XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;  
 XX cancer; autoimmune disease; cytostatic; immunosuppressive.

XX OS Homo sapiens.

XX PN US6376226-B1.

XX PD 23-APR-2002.

XX PF 26-APR-2000; 2000US-0561756.

XX PR 09-JAN-1998; 98US-070897P.

XX PR 08-JAN-1999; 99US-0227721.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 2002-451275/48.

XX New rev-caspases engineered to contain the small subunit fused in frame  
 XX N-terminal to the large subunit, which is in reverse order to the wild  
 XX type caspases, are useful to treat cancer and autoimmune diseases -

XX PS Disclosure; Fig 6; 81pp; English.

XX The present invention provides the protein and coding sequences of human

CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences  
 CC can be used in the gene therapy of cancer and autoimmune diseases. The  
 CC present sequence is a peptide described in the exemplification of the  
 CC invention.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
 ||||  
 DB 3 HGEE 6

RESULT 35

ABJ01267  
 ID ABJ01267 standard; Peptide; 6 AA.

XX AC ABJ01267;

XX DT 18-SEP-2002 (first entry)

XX DE Human caspase conserved region SEQ ID NO: 83.

XX KW Human; caspase; rev-caspase; gene therapy; protease; apoptosis;  
 XX cancer; autoimmune disease; cytostatic; immunosuppressive.

XX OS Homo sapiens.

XX PN US6376226-B1.

XX PD 23-APR-2002.

XX PF 26-APR-2000; 2000US-0561756.

XX PR 09-JAN-1998; 98US-070897P.

XX PR 08-JAN-1999; 99US-0227721.

XX PA (UYJE-) UNIV JEFFERSON THOMAS.

XX PI Alnemri ES;

XX DR WPI; 2002-451275/48.

XX New rev-caspases engineered to contain the small subunit fused in frame  
 XX N-terminal to the large subunit, which is in reverse order to the wild  
 XX type caspases, are useful to treat cancer and autoimmune diseases -

XX PS Disclosure; Fig 6; 81pp; English.

XX The present invention provides the protein and coding sequences of human  
 XX rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences  
 XX can be used in the gene therapy of cancer and autoimmune diseases. The  
 XX present sequence is a peptide described in the exemplification of the  
 XX invention.

SQ Sequence 6 AA;

Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
 ||||  
 DB 3 HGEE 6

RESULT 36

ABJ01272  
 ID ABJ01272 standard; Peptide; 6 AA.

XX

AC AEU01272;  
 XX 18-SEP-2002 (first entry)  
 XX Human caspase conserved region SEQ ID NO: 88.  
 DE  
 XX Human; caspase; rev-caspase; gene therapy; protease; apoptosis;  
 KW cancer; autoimmune disease; cytostatic; immunosuppressive.  
 KW  
 OS Homo sapiens.  
 XX  
 PN US6376226-B1.  
 XX  
 XX 23-APR-2002.  
 XX  
 XX 26-APR-2000; 2000US-0561756.  
 PF  
 XX 09-JAN-1998; 98US-070897P.  
 PR  
 PR 08-JAN-1999; 99US-0227721.  
 XX  
 PA (UVE-) UNIV JEFFERSON THOMAS.  
 XX  
 XX Alnemri ES;  
 PI  
 XX WPI; 2002-451275/48.  
 DR  
 XX New rev-caspases engineered to contain the small subunit fused in frame  
 PT N-terminal to the large subunit, which is in reverse order to the wild  
 PT type caspases, are useful to treat cancer and autoimmune diseases -  
 PT  
 XX Disclosure; Fig 6; 81pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of human  
 CC rev-caspase-3, uncleavable rev-caspase-3 and rev-caspase-6. The sequences  
 CC can be used in the gene therapy of cancer and autoimmune diseases. The  
 CC present sequence is a peptide described in the exemplification of the  
 CC invention.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 10 HGEE 13  
 Db |||||  
 3 HGEE 6  
 RESULT 37  
 AAO17301  
 ID AAO17301 standard; Peptide; 6 AA.  
 XX  
 AC AAO17301;  
 XX  
 DT 08-JUL-2002 (first entry)  
 XX  
 DE A thaliana receptor kinase RKS11 peptide fragment.  
 XX  
 KW Vegetative propagation; plant; phytochrome; receptor kinase-like SERK;  
 KW RKS.  
 XX Arabidopsis thaliana.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN EP1094113-A1.  
 XX  
 XX 25-APR-2001.  
 PD  
 XX 22-OCT-1999; 99EP-0203480.  
 PF  
 XX 22-OCT-1999; 99EP-0203480.  
 XX  
 PR (GENE-) GENETWISTER TECHNOLOGIES BV.  
 XX  
 PA

XX Schmidt EDL, Van Der Kop DAM, De Boer AD;  
 PI WPI; 2002-228902/29.  
 XX  
 DR In vitro culture propagation of a plant from plant starting material,  
 XX comprises stimulating root/shoot initiation by introducing a  
 PT recombinant gene product into the starting material, thus reducing  
 PT phytochrome addition to culture -  
 XX  
 XX Disclosure; Page 100; 171pp; English.  
 PS  
 XX The present invention relates to a culture method for propagating a plant  
 XX from a plant starting material, where root or shoot initiation is  
 CC stimulated by introducing a gene into the starting material which allows  
 CC the reduction or absence of phytochrome addition to the culture. The  
 CC method is used for the propagation (preferably, seedless propagation) of  
 CC a plant from a plant starting material in an in vitro culture method.  
 CC Nucleic acids encoding receptor-like kinases are useful in the method.  
 CC The present sequence is a fragment of a receptor-like kinase protein.  
 CC  
 XX  
 SQ Sequence 6 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 GEEI 14  
 Db |||||  
 2 GEEI 5  
 RESULT 38  
 AAU28695  
 ID AAU28695 standard; Peptide; 7 AA.  
 XX  
 AC AAU28695;  
 XX  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE DPI tryptic digest peptide #292.  
 XX  
 KW Human; depression associated protein isoform; tryptic digest peptide;  
 KW DPI; cerebrospinal fluid; CSF; BAD; bipolar affective disorder;  
 KW neuropsychiatric disorder; bipolar mood disorder; neuroleptic;  
 KW maniac-depressive illness; schizoaffective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200162787-A1.  
 PN  
 XX 30-AUG-2001.  
 PD  
 XX 23-FEB-2001; 2001WO-GB00786.  
 PF  
 XX 24-FEB-2000; 2000GB-0004412.  
 PR  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 PA  
 XX Herath HMC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 PI WPI; 2001-570626/64.  
 XX  
 DR Novel nucleic acid encoding a protein associated with bipolar affective  
 PT disorder, which is used for diagnosis, prophylaxis and therapy of  
 PT neuropsychiatric disorders, such as bipolar affective disorder -  
 XX  
 XX Disclosure; Page 37; 153pp; English.  
 PS  
 XX The present invention relates to the identification of depression  
 CC associated protein isoforms (DPis), particularly the tryptic digest

CC peptides of these proteins. Some of the DPIs (AAU28404-AAU28625)  
 CC described are decreased in the cerebrospinal fluid (CSF) of BAD  
 CC (bipolar affective disorder) subjects, whilst other DPIs  
 CC (AAU28626-AAU28887) are increased in BAD subjects. Also described  
 CC are peptide sequences identified from DPI-45 and DPI-213 and the  
 CC nucleic acid sequences they are encoded by. The sequences of the  
 CC invention are useful for clinical screening, diagnosis, prognosis,  
 CC therapy and prophylaxis of neuropsychiatric disorders e.g. BAD (also  
 CC known as bipolar mood disorder, BP), maniac-depressive illnesses,  
 CC attention deficit disorders, schizoaffective disorders, and unipolar  
 CC affective disorders. The present sequence represents one of the DPI  
 CC tryptic digest peptides of the present invention.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEIL 15  
 Db 2 EEIL 5  
 |||||

RESULT 39  
 AAU25065  
 ID AAU25065 standard; Peptide; 7 AA.  
 AC AAU25065;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Schizophrenia-Associated Protein Isoform (SPI) peptide #294.  
 XX  
 KW Schizophrenia-associated protein isoform; SPI; SPI-206; SPI-238; SPI-240;  
 KW neuroleptic; gene therapy; cerebrospinal fluid; serum; plasma.  
 XX  
 OS Homo sapiens.  
 XX  
 PI WO200162785-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00792.  
 XX  
 FR 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMWAC, Parekh RB, Rohlf C, Terrett JA, Tyson KL;  
 XX  
 DR WPI; 2001-570624/64.  
 XX  
 XX New schizophrenia associated protein isoforms and encoding nucleic acid  
 PT molecules, useful for treatment, diagnosis and prognosis of  
 PT schizophrenia and screening for potential drugs for treatment and new  
 PT drug targets -  
 XX  
 PS Disclosure; Page 35; 148pp; English.  
 XX  
 CC The sequence represents a schizophrenia-associated protein isoform (SPI).  
 CC These protein isoforms, e.g. SPI-206, SPI-238 and SPI-240 are detectable  
 CC in cerebrospinal fluid, serum or plasma and are useful markers of  
 CC schizophrenia. The sequences can be used for treatment and diagnosis of  
 CC schizophrenia, screening, prognosis, monitoring the results of therapy,  
 CC identifying patients most likely to respond to a particular therapy and  
 CC identification of new targets for drug treatment. SPI DNA is useful as a  
 CC nucleic acid probe to detect the presence of nucleic acids or SPIs.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEIL 15  
 Db 2 EEIL 5  
 |||||

RESULT 40  
 AAU26343  
 ID AAU26343 standard; Peptide; 7 AA.  
 AC AAU26343;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Depression-Associated Protein isoform DPI-174 #1.  
 XX  
 KW Human; Bipolar Affective Disorder; BAD; Depression-Associated feature;  
 KW DF; Depression-Associated protein isoform; DPI; Cerebro-spinal fluid;  
 KW CSF; antidepressant; antimanic; neuroleptic; tranquiliser; neuroleptic;  
 KW attention deficient disorder; schizoaffective disorder;  
 KW unipolar affective disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PI WO200163294-A2.  
 XX  
 PD 30-AUG-2001.  
 XX  
 PF 23-FEB-2001; 2001WO-GB00791.  
 XX  
 FR 24-FEB-2000; 2000GB-0004412.  
 PR 08-DEC-2000; 2000GB-0030050.  
 PR 12-DEC-2000; 2000US-0254830.  
 XX  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX  
 PI Herath HMWAC, Parekh RB, Rohlf C;  
 XX  
 DR WPI; 2001-582081/65.  
 XX  
 PT Preparation for diagnosing or treating bipolar affected disorder (BAD)  
 PT or unipolar depression, or for screening for modulators, comprises a  
 PT BAD-associated protein isoform -  
 XX  
 PS Claim 8; Page 37; 163pp; English.  
 XX  
 CC The invention relates to a preparation comprising an isolated Bipolar  
 CC Affected Disorder (BAD)-Associated Protein Isoform (DPIs). The DPI's are  
 CC used to screen, diagnose or prognosis of BAD or unipolar depression,  
 CC determine the stage or severity of BAD or unipolar depression, identify a  
 CC subject at risk of developing BAD or unipolar depression, or monitor the  
 CC effect of therapy in a subject. They are also used to screen for or  
 CC identify agents that interact with a DPI. These agents, antibodies  
 CC against the DPIs, and nucleic acids encoding the DPIs are used to treat  
 CC or prevent BAD or unipolar depression. Diseases that can be treated are  
 CC attention deficient disorder, a schizoaffective disorder, a bipolar or a  
 CC unipolar affective disorder. The DPIs are used in proteomics. The  
 CC proteomic approach of using DPIs for screening, diagnosis or prognosis of  
 CC BAD or unipolar depression overcomes the problems of using gene  
 CC expression analysis, such as not being able to obtain central nervous  
 CC system (CNS) tissue from a living patient under normal circumstances.  
 CC The present sequence is a DIP increased in the CSF (cerebro-spinal  
 CC fluid) of subjects having BAD.

XX SQ Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EEIL 15



```

Db          |||||
            2 EUIL 5

RESULT 41
AAM44583
ID AAM44583 standard; Peptide; 7 AA.
AC
XX
XX AAM44583;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #854.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 104; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 RYQD 8
XX |||||
XX 3 RYQD 6
XX
XX RESULT 43
XX AAU15409
XX ID AAU15409 standard; Peptide; 7 AA.
XX
XX

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RESULT 42
AAM44588
ID AAM44588 standard; Peptide; 7 AA.
XX
XX AAM44588;
XX
XX 25-OCT-2001 (first entry)
XX
XX H11 binding site consensus conforming peptide (CCP) #859.
XX
XX Antigen-binding; tumour; diagnosis; stress protein-peptide complex; SPPC;
XX immunogenically cross-reactive; cancer; immunogenic cancer cell;
XX cytostatic; vaccine; tumour-specific immunogenic response inducer;
XX astrocytoma; fibrosarcoma; myxosarcoma; liposarcoma; oligodendroglioma;
XX ependymoma; medulloblastoma; primitive neural ectodermal tumour.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX CA2290722-A1.
XX
XX 08-JUN-2001.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX 08-DEC-1999; 99CA-2290722.
XX
XX (NOVO-) NOVOPHARM BIOTECH INC.
XX
XX Kaplan HA, Maiti PK, Fast DG, Herman W, Dan MD, Lewis KE;
XX Entwistle JM, MacDonald GC;
XX WPI; 2001-425937/46.
XX
XX Composition useful for treating and diagnosing cancer, comprises stress
XX protein-peptide complexes associated with tumor, and isolated
XX antigen-binding fragments of an antibody that binds specifically to the
XX complex -
XX
XX Example 4; Page 104; 154pp; English.
XX
XX The present invention describes a composition (I) comprising stress
XX protein-peptide complexes (SPPC) associated with tumours that is
XX specifically immunogenically cross-reactive with cell surface-associated
XX SPPCs specific to target cancer (TC). Also described is an isolated
XX antigen-binding fragment of an antibody that binds specifically to SPPCs
XX or a population of different SPPCs consisting of immunogenic cancer cell
XX surface-associated SPPC of TC. (I) has cytostatic activity and can be
XX used in vaccine production and as a tumour-specific immunogenic response
XX inducer. (I) is useful for treating 71 types of cancers or tumours in a
XX subject, such as astrocytoma, fibrosarcoma, myxosarcoma, liposarcoma,
XX oligodendroglioma, ependymoma, medulloblastoma, and primitive neural
XX ectodermal tumour (PNET). (I) is useful as cancer immunogen including
XX vaccines. (I) is useful for diagnostic and palliative use, for detecting
XX or imaging cancer cells, and to monitor the course of amelioration of
XX malignancy in an individual. AAM43707 to AAM47109 represent peptides
XX which are used in the exemplification of the present invention.
XX
XX Sequence 7 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 7;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 5 RYQD 8
XX |||||
XX 3 RYQD 6
XX
XX RESULT 43
XX AAU15409
XX ID AAU15409 standard; Peptide; 7 AA.
XX
XX

```

AC AAU15409;  
 XX 24-OCT-2001 (first entry)  
 XX Schizophrenia-associated isoform peptide #294.  
 XX Schizophrenia; neuroleptic; diagnostic; neuropsychiatric disorder;  
 XX neurological disorder; neuropathy.  
 XX Homo sapiens.  
 XX WO200163293-A2.  
 PN 30-AUG-2001.  
 XX 23-FEB-2001; 2001WO-GB00783.  
 XX 24-FEB-2000; 2000GB-0004415.  
 PR 28-NOV-2000; 2000US-0750395.  
 XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
 PA Herath HMC, Parekh RB, Rohlf C;  
 PI WPI; 2001-502868/55.  
 XX Diagnosing and monitoring Schizophrenia by detecting the presence of  
 PT Schizophrenia Associated Features and Schizophrenia Associated Protein  
 PT Isoforms in samples of cerebrospinal fluid -  
 XX Claim 6; Page 35; 160pp; English.  
 XX The invention relates to methods and compositions for screening,  
 CC diagnosis and prognosis of Schizophrenia. The method involves detecting  
 CC the presence of Schizophrenia (SCH) Associated Features (SFS) and SCH  
 CC Associated Protein Isoforms (SPIs) in samples, e.g. by electrophoresis,  
 CC immunoblotting or hybridization assay, for diagnosing and monitoring SCH;  
 CC studying the effectiveness of treatments and for identifying potential  
 CC therapeutic agents. The method is used for (1) screening or diagnosis of  
 CC SCH and the relative abundance of at least 1 chosen feature correlates  
 CC with the presence or absence of SCH; and (2) monitoring the effect of  
 CC therapy administered to a subject with SCH and the relative abundance of  
 CC at least 1 chosen feature which correlates with the severity of SCH.  
 CC The expression and activity of the SFS, SPIs and related molecules  
 CC (e.g. secondary messengers) are studied to diagnose SCH, monitor the  
 CC progress of the disorder and the effectiveness of treatment and as  
 CC targets to identify and produce potential therapeutic agents for the  
 CC treatment of SCH. The paucity of detectable neuroalgal defects  
 CC distinguishes neuropsychiatric disorders such as SCH from neurological  
 CC disorders, where manifestations of anatomical and biochemical changes  
 CC have been identified in many cases. Consequently the identification and  
 CC characterisation of cellular and/or molecular causative defects and  
 CC neuropathies are necessary for improved treatment of neuropsychiatric  
 CC disorders. AAU15114-AAU15762 represent the amino acid sequences of  
 CC schizophrenia-associated isoforms used in the method of the invention.  
 XX SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 12 EEIL 15  
 DB 2 EEIL 5  
 RESULT 44  
 AAB55643  
 ID AAB55643 standard; Peptide; 7 AA.  
 XX AAB55643;  
 AC AAB55643;  
 XX

DT 07-MAR-2001 (first entry)  
 XX Monocyte surface receptor PDZ domain sequence #14.  
 XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;  
 KW allergy; asthma; multiple sclerosis; cancer; infection.  
 XX Synthetic.  
 OS WO200069896-A2.  
 XX 23-NOV-2000.  
 PD 12-MAY-2000; 2000WO-US13161.  
 XX 14-MAY-1999; 99US-0134114.  
 PR 14-MAY-1999; 99US-0134117.  
 PR 21-OCT-1999; 99US-0134118.  
 PR 29-OCT-1999; 99US-0160860.  
 PR 13-DEC-1999; 99US-0162498.  
 PR 14-JAN-2000; 2000US-0176195.  
 PR 14-FEB-2000; 2000US-0182296.  
 PR 11-APR-2000; 2000US-0196460.  
 PR 11-APR-2000; 2000US-0196527.  
 XX (ARBO-) ARBOR VITA CORP.  
 PA Lu PS;  
 XX WPI; 2001-080245/09.  
 XX Modulating a biological function of an endothelial cell or  
 PT hematopoietic cell, useful for treating autoimmune diseases and  
 PT infectious diseases, by administering an antagonist that inhibits  
 PT binding between a PDZ protein and a PL protein -  
 XX Disclosure; Page 87-94; 141pp; English.  
 XX The present invention relates to a new method for modulating a  
 CC biological function of an endothelial cell or hematopoietic cell. The  
 CC method involves introducing into a cell, an antagonist that inhibits  
 CC binding between a PDZ protein and a PL protein. The inhibitor is used  
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune  
 CC disease. It may also be used to prevent transplantation rejection of  
 CC a solid organ transplant. The method may also be used in the treatment  
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative  
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,  
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,  
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.  
 XX SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 DB 3 LKSL 6  
 RESULT 45  
 AAB57490  
 ID AAB57490 standard; Peptide; 7 AA.  
 XX AAB57490;  
 AC AAB57490;  
 XX 12-MAR-2001 (first entry)  
 DT CD61 C-terminal core sequence #4.  
 XX

XX Endothelial cell; haematopoietic cell; PDZ domain protein;  
 KW PD domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200069897-A2.  
 XX  
 XX 23-NOV-2000.  
 XX  
 XX 12-MAY-2000; 2000WO-US13166.  
 XX  
 XX 14-MAY-1999; 99US-0134114.  
 XX 14-MAY-1999; 99US-0134117.  
 XX 14-MAY-1999; 99US-0134118.  
 XX 21-OCT-1999; 99US-0160860.  
 XX 29-OCT-1999; 99US-0162498.  
 XX 13-DEC-1999; 99US-0170453.  
 XX 14-JAN-2000; 2000US-0176195.  
 XX 14-FEB-2000; 2000US-0182296.  
 XX 11-APR-2000; 2000US-0196460.  
 XX 11-APR-2000; 2000US-0196527.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Lu PS;  
 XX  
 XX WPI; 2001-025003/03.  
 XX  
 XX New inhibitors of binding of a PDZ protein and PL protein for  
 PT inhibiting T cell-mediated response by haematopoietic cells, or for  
 PT treating diseases characterized by inflammatory and humoral immune  
 PT responses, e.g. inflammation, cancer -  
 XX  
 XX Disclosure; Page 90; 139pp; English.  
 XX  
 XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.  
 XX  
 XX Sequence 7 AA;  
 XX  
 XX Query Match 22.2%; Score 4; DB 22; Length 7;  
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 15 LKSL 18  
 XX 3 LKSL 6

RESULT 46  
 AAB57900  
 ID AAB57900 standard; Peptide; 7 AA.  
 XX  
 AC AAB57900;  
 XX  
 DT 12-MAR-2001 (first entry)  
 XX  
 DE CD61 C-terminal core sequence #4.  
 XX  
 XX Endothelial cell; haematopoietic cell; PDZ domain protein;  
 KW PD domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200069898-A2.  
 XX  
 XX 23-NOV-2000.  
 XX  
 XX 12-MAY-2000; 2000WO-US13205.  
 XX  
 XX 14-MAY-1999; 99US-0134114.  
 XX 14-MAY-1999; 99US-0134117.  
 XX 14-MAY-1999; 99US-0134118.  
 XX 21-OCT-1999; 99US-0160860.  
 XX 29-OCT-1999; 99US-0162498.  
 XX 13-DEC-1999; 99US-0170453.  
 XX 14-JAN-2000; 2000US-0176195.  
 XX 14-FEB-2000; 2000US-0182296.  
 XX 11-APR-2000; 2000US-0196460.  
 XX 11-APR-2000; 2000US-0196527.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Lu PS;  
 XX  
 XX WPI; 2001-061214/07.  
 XX  
 XX Modulating a biological function of a haematopoietic cell for treating  
 PT an allergic response, or diseases mediated by immune system cells,  
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
 PT inhibitor -  
 XX  
 XX Disclosure; Page 93; 143pp; English.  
 XX  
 XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.  
 XX  
 XX Sequence 7 AA;

Query Match 22.2%; Score 4; DB 22; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 3 LKSL 6

RESULT 47  
 ABJ05122  
 ID ABJ05122 standard; Peptide; 7 AA.  
 XX  
 AC ABJ05122;  
 XX  
 DT 07-NOV-2002 (first entry)  
 XX  
 DE T-cell surface receptor C-terminal core peptide SEQ ID No 117.  
 XX  
 KW Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;  
 KW T-cell surface receptor.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200231512-A2.  
 XX  
 PD 18-APR-2002.  
 XX  
 XX 11-OCT-2001; 2001WO-US32150.  
 XX  
 XX 13-OCT-2000; 2000US-0688017.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Rabinowitz JD, Lu PS, Schweizer J;  
 XX WPI; 2002-416978/44.  
 XX  
 XX Assays for determining the affinity of binding between a PDZ domain and  
 XX a ligand, and determining the Ki of an inhibitor of the binding,  
 XX comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 XX domain -  
 XX  
 XX Disclosure; Page 114; 164pp; English.

The invention relates to methods and reagents for determining the  
 apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
 invention also relates to methods and reagents for determining the Ki of  
 an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 agent that enhances binding of a PDZ domain and a ligand, and determining  
 the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 determining the ligand bound with an immobilised polypeptide comprising a  
 PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 an inhibitor) of interaction between PDZ and PL is useful for treating a  
 disease characterised by leukocyte activation, e.g., an autoimmune  
 disease that is characterised by inflammation in a subject. This sequence represents a T-  
 cell surface receptor C-terminal core peptide relating to the PDZ  
 containing proteins of the invention.

Sequence 7 AA;  
 QY 15 LKSL 18  
 ||||  
 Db 3 LKSL 6

Query Match 22.2%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 3 LKSL 6

RESULT 48  
 ABP63415  
 ID ABP63415 standard; Peptide; 7 AA.  
 XX  
 AC ABP63415;  
 XX  
 DT 28-OCT-2002 (first entry)  
 XX  
 DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:117.  
 XX  
 KW Molecular interaction; haematopoietic cell; immune response; T cell;  
 KW PDZ domain; B cell; endothelial cell; PDZ protein; PSD95; PDZ ligand;  
 KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
 KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;  
 KW antitumor; antiproliferative; dermatological; antisthmatic; cytostatic;  
 KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
 KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
 KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
 KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
 KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
 KW angiogenesis-dependent disorder; infectious disease.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200242422-A2.  
 XX  
 PD 30-MAY-2002.  
 XX  
 XX 09-NOV-2001; 2001WO-US44138.  
 XX  
 XX 11-NOV-2000; 2000US-0710059.  
 XX  
 XX 24-NOV-2000; 2000US-0721915.  
 XX  
 XX 24-NOV-2000; 2000US-0722069.  
 XX  
 XX 28-NOV-2000; 2000US-0724553.  
 XX  
 XX (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Lu P, Rabinowitz JD, Schweizer J;  
 XX WPI; 2002-608221/65.  
 XX  
 XX Modulating the biological function of an endothelial cell or  
 XX haematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
 XX the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
 XX ligand protein in the cell -  
 XX  
 XX Disclosure; Page 132; 207pp; English.

The present invention describes a method (M1) for modulating a biological  
 function of an endothelial cell or haematopoietic cell. M1 comprises  
 introducing into the cell, an agent that inhibits binding of a PDZ  
 protein and a PDZ ligand (PL) protein, and Zonula Occludin 1 protein)  
 (PSD95, Drosophila large disc protein, and Zonula Occludin 1 protein)  
 biological function. Also described is a method (M2) for determining  
 whether a test compound is an inhibitor of binding between a PDZ protein  
 and a PL protein. M1 is used for modulating a biological function of an  
 endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
 inflammatory or humoral immune response, or an autoimmune disease. An  
 inhibitor (I) is useful for treating a disease characterised by leukocyte  
 activation, where the disease is characterised by an inflammatory or  
 humoral immune response, e.g., an autoimmune disease. The compounds  
 e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
 symptoms of) a variety of diseases and conditions characterised by  
 inflammatory and humoral immune responses e.g., inflammation, allergy,  
 inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
 psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
 diseases such as asthma, allergic rhinitis, transplantation rejection  
 (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
 autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
 angiogenesis-dependent disorders, infectious diseases and ischaemia.  
 CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
 CC in the exemplification of the present invention.

XX SQ Sequence 7 AA;  
 Query Match 22.2%; Score 4; DB 23; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 DB 3 LKSL 6

RESULT 49  
 ABP11644  
 ID ABP11644 standard; Peptide; 8 AA.  
 XX AC  
 XX ABP11644;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A01 super motif gag peptide #16.  
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX OS Human immunodeficiency virus type 1.  
 XX PN WO200124810-A1.  
 XX PD 12-APR-2001.  
 XX PF 05-OCT-2000; 2000WO-US27766.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -  
 Claim 32; Page 107; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 DB 4 LKSL 7

RESULT 50  
 ABP12644  
 ID ABP12644 standard; Peptide; 8 AA.  
 XX AC ABP12644;  
 XX DT 15-JUL-2002 (first entry)  
 XX DE HIV A02 super motif gag peptide #115.  
 XX KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX OS Human immunodeficiency virus type 1.  
 XX PN WO200124810-A1.  
 XX PD 12-APR-2001.  
 XX PF 05-OCT-2000; 2000WO-US27766.  
 XX PR 05-OCT-1999; 99US-0412863.  
 XX PA (EPIM-) EPIMUNE INC.  
 XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -  
 Claim 32; Page 128; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      15 LKSL 18
Db      ||||
        5 LKSL 8

RESULT 51
ABP12645
ID  ABP12645 standard; Peptide; 8 AA.
XX  AC
XX  ABP12645;
XX  DT
XX  15-JUL-2002 (first entry)
XX  DE
XX  HIV A02 super motif gag peptide #116.
XX  KW
XX  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX  vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX  antigen; vaccine; HIV infection; immunisation; virucide.
XX  OS
XX  Human immunodeficiency virus type 1.
XX  PN
XX  WO200124810-A1.
XX  PD
XX  12-APR-2001.
XX  PF
XX  05-OCT-2000; 2000WO-US27766.
XX  PR
XX  05-OCT-1999; 99US-0412863.
XX  PA
XX  (EPIM-) EPIMMUNE INC.
XX  PI
XX  Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX  Baker DM, Cellis E, Kubo RT, Grey HM;
XX  WPI; 2001-354887/37.
XX  VT
XX  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX  peptide groups, useful for vaccinating against HIV-1 -
XX  Claim 32; Page 128; 448pp; English.
XX  PS
XX  The present invention describes a composition (I) comprising a prepared
XX  human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX  sequence selected from 51 defined amino acid sequences (AB125347 to
XX  AB25397). (I) has virucide activity and can be used in vaccines. (I)
XX  may be used for immunising subjects against HIV-1 infections. The use of
XX  group-based vaccines has several advantages over traditional vaccines,
XX  particularly when compared to the use of whole antigens in vaccine
XX  compositions. There is evidence that the immune response to whole
XX  antigens is directed largely toward variable regions of the antigen,
XX  allowing for immune escape due to mutations. The groups for inclusion in
XX  an group-based vaccine may be selected from conserved regions of viral or
XX  tumour-associated antigens, which therefore reduces the likelihood of
XX  escape mutants. Furthermore, immunosuppressive groups that may be present
XX  in whole antigens can be avoided with the use of group-based vaccines.
XX  An additional advantage of an group-based vaccine approach is the ability
XX  to combine selected groups (CTL and HTL), and further, to modify the
XX  composition of the groups, achieving, for example, enhanced
XX  immunogenicity. Accordingly, the immune response can be modulated, as
XX  appropriate, for the target disease. Similar engineering of the response
XX  is not possible with traditional approaches. ABP1501 to ABP25412
XX  represent peptide sequences used in the exemplification of the present
XX  invention.
XX  SQ      Sequence      8 AA;

Query Match      22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
Db      ||||

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Db      5 LKSL 8

RESULT 52
ABP15564
ID  ABP15564 standard; Peptide; 8 AA.
XX  AC
XX  ABP15564;
XX  DT
XX  15-JUL-2002 (first entry)
XX  DE
XX  HIV A24 super motif gag peptide #50.
XX  KW
XX  HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX  vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX  antigen; vaccine; HIV infection; immunisation; virucide.
XX  OS
XX  Human immunodeficiency virus type 1.
XX  PN
XX  WO200124810-A1.
XX  PD
XX  12-APR-2001.
XX  PF
XX  05-OCT-2000; 2000WO-US27766.
XX  PR
XX  05-OCT-1999; 99US-0412863.
XX  PA
XX  (EPIM-) EPIMMUNE INC.
XX  PI
XX  Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX  Baker DM, Cellis E, Kubo RT, Grey HM;
XX  WPI; 2001-354887/37.
XX  VT
XX  Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX  peptide groups, useful for vaccinating against HIV-1 -
XX  Claim 32; Page 187; 448pp; English.
XX  PS
XX  The present invention describes a composition (I) comprising a prepared
XX  human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX  sequence selected from 51 defined amino acid sequences (AB125347 to
XX  AB25397). (I) has virucide activity and can be used in vaccines. (I)
XX  may be used for immunising subjects against HIV-1 infections. The use of
XX  group-based vaccines has several advantages over traditional vaccines,
XX  particularly when compared to the use of whole antigens in vaccine
XX  compositions. There is evidence that the immune response to whole
XX  antigens is directed largely toward variable regions of the antigen,
XX  allowing for immune escape due to mutations. The groups for inclusion in
XX  an group-based vaccine may be selected from conserved regions of viral or
XX  tumour-associated antigens, which therefore reduces the likelihood of
XX  escape mutants. Furthermore, immunosuppressive groups that may be present
XX  in whole antigens can be avoided with the use of group-based vaccines.
XX  An additional advantage of an group-based vaccine approach is the ability
XX  to combine selected groups (CTL and HTL), and further, to modify the
XX  composition of the groups, achieving, for example, enhanced
XX  immunogenicity. Accordingly, the immune response can be modulated, as
XX  appropriate, for the target disease. Similar engineering of the response
XX  is not possible with traditional approaches. ABP1501 to ABP25412
XX  represent peptide sequences used in the exemplification of the present
XX  invention.
XX  SQ      Sequence      8 AA;

Query Match      22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches      4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
Db      ||||

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RESULT 53
ABP15565
ID ABP15565 standard; Peptide; 8 AA.
XX
AC ABP15565;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif gag peptide #51.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 3; Page 187; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LKSL 18
Db 5 LKSL 8
RESULT 54
ABP15567
ID ABP15567 standard; Peptide; 8 AA.

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XX ABP15567;
AC
XX 15-JUL-2002 (first entry)
DT
XX
DE HIV A24 super motif gag peptide #53.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpr; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 3; Page 187; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;
Query Match 22.2%; Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 LKSL 18
Db 4 LKSL 7
RESULT 55
ABP17830
ID ABP17830 standard; Peptide; 8 AA.
XX
AC ABP17830;
XX

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DT 15-JUL-2002 (first entry)  
 XX HIV B58 super motif gag peptide #49.  
 DE  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 FN 12-APR-2001.  
 XX  
 XX 05-OCT-2000; 2000WO-US27766.  
 PD  
 XX 05-OCT-1999; 99US-0412863.  
 PF  
 XX (EPIM-) EPIMMUNE INC.  
 PR Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX Baker DM, Celis E, Kubo RT, Grey HM;  
 PI WPI; 2001-354887/37.  
 PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 XX Claim 32; Page 234; 448pp; English.  
 PS  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 LKSL 18  
 Db 5 LKSL 8  
 RESULT 56  
 ABP17849  
 ID ABP17849 standard; Peptide; 8 AA.  
 XX  
 AC ABP17849;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX HIV B58 super motif gag peptide #68.  
 DE

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 XX WO200124810-A1.  
 FN 12-APR-2001.  
 XX  
 XX 05-OCT-2000; 2000WO-US27766.  
 PD  
 XX 05-OCT-1999; 99US-0412863.  
 PF  
 XX (EPIM-) EPIMMUNE INC.  
 PR Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 XX Baker DM, Celis E, Kubo RT, Grey HM;  
 PI WPI; 2001-354887/37.  
 PI Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 XX  
 XX Claim 32; Page 234; 448pp; English.  
 PS  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 LKSL 18  
 Db 4 LKSL 7  
 RESULT 57  
 ABP17869  
 ID ABP17869 standard; Peptide; 8 AA.  
 XX  
 AC ABP17869;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT  
 XX HIV B58 super motif gag peptide #88.  
 DE  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW



KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX Human immunodeficiency virus type 1.  
 XX WO200124810-A1.  
 XX 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PT  
 XX Claim 32; Page 235; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db 4 LKSL 7  
 RESULT 58  
 ABP20480  
 ID ABP20480 standard; Peptide; 8 AA.  
 XX  
 AC ABP20480;  
 XX  
 DT 15-JUL-2002 (first entry)  
 DE  
 DE HIV A03 motif gag peptide #143.  
 XX  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.

XX WO200124810-A1.  
 XX 12-APR-2001.  
 XX 05-OCT-2000; 2000WO-US27766.  
 XX 05-OCT-1999; 99US-0412863.  
 XX (EPIM-) EPIMUNE INC.  
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX WPI; 2001-354887/37.  
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1 -  
 PT  
 XX Claim 32; Page 289; 448pp; English.  
 XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)  
 CC may be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines.  
 CC An additional advantage of an group-based vaccine approach is the ability  
 CC to combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP1501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 8 AA;  
 Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db 4 LKSL 7  
 RESULT 59  
 ABP20520  
 ID ABP20520 standard; Peptide; 8 AA.  
 XX  
 AC ABP20520;  
 XX  
 DT 15-JUL-2002 (first entry)  
 DE  
 DE HIV A03 motif gag peptide #183.  
 XX  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;  
 KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;  
 KW antigen; vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus type 1.  
 XX  
 PN WO200124810-A1.  
 XX

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PD 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US-0412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 290; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 8 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 15 LKSL 18
XX ||||
XX 4 LKSL 7
XX
XX RESULT 60
XX ABP23517
XX ID ABP23517 standard; Peptide; 8 AA.
XX
XX AC ABP23517;
XX
XX 15-JUL-2002 (first entry)
XX
XX DE HIV A11 motif pol peptide #459.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX OS Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US27766.
XX

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XX 05-OCT-1999; 99US-0412863.
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1 -
XX
XX Claim 32; Page 350; 448pp; English.
XX
XX The present invention describes a composition (I) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABL25347 to
XX ABP25397). (I) has virucide activity and can be used in vaccines. (I)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 8 AA;
XX
XX Query Match 22.2%; Score 4; DB 22; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 EILK 16
XX ||||
XX 1 EILK 4
XX
XX RESULT 61
XX AAB55644
XX ID AAB55644 standard; Peptide; 8 AA.
XX
XX AC AAB55644;
XX
XX 07-MAR-2001 (first entry)
XX
XX DE Monocyte surface receptor PDZ domain sequence #15.
XX
XX Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
XX allergy; asthma; multiple sclerosis; cancer; infection.
XX
XX OS Synthetic.
XX
XX WO200069896-A2.
XX
XX 23-NOV-2000.
XX
XX 12-MAY-2000; 2000WO-US13161.
XX
XX 14-MAY-1999; 99US-0134114.
XX
XX 14-MAY-1999; 99US-0134117.
XX
XX 14-MAY-1999; 99US-0134118.
XX

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PR 21-OCT-1999; 99US-0160860.  
 PR 29-OCT-1999; 99US-0162498.  
 PR 13-DEC-1999; 99US-0170453.  
 PR 14-JAN-2000; 2000US-0176195.  
 PR 14-FEB-2000; 2000US-0182296.  
 PR 11-APR-2000; 2000US-0196460.  
 PR 11-APR-2000; 2000US-0196527.  
 XX (ARBO-) ARBOR VITA CORP.  
 XX PA  
 XX Lu PS;  
 XX WPI; 2001-080245/09.

XX Modulating a biological function of an endothelial cell or  
 PT hematopoietic cell, useful for treating autoimmune diseases and  
 PT infectious diseases, by administering an antagonist that inhibits  
 PT binding between a PDZ protein and a PL protein -  
 XX  
 PS Disclosure; Page 87-94; 141pp; English.

XX The present invention relates to a new method for modulating a  
 CC biological function of an endothelial cell or hematopoietic cell. The  
 CC method involves introducing into a cell, an antagonist that inhibits  
 CC binding between a PDZ protein and a PL protein. The inhibitor is used  
 CC to treat a disease mediated by hematopoietic cells, e.g. autoimmune  
 CC disease. It may also be used to prevent transplantation rejection of  
 CC a solid organ transplant. The method may also be used in the treatment  
 CC of inflammation, allergy, inflammatory bowel diseases, ulcerative  
 CC colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune  
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis,  
 CC insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis,  
 CC graft rejection, transplantation rejection), atherosclerosis, cancers,  
 CC infectious diseases, ischemia, vasculitis and Crohn's disease.

XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 4 LKSL 7

RESULT 62  
 AAB57491  
 ID AAB57491 standard; Peptide; 8 AA.

XX AC AAB57491;

XX 12-MAR-2001 (first entry)

XX CD61 C-terminal core sequence #5.

XX Endothelial cell; hematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.

XX OS Homo sapiens.

XX WO200069897-A2.

XX 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13166.

XX 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.  
 PR 14-MAY-1999; 99US-0134118.  
 PR 21-OCT-1999; 99US-0160860.  
 PR 29-OCT-1999; 99US-0162498.  
 PR 13-DEC-1999; 99US-0170453.  
 PR 14-JAN-2000; 2000US-0176195.  
 PR 14-FEB-2000; 2000US-0182296.  
 PR 11-APR-2000; 2000US-0196460.  
 PR 11-APR-2000; 2000US-0196527.  
 XX (ARBO-) ARBOR VITA CORP.  
 XX PA  
 XX Lu PS;  
 XX WPI; 2001-025003/03.

XX New inhibitors of binding of a PDZ protein and PL protein for  
 PT inhibiting T cell-mediated response by hematopoietic cells, or for  
 PT treating diseases characterized by inflammatory and humoral immune  
 PT responses, e.g. inflammation, cancer -  
 XX  
 PS Disclosure; Page 90; 139pp; English.

XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or hematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organizing transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC hematopoietic cells, e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteo-  
 CC arthrititis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.

SQ Sequence 8 AA;

Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 4 LKSL 7

RESULT 63

AAB57901

ID AAB57901 standard; Peptide; 8 AA.

XX AC AAB57901;

XX 12-MAR-2001 (first entry)

XX CD61 C-terminal core sequence #5.

XX Endothelial cell; hematopoietic cell; PDZ domain protein;  
 KW PL domain protein; leukocyte activation; T cell surface receptor;  
 KW synapse formation; transmembrane neurotransmitter receptor;  
 KW autoimmune disease; transplantation rejection; inflammation; allergy;  
 KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;  
 KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;  
 KW ischaemia; vasculitis; Crohn's disease.

OS Homo sapiens.  
 XX WO200069898-A2.  
 XX 23-NOV-2000.  
 XX 12-MAY-2000; 2000WO-US13205.  
 XX 14-MAY-1999; 99US-0134114.  
 XX 14-MAY-1999; 99US-0134117.  
 XX 14-MAY-1999; 99US-0134118.  
 XX 21-OCT-1999; 99US-0160860.  
 XX 29-OCT-1999; 99US-0162498.  
 XX 13-DEC-1999; 99US-0170453.  
 XX 14-JAN-2000; 2000US-0176195.  
 XX 14-FEB-2000; 2000US-0182296.  
 XX 11-APR-2000; 2000US-0196460.  
 XX 11-APR-2000; 2000US-0196527.  
 XX (ARBO-) ARBOR VITA CORP.  
 XX PI Lu PS;  
 XX WPI; 2001-061214/07.  
 XX Modulating a biological function of a hematopoietic cell for treating  
 PT an allergic response, or diseases mediated by immune system cells,  
 PT comprises introducing into the cell a PDZ-PL interaction enhancer or  
 PT inhibitor.  
 XX Disclosure; Page 93; 143pp; English.  
 XX The present invention relates to a method for modulating a biological  
 CC function of an endothelial cell or haematopoietic cell, comprises  
 CC introducing into a cell an antagonist that inhibits binding between a  
 CC PDZ domain protein and a PL domain protein to result in inhibition of  
 CC leukocyte activation. The present sequence is a core sequence of a PL  
 CC domain protein (a T cell surface receptor). PDZ domains of proteins are  
 CC named after three prototypical proteins: PSD95, Drosophila large disc  
 CC protein and Zonula Occludin 1 protein. PDZ domain proteins are involved  
 CC in synapse formation by organising transmembrane neurotransmitter  
 CC receptors through intracellular interactions. The inhibitors identified  
 CC by the present invention can be used to treat a disease mediated by  
 CC haematopoietic cells; e.g. autoimmune disease, inflammation, allergy  
 CC (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis,  
 CC ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic  
 CC dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple  
 CC sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis,  
 CC osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g.  
 CC viral infection), ischaemia, vasculitis and Crohn's disease. The  
 CC inhibitors can also be used to prevent transplantation rejection of a  
 CC solid organ transplant.  
 XX Sequence 8 AA;  
 SQ Query Match 22.2%; Score 4; DB 22; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db 4 LKSL 7  
 RESULT 64  
 ABJ05123  
 ID ABJ05123 standard; Peptide; 8 AA.  
 XX AC ABJ05123;  
 XX 07-NOV-2002 (first entry)  
 DT T-cell surface receptor C-terminal core peptide SEQ ID No 118.  
 DE

XX Immunosuppressive; antiinflammatory; affinity; Kd; binding; PDZ domain;  
 KW ligand; Ki; inhibitor; K-enhancer; leukocyte; autoimmune disease;  
 KW inflammatory; humoral immune response; inflammation; C-terminal core;  
 KW T-cell surface receptor.  
 XX Unidentified.  
 XX WO200231512-A2.  
 XX 18-APR-2002.  
 XX 11-OCT-2001; 2001WO-US32150.  
 XX 13-OCT-2000; 2000US-0688017.  
 XX (ARBO-) ARBOR VITA CORP.  
 XX Rabinowitz JD, Lu PS, Schweizer J;  
 XX WPI; 2002-416878/44.  
 XX Assays for determining the affinity of binding between a PDZ domain and  
 PT a ligand, and determining the Ki of an inhibitor of the binding,  
 PT comprises using a polypeptide comprising a PDZ domain and a non-PDZ  
 PT domain.  
 XX Disclosure; Page 114; 164pp; English.  
 XX The invention relates to methods and reagents for determining the  
 CC apparent affinity (Kd) of binding between a PDZ domain and a ligand. The  
 CC invention also relates to methods and reagents for determining the Ki of  
 CC an inhibitor of binding between a PDZ domain and a ligand, identifying an  
 CC agent that enhances binding of a PDZ domain and a ligand, and determining  
 CC the potency (K-enhancer) of binding between a PDZ domain and a ligand, by  
 CC determining the ligand bound with an immobilised polypeptide comprising a  
 CC PDZ domain and a non-PDZ domain on a surface. The modulator (preferably,  
 CC an inhibitor) of interaction between PDZ and PL is useful for treating a  
 CC disease characterised by leukocyte activation, e.g., an autoimmune  
 CC disease that is characterised by inflammatory or humoral immune response,  
 CC and for reducing inflammation in a subject. This sequence represents a T-  
 CC cell surface receptor C-terminal core peptide relating to the PDZ  
 CC containing proteins of the invention.  
 XX Sequence 8 AA;  
 SQ Query Match 22.2%; Score 4; DB 23; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db 4 LKSL 7  
 RESULT 65  
 ABJ06021  
 ID ABJ06021 standard; Peptide; 8 AA.  
 XX AC ABJ06021;  
 XX 14-NOV-2002 (first entry)  
 DT Hepatitis B virus epitope #239.  
 DE Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;  
 KW virucide; hepatotropic; antiinflammatory.  
 XX Hepatitis B virus.  
 OS WO200219986-A1.  
 XX 14-MAR-2002.  
 PD

XX 08-SEP-2000; 2000WO-US24802.  
XX  
XX  
XX 08-SEP-2000; 2000WO-US24802.  
XX  
XX (EPIM-) EPIMMUNE INC.  
XX PA (SETT/) SETTE A.  
XX  
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;  
XX PI Celis E, Kubo RT, Grey HM, Chesnut RW;  
XX  
XX WPI; 2002-643192/69.  
XX  
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)  
PT infection, and/or for stimulating an immune response to HBV, comprises  
PT a HBV peptide epitope -  
XX  
XX Disclosure; Page 114; 228pp; English.  
XX  
XX The present invention relates to a composition comprising at least one  
CC hepatitis B virus epitope. This can be used in the production of a  
CC vaccine for use in preventing or treating hepatitis B virus infection.  
CC The present sequence is a peptide described in the exemplification of the  
CC invention.  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 22.2%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 GEEI 14  
Db 3 GEEI 6  
RESULT 66  
ABJ06547  
XX ID ABJ06547 standard; Peptide; 8 AA.  
XX AC ABJ06547;  
XX  
XX DT 14-NOV-2002 (first entry)  
XX DE Hepatitis B virus epitope #765.  
XX  
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;  
KW virucide; hepatotropic; antiinflammatory.  
XX  
XX Hepatitis B virus.  
OS  
XX WO200219986-A1.  
XX PN  
XX PD 14-MAR-2002.  
XX  
XX PF 08-SEP-2000; 2000WO-US24802.  
XX PR 08-SEP-2000; 2000WO-US24802.  
XX PA (EPIM-) EPIMMUNE INC.  
XX PA (SETT/) SETTE A.  
XX  
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;  
XX PI Celis E, Kubo RT, Grey HM, Chesnut RW;  
XX  
XX WPI; 2002-643192/69.  
XX  
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)  
PT infection, and/or for stimulating an immune response to HBV, comprises  
PT a HBV peptide epitope -  
XX  
XX Disclosure; Page 127; 228pp; English.

CC The present invention relates to a composition comprising at least one  
CC hepatitis B virus epitope. This can be used in the production of a  
CC vaccine for use in preventing or treating hepatitis B virus infection.  
CC The present sequence is a peptide described in the exemplification of the  
CC invention.  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 22.2%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 GEEI 14  
Db 3 GEEI 6  
RESULT 67  
ABJ07394  
XX ID ABJ07394 standard; Peptide; 8 AA.  
XX AC ABJ07394;  
XX  
XX DT 14-NOV-2002 (first entry)  
XX DE Hepatitis B virus epitope #1612.  
XX  
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;  
KW virucide; hepatotropic; antiinflammatory.  
XX  
XX Hepatitis B virus.  
OS  
XX WO200219986-A1.  
XX PN  
XX PD 14-MAR-2002.  
XX  
XX PF 08-SEP-2000; 2000WO-US24802.  
XX PR 08-SEP-2000; 2000WO-US24802.  
XX PA (EPIM-) EPIMMUNE INC.  
XX PA (SETT/) SETTE A.  
XX  
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;  
XX PI Celis E, Kubo RT, Grey HM, Chesnut RW;  
XX  
XX WPI; 2002-643192/69.  
XX  
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)  
PT infection, and/or for stimulating an immune response to HBV, comprises  
PT a HBV peptide epitope -  
XX  
XX Disclosure; Page 143; 228pp; English.  
XX  
XX The present invention relates to a composition comprising at least one  
CC hepatitis B virus epitope. This can be used in the production of a  
CC vaccine for use in preventing or treating hepatitis B virus infection.  
CC The present sequence is a peptide described in the exemplification of the  
CC invention.  
XX  
XX Sequence 8 AA;  
SQ  
Query Match 22.2%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 11 GEEI 14  
Db 3 GEEI 6  
RESULT 68  
ABF63416

ID ABP63416 standard; Peptide; 8 AA.  
XX AC ABP63416;  
XX DT 28-OCT-2002 (first entry)  
XX DE Monocyte surface receptor PDZ motif (PL) peptide SEQ ID NO:118.  
XX KW Molecular interaction; haematopoietic cell; immune response; T cell;  
KW PDZ domain; B cell; endothelial cell; PDZ protein; PSB95; PDZ ligand;  
KW Drosophila large disc protein; Zonula Occludin 1 protein; PL protein;  
KW immunosuppressive; antiinflammatory; antiallergic; antiatherosclerotic;  
KW antitumor; antiproliferative; dermatological; antiasthmatic; cytostatic;  
KW antimicrobial; vasotropic; inflammatory immune response; inflammation;  
KW humoral immune response; autoimmune disease; allergy; ulcerative colitis;  
KW inflammatory bowel disease; ileitis; enteritis; psoriasis; scleroderma;  
KW inflammatory dermatosis; respiratory allergic disease; asthma; cancer;  
KW allergic rhinitis; transplantation rejection; atherosclerosis; ischaemia;  
KW angiogenesis-dependent disorder; infectious disease.  
XX OS Homo sapiens.  
XX OS Synthetic.  
XX PN WO200242422-A2.  
XX PD 30-MAY-2002.  
XX PF 09-NOV-2001; 2001WO-US44138.  
XX PR 11-NOV-2000; 2000US-0710059.  
XX PR 24-NOV-2000; 2000US-0721915.  
XX PR 24-NOV-2000; 2000US-0722069.  
XX PR 28-NOV-2000; 2000US-0724553.  
XX PA (ARBO-) ARBOR VITA CORP.  
XX PI Lu P, Rabinowitz JD, Schweizer J;  
XX DR WPI; 2002-608221/65.  
XX PT Modulating the biological function of an endothelial cell or  
PT hematopoietic cell e.g., a T-cell or B-cell comprises introducing into  
PT the cell, an agent that inhibits binding of a PDZ protein and a PDZ  
PT ligand protein in the cell -  
XX PS Disclosure; Page 132; 207pp; English.  
XX CC The present invention describes a method (M1) for modulating a biological  
CC function of an endothelial cell or haematopoietic cell. M1 comprises  
CC introducing into the cell, an agent that inhibits binding of a PDZ  
CC (PSB95, Drosophila large disc protein, and Zonula Occludin 1 protein)  
CC protein and a PDZ ligand (PL) protein in the cell, and so modulates the  
CC biological function. Also described is a method (M2) for determining  
CC whether a test compound is an inhibitor of binding between a PDZ protein  
CC and a PL protein. M1 is used for modulating a biological function of an  
CC endothelial cell or haematopoietic cell e.g., T-cell or B-cell, by an  
CC inflammatory or humoral immune response, or an autoimmune disease. An  
CC inhibitor (I) is useful for treating a disease characterised by leukocyte  
CC activation, where the disease is characterised by an inflammatory or  
CC humoral immune response, e.g., an autoimmune disease. The compounds  
CC e.g., PL-PDZ interaction inhibitors are useful for treating (ameliorating  
CC symptoms of) a variety of diseases and conditions characterised by  
CC inflammatory and humoral immune responses e.g., inflammation, allergy,  
CC inflammatory bowel diseases, ulcerative colitis, ileitis and enteritis,  
CC psoriasis and inflammatory dermatoses, scleroderma, respiratory allergic  
CC diseases such as asthma, allergic rhinitis, transplantation rejection  
CC (cardiac, kidney, lung, liver, small bowel, cornea, pancreas, cadaver,  
CC autologous, bone marrow, xenotransplantation), atherosclerosis, cancers,  
CC angiogenesis-dependent disorders, infectious diseases and ischaemia  
CC ABQ96620 to ABQ96732 and ABP63153 to ABP63578 represent sequences used  
CC in the exemplification of the present invention.  
XX XX Sequence 8 AA;

Query Match 22.2%; Score 4; DB 23; Length 8;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 LKSL 18  
DB 4 LKSL 7  
RESULT 69  
ID AAR66006 standard; peptide; 9 AA.  
XX AAR66006;  
XX AC AAR66006;  
XX DT 30-JUN-1995 (first entry)  
XX DE Peptide which binds immune complexes.  
XX KW Immune complex; immunoadsorbent.  
XX OS Synthetic.  
XX PN JP06263795-A.  
XX PD 20-SEP-1994.  
XX PF 30-SEP-1993; 93JP-0245367.  
XX PR 30-SEP-1992; 93JP-0261821.  
XX PR 18-JAN-1993; 93JP-0006099.  
XX PA (KURS) KURARAY CO LTD.  
XX DR WPI; 1994-338300/42.  
XX PT Peptide(s) capable of binding to immune complex, and adsorbents  
PT contg them - useful for removal of immune complexes from body  
PT fluid and for treatment of associated diseases.  
XX Example 8; Page 6; 15pp; Japanese.  
XX CC The invention relates to new peptides of formula H-X-A-Y-Z in which  
CC A is a peptide fragment of 6-12 amino acids containing the sequence  
CC Ala-B-C-Glu-Ile-Leu, where B and C are Trp, Tyr and/or Phe; X and Y  
CC are each a single bond, or an amino acid or peptide composed of 2-10  
CC amino acids selected from Asp, Glu, Arg, Lys and His, provided at  
CC least one of X and Y is not a bond; and Z is OH or amide.  
CC The peptides can bind to immune complexes. They can be fixed to a  
CC support and used for selective removal of immune complexes from body  
CC fluids without removal of useful components. They can thus be used for  
CC treating diseases involving the complexes. In Examples, the  
CC activity of the peptides is compared to that of reference peptides  
CC in which neither X nor Y is present.  
XX CC The present sequence is a specific example of the new peptides.  
SQ Sequence 9 AA;  
Query Match 22.2%; Score 4; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 BILK 16  
DB 5 BILK 8  
RESULT 70  
ID AAR65863 standard; peptide; 9 AA.  
XX AAR65863;  
XX AC AAR65863;

XX DT 26-JUN-1995 (first entry)  
 XX DE Antideoxyribonucleic acid antibody adsorbent peptide.  
 XX KW Antideoxyribonucleic acid adsorbent peptide; kidney inflammation;  
 XX KW systemic lupus erythematosus.  
 XX OS Synthetic.  
 XX PN JP06261941-A.  
 XX PD 20-SEP-1994.  
 XX PF 13-OCT-1993; 93JP-0256111.  
 XX PR 18-JAN-1993; 93JP-0006100.  
 XX PA (KURS ) KURARAY CO LTD.  
 XX DR WPI; 1994-337461/42.  
 XX PT Adsorbents of antideoxyribonucleic - comprising a peptide,  
 XX PT immobilised on a carrier.  
 XX PS Claim 1; Page 14; 16pp; Japanese.  
 XX CC AAR65841-R65879 are antideoxyribonucleic (ADN) acid adsorbent peptides  
 CC derived from the highly generic peptide in the specification. When these  
 CC peptides are immobilised on a carrier (either cellulose, porous  
 CC glass, polyvinyl alcohol or polyacrylamide) they can be used to  
 CC remove ADN antibodies, which can result in kidney inflammation and  
 CC systemic lupus erythematosus.  
 XX SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 15; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 13 EILK 16  
 Db 5 EILK 8  
 ||||  
 RESULT 71  
 AAR70537  
 ID AAR70537 standard; Peptide; 9 AA.  
 XX AC AAR70537;  
 XX DT 09-JAN-1996 (first entry)  
 XX DE HIV peptide fragment 6 capable of binding to HLA-B3501.  
 XX KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX OS Human immunodeficiency virus.  
 XX PN WO9511255-A1.  
 XX PD 27-APR-1995.  
 XX PF 19-OCT-1994; 94WO-JP01756.  
 XX PR 19-OCT-1993; 93JP-0261302.  
 XX PA (AJIN ) AJINOMOTO CO INC.  
 XX PA (AJIN ) AJINOMOTO KK.  
 XX PI Miwa K, Takiguchi M;  
 XX DR WPI; 1995-170188/22.  
 XX PT HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 XX anti-HIV vaccines  
 XX PS Claim 1; Page 29; 93JP-0261302.  
 XX CC (AJIN ) AJINOMOTO CO INC.  
 CC (AJIN ) AJINOMOTO KK.  
 CC PI Miwa K, Takiguchi M;  
 CC AAR70544 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) protein and is capable of binding to human  
 CC lymphocyte antigen (HLA) B51. Peptides shown in AAR70543-64 are all  
 CC capable of binding to HLA-B51, and other peptide fragments bind to other

XX WPI; 1995-170188/22.  
 XX HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 PT anti-HIV vaccines  
 XX PS Claim 1; Page 27; 61pp; Japanese.  
 XX CC AAR70537 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) protein which is capable of binding to human  
 CC lymphocyte antigen (HLA) B\*3501. Peptides shown in AAR70519-42 are all  
 CC capable of binding to HLA-B\*3501, and other peptide fragments bind to  
 CC other specific HLA's. Pref. peptides have Pro, Ala or Gly as the second  
 CC residue (from the N-terminal) and Ieu, Ile, Met, Phe, Val (or Tyr or Ala)  
 CC at the carboxy terminal. The peptides induce killer cells which target  
 CC HIV-infected cells. They are useful in the prevention and treatment of  
 CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may  
 CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the  
 CC peptides.  
 XX SQ Sequence 9 AA;  
 Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 15 LKSL 18  
 Db 6 LKSL 9  
 ||||  
 RESULT 72  
 AAR70544  
 ID AAR70544 standard; Peptide; 9 AA.  
 XX AC AAR70544;  
 XX DT 11-JAN-1996 (first entry)  
 XX DE HIV peptide fragment 12 capable of binding to HLA-B51.  
 XX KW HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX OS Human immunodeficiency virus.  
 XX PN WO9511255-A1.  
 XX PD 27-APR-1995.  
 XX PF 19-OCT-1994; 94WO-JP01756.  
 XX PR 19-OCT-1993; 93JP-0261302.  
 XX PA (AJIN ) AJINOMOTO CO INC.  
 XX PA (AJIN ) AJINOMOTO KK.  
 XX PI Miwa K, Takiguchi M;  
 XX DR WPI; 1995-170188/22.  
 XX PT HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 XX anti-HIV vaccines  
 XX PS Claim 1; Page 29; 61pp; Japanese.  
 XX CC AAR70544 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency Virus) protein and is capable of binding to human  
 CC lymphocyte antigen (HLA) B51. Peptides shown in AAR70543-64 are all  
 CC capable of binding to HLA-B51, and other peptide fragments bind to other

CC specific HLA's. Pref. peptides have Pro, Ala or Gly as the second residue  
 CC (from the N-terminal) and Leu, Ile, Met, Phe, Val (or Tyr or Ala) at the  
 CC carboxy terminal. The peptides induce killer cells which target  
 CC HIV-infected cells. They are useful in the prevention and treatment of  
 CC HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may  
 CC incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the  
 CC peptides.  
 XX  
 SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 6 LKSL 9

RESULT 73  
 AAR77554  
 ID AAR77554 standard; Peptide; 9 AA.

XX  
 AC AAR77554;

XX 14-FEB-1996 (first entry)

XX HIV(B35)GAG-29, human immunodeficiency virus epitope.

XX HLA; human lymphocyte antigen; HIV; human immunodeficiency virus;  
 KW binding peptide; induce killer cell; prevention; treatment; AIDS;  
 KW autoimmune disease syndrome; vaccine.  
 XX

OS Human immunodeficiency virus (MN isolate).

XX WO9511255-A1.

XX 27-APR-1995.

XX 19-OCT-1994; 94WO-JP01756.

XX 19-OCT-1993; 93JP-0261302.

XX (AJIN ) AJINOMOTO CO INC.

XX (AJIN ) AJINOMOTO KK.

XX Miwa K, Takiguchi M;

XX WPI; 1995-170188/22.

XX HLA-binding peptide fragments from HIV proteins - induce killer  
 PT cells which target HIV-infected cells and can be incorporated into  
 PT anti-HIV vaccines

XX Example 1; Page 16; 61pp; Japanese.

XX R775540 is a peptide fragment derived from an HIV (Human  
 CC Immunodeficiency virus) gag protein (residues 490-498) and is capable of  
 CC binding to a human lymphocyte antigen. The peptide can induce killer  
 CC cells which target HIV-infected cells. It is also useful in the  
 CC prevention and treatment of HIV and AIDS. Anti-HIV vaccines may  
 CC incorporate the peptides, or may incorporate a vector (such as vaccinia  
 CC or BCG) contg. DNA encoding the peptides.  
 XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 16; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
 ||||  
 Db 6 LKSL 9

RESULT 74  
 AAW49244

ID AAW49244 standard; peptide; 9 AA.

XX  
 AC AAW49244;

XX 05-JUN-1998 (first entry)

XX Human leucocyte antigen DQ4 binding peptide #135.

XX Human leucocyte antigen; HLA-DQ4; combinatorial library;  
 KW autoimmune disease; chronic articular rheumatism.  
 XX

OS Synthetic.

XX JP08151396-A.

XX 11-JUN-1996.

XX 28-NOV-1994; 94JP-0292657.

XX 28-NOV-1994; 94JP-0292657.

XX (TEIJ ) TEIJIN LTD.

XX WPI; 1996-329479/33.

XX HLA-binding oligopeptide and an immuno:regulator contg it - used in  
 PT the treatment of auto:immune disease  
 XX

PS Claim 4; Page 23; 61pp; Japanese.

XX This peptide is an example of a peptide which binds to a human leucocyte  
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid  
 CC combinatorial library comprising the sequence AAV05953, by screening  
 CC with an HLA-DQ4 molecule. The peptide is used for the treatment of  
 CC autoimmune disease, or especially for treatment of viral diseases.  
 XX

SQ Sequence 9 AA;

Query Match 22.2%; Score 4; DB 17; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEEI 14  
 ||||  
 Db 1 GEEI 4

RESULT 75  
 AAY96353

ID AAY96353 standard; peptide; 9 AA.

XX  
 AC AAY96353;

XX 29-AUG-2000 (first entry)

XX HLA-A3 binding peptide hTERT R535.

XX hTERT; telomerase complex; reverse transcriptase; MHC; HLA; CTL; cancer;  
 KW human leukocyte antigen; tumour-associated antigen; cytostatic; vaccine;  
 KW major histocompatibility complex; cytotoxic T lymphocyte; immunotherapy.  
 XX

OS Homo sapiens.

XX WO200025813-A1.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US25438.



```

PR 29-OCT-1998; 98US-0106106.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX Nadler LM, Hahn WC, Schultze JL, Vonderheide RH;
XX
XX WPI; 2000-365402/31.
XX
XX Universal tumor-associated antigens such as telomerase catalytic
XX subunit capable of binding major histocompatibility complex molecule
XX useful for diagnosis, prevention and treatment of cancer
XX
XX Disclosure; Page 74; 136pp; English.
XX
XX Human telomerase complex reverse transcriptase (hTERT) is expressed in
XX more than 85 percent of human cancers. hTERT is useful as a universal
XX tumour-associated antigen (TAA) that binds to a major histocompatibility
XX complex molecule (MHC). hTERT peptides were analyzed for the ability to
XX bind to HLA (human leukocyte antigen) class I molecules. Cytotoxic T
XX lymphocytes (CTL) were then generated that kill a cell expressing hTERT
XX or a hTERT-TAA, in a hTERT or TAA specific MHC-restricted fashion.
XX Antigen presenting cells (APC) were also generated ex vivo for
XX presentation of a TAA peptide or hTERT. The APC can be used to activate
XX CTL to kill cells expressing the TAA. The TAA, hTERT peptides, APC and
XX CTL are useful for cancer immunotherapy. Measuring the level of CTL in a
XX sample is useful for assessing the level of immunity of a patient to a
XX TAA or a peptide, where the sample is obtained before or after a cancer
XX treatment is given to the patient. TAA peptides (e.g. hTERT) are also
XX useful for diagnosis and prophylactic treatment of cancer.
XX
SQ Sequence 9 AA;
Query Match 22.2%; Score 4; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 12 BEIL 15
Db 4 BEIL 7

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Job time : 46.9419 secs

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QM protein - protein search, using sw model

Run on: November 25, 2003, 20:25:48 ; Search time 28.8837 Seconds  
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114.943 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

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Scoring table:

Gapop 60.0 , Gapext 60.0

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Total number of hits satisfying chosen parameters: 139996

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	18	100.0	18	15	US-10-281-652-30
2	16	33.3	18	10	US-09-734-520-33
3	6	33.3	18	14	US-10-012-034A-33
4	5	27.8	9	14	US-10-153-159-28
5	5	27.8	9	15	US-10-153-176-28
6	4	22.2	5	10	US-09-976-736-56
7	4	22.2	5	10	US-09-976-736-60
8	4	22.2	5	10	US-09-976-736-64
9	4	22.2	6	9	US-09-952-768-23
10	4	22.2	6	9	US-09-952-768-33
11	4	22.2	6	9	US-09-954-697-72
12	4	22.2	6	10	US-09-954-697-83
13	4	22.2	6	10	US-09-954-697-88
14	4	22.2	6	10	US-09-954-697-88
15	4	22.2	6	10	US-09-867-852-205
16	4	22.2	6	10	US-09-867-852-207
17	4	22.2	6	14	US-10-059-749-34
18	4	22.2	6	14	US-10-059-749-45
19	4	22.2	6	14	US-10-059-749-50
20	4	22.2	7	10	US-09-791-378-294
21	4	22.2	7	11	US-09-791-393-189
22	4	22.2	7	11	US-09-791-393-189
23	4	22.2	9	10	US-09-753-831-6
24	4	22.2	9	10	US-09-791-378-204
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26	4	22.2	9	12	US-09-943-052-132
27	4	22.2	9	12	US-09-943-052-137
28	4	22.2	9	12	US-09-942-052-215
29	4	22.2	9	12	US-09-942-052-241
30	4	22.2	9	12	US-09-942-052-310
31	4	22.2	9	12	US-09-942-052-310
32	4	22.2	9	12	US-09-942-052-343
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38	4	22.2	9	12	US-09-942-052-603
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41	4	22.2	9	14	US-10-153-159-29
42	4	22.2	9	14	US-10-153-159-30
43	4	22.2	9	15	US-10-153-176-21
44	4	22.2	9	15	US-10-153-176-24
45	4	22.2	9	15	US-10-153-176-29
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47	4	22.2	10	9	US-09-912-917-3
48	4	22.2	10	11	US-09-572-404B-722
49	4	22.2	10	11	US-09-572-404B-724
50	4	22.2	10	12	US-09-572-270A-611
51	4	22.2	10	12	US-09-572-270A-948
52	4	22.2	10	12	US-09-572-270A-950
53	4	22.2	10	12	US-09-942-052-152
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56	4	22.2	10	12	US-09-942-052-294
57	4	22.2	10	12	US-09-942-052-357
58	4	22.2	10	12	US-09-942-052-375
59	4	22.2	10	12	US-09-942-052-474
60	4	22.2	10	12	US-09-942-052-484
61	4	22.2	10	12	US-09-942-052-488
62	4	22.2	10	12	US-09-942-052-493
63	4	22.2	10	12	US-09-942-052-560
64	4	22.2	10	12	US-09-942-052-566
65	4	22.2	10	12	US-09-942-052-582
66	4	22.2	10	12	US-09-942-052-597
67	4	22.2	10	12	US-09-942-052-667
68	4	22.2	10	12	US-09-942-052-681
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71	4	22.2	10	12	US-10-239-313A-5
72	4	22.2	10	12	US-10-239-313A-80
73	4	22.2	10	12	US-10-200-708-29
74	4	22.2	10	12	US-10-200-708-440
75	4	22.2	10	12	US-10-200-708-594
76	4	22.2	10	12	US-09-573-822C-22
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78	4	22.2	10	12	US-09-573-822C-265
79	4	22.2	10	12	US-10-277-292-58
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84	4	22.2	10	12	US-10-280-340-394
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87	4	22.2	11	10	US-09-795-006A-137
88	4	22.2	11	11	US-09-852-910-149
89	4	22.2	11	11	US-09-852-910-149
90	4	22.2	11	11	US-09-852-910-149
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89                   4   22.2   12   15   US-10-033-662-16                   Sequence 16, Appl  
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91                   4   22.2   13   9   US-09-813-329-39                   Sequence 39, Appl  
92                   4   22.2   13   9   US-09-813-329-49                   Sequence 49, Appl  
93                   4   22.2   13   9   US-09-813-329-60                   Sequence 60, Appl  
94                   4   22.2   13   9   US-09-873-676-13                   Sequence 13, Appl  
95                   4   22.2   13   12   US-10-153-244-61                   Sequence 61, Appl  
96                   4   22.2   13   12   US-10-153-244-124                   Sequence 124, App  
97                   4   22.2   13   12   US-10-153-244-174                   Sequence 174, App  
98                   4   22.2   13   12   US-10-153-244-224                   Sequence 224, App  
99                   4   22.2   14   10   US-09-957-143-5                   Sequence 5, Appl  
100                  4   22.2   15   11   US-09-907-969-502                   Sequence 502, App

## ALIGNMENTS

RESULT 1  
US-10-281-652-30  
; Sequence 30, Application US/10281652  
; Publication No. US20030091606A1  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; FILE REFERENCE: 265.00220101  
; CURRENT APPLICATION NUMBER: US/10/281.652  
; CURRENT FILING DATE: 2002-10-28  
; PRIOR APPLICATION NUMBER: US/09/641,803  
; PRIOR FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 30  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-10-281-652-30

Query Match                   100.0%; Score 18; DB 15; Length 18;  
Best Local Similarity       100.0%; Pred. No. 1.5e-12;  
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1   ATFNRYQDDHGEILKSL 18  
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Db   1   ATFNRYQDDHGEILKSL 18

RESULT 2  
US-09-734-520-33  
; Sequence 33, Application US/09734520  
; Patent No. US20020115173A1  
; GENERAL INFORMATION:  
; APPLICANT: Ben-Sasson, Shmuel  
; TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF  
; TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE  
; FILE REFERENCE: 1242.2003-000  
; CURRENT APPLICATION NUMBER: US/09/734,520  
; CURRENT FILING DATE: 2000-12-11  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:

; OTHER INFORMATION: Jak2  
US-09-734-520-33

Query Match                   33.3%; Score 6; DB 10; Length 18;  
Best Local Similarity       100.0%; Pred. No. 7.5;  
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   13   EILKSL 18  
     |||||  
Db   2   EILKSL 7

RESULT 3  
US-10-012-034A-33  
; Sequence 33, Application US/10012034A  
; Publication No. US20020137141A1  
; GENERAL INFORMATION:  
; APPLICANT: Ben-Sasson, Shmuel  
; TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF  
; TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE  
; FILE REFERENCE: BEN-SASSON=5A  
; CURRENT APPLICATION NUMBER: US/10/012,034A  
; CURRENT FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 09/734,520  
; PRIOR FILING DATE: 2000-12-11  
; NUMBER OF SEQ ID NOS: 133  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Jak2  
; FEATURE:  
; NAME/KEY: MYRISTATE  
; LOCATION: (1)...(0)  
; FEATURE:  
; NAME/KEY: AMIDATION  
; LOCATION: (0)...(18)  
US-10-012-034A-33

Query Match                   33.3%; Score 6; DB 14; Length 18;  
Best Local Similarity       100.0%; Pred. No. 7.5;  
Matches   6; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   13   EILKSL 18  
     |||||  
Db   2   EILKSL 7

RESULT 4  
US-10-153-159-28  
; Sequence 28, Application US/10153159  
; Publication No. US20020177170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu  
; APPLICANT: Wang, Caili  
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY  
; FILE REFERENCE: 26050-704  
; CURRENT APPLICATION NUMBER: US/10/153,159  
; CURRENT FILING DATE: 2002-05-20  
; PRIOR APPLICATION NUMBER: US 10/125,687  
; PRIOR FILING DATE: 2002-04-17  
; PRIOR APPLICATION NUMBER: US 60/284,407  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 125  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-28

Query Match      27.8%; Score 5; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TENRY 6
      |||||
Db      3 TENRY 7

RESULT 5
US-10-153-176-28
; Sequence 28, Application US/10153176
; Patent No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT FILING DATE: US/10/153,176
; CURRENT APPLICATION NUMBER: 2002-05-20
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-28

Query Match      27.8%; Score 5; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 TENRY 6
      |||||
Db      3 TENRY 7

RESULT 6
US-09-976-736-56
; Sequence 56, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: US/09/161,241
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-976-736-64

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5

RESULT 7
US-09-976-736-60
; Sequence 60, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-976-736-60

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5

RESULT 8
US-09-976-736-64
; Sequence 64, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-976-736-64

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5
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; TYPE: PRT
; ORGANISM: Human
US-09-976-736-56

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5

RESULT 7
US-09-976-736-60
; Sequence 60, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-976-736-60

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5

RESULT 8
US-09-976-736-64
; Sequence 64, Application US/09976736
; Patent No. US20020161178A1
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Sullivan, John K
; APPLICANT: Theill, Lars E
; APPLICANT: Wang, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; FILE REFERENCE: A-548
; CURRENT APPLICATION NUMBER: US/09/976,736
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/161,241
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Human
US-09-976-736-64

Query Match      22.2%; Score 4; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GEEI 14
      |||||
Db      2 GEEI 5
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Db      2 GEEI 5

RESULT 9
US-09-952-768-23
; Sequence 23, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
;               Armstrong, Robert
;               Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
;                   NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-952-768-23

Query Match      22.2%  Score 4;  DB 9;  Length 6;
Best Local Similarity 100.0%; Pred.No. 6.1e+05;
Matches 4;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGEE 13
      ||||
Db      3 HGEE 6

RESULT 11
US-09-952-768-38
; Sequence 38, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
;               Armstrong, Robert
;               Tomaselli, Kevin
; TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,
;                   NUCLEIC ACIDS ENCODING AND METHODS OF USE
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: Suite 6300, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-952-768-38

Query Match      22.2%  Score 4;  DB 9;  Length 6;
Best Local Similarity 100.0%; Pred.No. 6.1e+05;
Matches 4;  Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGEE 13
      ||||
Db      3 HGEE 6

RESULT 10
US-09-952-768-33
; Sequence 33, Application US/09952768
; Patent No. US20020035242A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
;               Fernandes-Alnemri, Teresa
;               Litwack, Gerald
;               Armstrong, Robert
;               Tomaselli, Kevin

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/952,768
; FILING DATE: 10-Sep-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Christiansen, William T.
; REGISTRATION NUMBER: 44,614
; REFERENCE/DOCKET NUMBER: 480140.424C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CED-3"
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-952-768-38

Query Match      22.2%; Score 4; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
DB      3 HGEE 6

RESULT 12
US-09-954-697-72
; Sequence 72, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 72
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-72

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
DB      3 HGEE 6

RESULT 13
US-09-954-697-83
; Sequence 83, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
```

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; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 83
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-83

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
DB      3 HGEE 6

RESULT 14
US-09-954-697-88
; Sequence 88, Application US/09954697
; Patent No. US20020106631A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USSES
; FILE REFERENCE: 480140.431D2
; CURRENT APPLICATION NUMBER: US/09/954,697
; CURRENT FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 88
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-954-697-88

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 HGEE 13
DB      3 HGEE 6

RESULT 15
US-09-867-852-205
; Sequence 205, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Staskawicz, Frederick M.
; APPLICANT: Brent, Andrew P.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
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;
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-205

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 LKSL 18
      ||||
Db      3 LKSL 6

RESULT 16
US-09-867-852-207
; Sequence 207, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-207

Query Match      22.2%; Score 4; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 LKSL 18
      ||||
Db      3 LKSL 6

RESULT 17
US-10-059-749-34
; Sequence 34, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:
US-10-059-749-34

Query Match      22.2%; Score 4; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGEE 13
      ||||
Db      3 HGEE 6

RESULT 18
US-10-059-749-45
; Sequence 45, Application US/10059749
; Publication No. US20020183504A1
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; Encoding Same and Methods of Use
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/059,749
; FILING DATE: 29-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
```





; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 189  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-389-189

Query Match 22.2%; Score 4; DB 11; Length 7;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEIL 15  
Db 2 EEIL 5

## RESULT 23

US-09-753-831-6  
; Sequence 6, Application US/09753831  
; Patent No. US20020137693A1  
; GENERAL INFORMATION:  
; APPLICANT: Hogan, Kevin T.  
; APPLICANT: Ross, Mark M.  
; TITLE OF INVENTION: C-SKI Oncogene-Derived Peptides for Prevention,  
; TITLE OF INVENTION: Treatment and Diagnosis of Cancer  
; FILE REFERENCE: 26747-27  
; CURRENT APPLICATION NUMBER: US/09/753,831  
; CURRENT FILING DATE: 2001-01-03  
; PRIOR APPLICATION NUMBER: U.S. 60/174296  
; PRIOR FILING DATE: 2000-01-03  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: No. US20020137693A1a1apeptide  
; OTHER INFORMATION: derived from the human C-SKI oncoprotein.  
US-09-753-831-6

Query Match 22.2%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
Db 6 EILK 9

## RESULT 24

US-09-791-378-204  
; Sequence 204, Application US/09791378  
; Patent No. US20020142303A1  
; GENERAL INFORMATION:

; APPLICANT: Parekh, Rajesh  
; TITLE OF INVENTION: PROTEINS, GENES AND THEIR USE FOR DIAGNOSIS AND TREATMENT OF  
; TITLE OF INVENTION: SCHIZOPHRENIA  
; FILE REFERENCE: 9195-061-999  
; CURRENT APPLICATION NUMBER: US/09/791,378  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 09/750,395  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 677  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 204  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-378-204

Query Match 22.2%; Score 4; DB 10; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEIL 15  
Db 1 EEIL 4

## RESULT 25

US-10-282-960-87  
; Sequence 87, Application US/10282960  
; Publication No. US20030143228A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Si-Yi  
; APPLICANT: ZhaoYang, You  
; APPLICANT: Schroers, Roland  
; TITLE OF INVENTION: Human Telomerase Reverse Transcriptase as a Class-II Restrict  
; TITLE OF INVENTION: Associated Antigen  
; FILE REFERENCE: P02193US1  
; CURRENT APPLICATION NUMBER: US/10/282,960  
; CURRENT FILING DATE: 2002-10-29  
; PRIOR APPLICATION NUMBER: US 60/345,012  
; PRIOR FILING DATE: 2001-10-29  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 87  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human  
US-10-282-960-87

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TFNR 5  
Db 4 TFNR 7

## RESULT 26

US-09-942-052-132  
; Sequence 132, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28

; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 132  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-132

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 6 LKSL 9

RESULT 27  
US-09-942-052-137  
; Sequence 137, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 137  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-137

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 2 LKSL 5

RESULT 28  
US-09-942-052-215  
; Sequence 215, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052

; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 215  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-215

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 2 LKSL 5

RESULT 29  
US-09-942-052-241  
; Sequence 241, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 241  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-241

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 4 LKSL 7

RESULT 30  
US-09-942-052-310  
; Sequence 310, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00

; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 310  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-310

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|  
|  
|  
|  
Db 4 LKSL 7

RESULT 31  
US-09-942-052-343  
; Sequence 343, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 343  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-343

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|  
|  
|  
|  
Db 2 LKSL 5

RESULT 32  
US-09-942-052-345  
; Sequence 345, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 345  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-345

; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 345  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-345

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|  
|  
|  
|  
Db 6 LKSL 9

RESULT 33  
US-09-942-052-405  
; Sequence 405, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 405  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-405

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|  
|  
|  
|  
Db 2 LKSL 5

RESULT 34  
US-09-942-052-421  
; Sequence 421, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 421  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-421

; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 421  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-421

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 6 LKSL 9

RESULT 35  
US-09-942-052-513  
; Sequence 513, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 513  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-513

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 6 LKSL 9

RESULT 36  
US-09-942-052-517  
; Sequence 517, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 517  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-517

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 2 LKSL 5

RESULT 37  
US-09-942-052-603  
; Sequence 603, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 603  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-603

Query Match 22.2%; Score 4; DB 12; Length 9;  
Best Local Similarity 100.0%; Pred. No. 6.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 2 LKSL 5

RESULT 38  
US-09-942-052-635  
; Sequence 635, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao

```

RESULT 40
US-10-153-159-24
; Sequence 24, Application US/10153159
; Publication NO. US2020177170A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caiji

```

RESULT 42  
US-10-153-159-30  
; Sequence 30, Application US/10153159  
; Publication No. US20020177170A1  
; GENERAL INFORMATION:  
; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark  
; APPLICANT: Zhong, Pingyu

```
; APPLICANT: Wang, Caili
; TITLE OF INVENTION: STRUCTURE-BASED SELECTION AND AFFINITY MATURATION OF ANTIBODY LIB
; TITLE OF INVENTION: SILICO
; FILE REFERENCE: 26050-704
; CURRENT APPLICATION NUMBER: US/10/153,159
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-159-30

Query Match                22.2%; Score 4; DB 14; Length 9;
Best Local Similarity      100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNRV 6
        |||||
Db       4 FNRV 7

RESULT 43
US-10-153-176-21
; Sequence 21, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-21

Query Match                22.2%; Score 4; DB 15; Length 9;
Best Local Similarity      100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNRV 6
        |||||
Db       4 FNRV 7

RESULT 44
US-10-153-176-24
; Sequence 24, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-24

Query Match                22.2%; Score 4; DB 15; Length 9;
Best Local Similarity      100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNRV 6
        |||||
Db       4 FNRV 7

RESULT 45
US-10-153-176-29
; Sequence 29, Application US/10153176
; Publication No. US20030022240A1
; GENERAL INFORMATION:
; APPLICANT: Luo, Peter
; APPLICANT: Hsieh, Mark
; APPLICANT: Zhong, Pingyu
; APPLICANT: Wang, Caili
; APPLICANT: Cao, Yicheng
; APPLICANT: Li, Shengfeng
; APPLICANT: Liu, Shengjiang
; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO
; FILE REFERENCE: 26050-701
; CURRENT APPLICATION NUMBER: US/10/153,176
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 10/125,687
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VH CDR1 Variant
US-10-153-176-29

Query Match                22.2%; Score 4; DB 15; Length 9;
Best Local Similarity      100.0%; Pred. No. 6.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 FNRV 6
        |||||
Db       4 FNRV 7
```

## RESULT 46

US-10-153-176-30  
; Sequence 30, Application US/10153176  
; Publication No. US20030022240A1  
; GENERAL INFORMATION:

; APPLICANT: Luo, Peter  
; APPLICANT: Hsieh, Mark

; APPLICANT: Zhong, Pingyu

; APPLICANT: Wang, Caili

; APPLICANT: Cao, Yicheng

; APPLICANT: Li, Shengfeng

; APPLICANT: Liu, Shengjiang

; TITLE OF INVENTION: GENERATION AND AFFINITY MATURATION OF ANTIBODY LIBRARY IN SILICO

; FILE REFERENCE: 26050-701

; CURRENT APPLICATION NUMBER: US/10/153,176

; CURRENT FILING DATE: 2002-05-20

; PRIOR APPLICATION NUMBER: US 10/125,687

; PRIOR FILING DATE: 2002-04-17

; PRIOR APPLICATION NUMBER: US 60/284,407

; PRIOR FILING DATE: 2001-04-17

; NUMBER OF SEQ ID NOS: 125

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 30

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: VH CDR1 Variant

US-10-153-176-30

Query Match

Best Local Similarity 22.2%; Score 4; DB 15; Length 9;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FNRY 6

Db 4 FNRY 7

## RESULT 47

US-09-912-917-3

; Sequence 3, Application US/09912917

; Patent No. US2002028487A1

; GENERAL INFORMATION:

; APPLICANT: Lathangue, Nicholas B

; APPLICANT: Shikama, No. US2002028487A1iko

; TITLE OF INVENTION: The University Court of the University of Glasgow

; TITLE OF INVENTION: JWY, a co-activator for p300/CBP, nucleic acid encoding

; FILE REFERENCE: ABB/LP5731500

; CURRENT APPLICATION NUMBER: US/09/912,917

; CURRENT FILING DATE: 2001-07-25

; PRIOR APPLICATION NUMBER: 09/311,236

; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: GB 9818235.5

; PRIOR FILING DATE: 1998-08-20

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-912-917-3

Query Match

Best Local Similarity 22.2%; Score 4; DB 9; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 BILK 16

Db 5 BILK 8

## RESULT 48

US-09-572-404B-722

; Sequence 722, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 722

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in PRKAR2A OR PKR2 OR PRKAR2 at 273-282 and

; OTHER INFORMATION: interact with Sequence 721 in this patent.

US-09-572-404B-722

Query Match

Best Local Similarity 22.2%; Score 4; DB 11; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18

Db 4 LKSL 7

## RESULT 49

US-09-572-404B-724

; Sequence 724, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 724

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in PRKAR2A OR PKR2 OR PRKAR2 at 272-281 and

; OTHER INFORMATION: interact with Sequence 723 in this patent.

US-09-572-404B-724

Query Match

Best Local Similarity 22.2%; Score 4; DB 11; Length 10;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18

Db 5 LKSL 8

## RESULT 50

US-09-572-270A-611

; Sequence 611, Application US/09572270A

; Publication No. US20030148368A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Inter- complementary peptide listing

; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/09/572,270A

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 1144

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 611

; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in Unknown at 379-388 and may interact with  
US-09-572-270A-611

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 ILKS 17  
Db 7 ILKS 10

RESULT 51  
US-09-572-270A-948  
; Sequence 948, Application US/09572270A  
; Publication No. US20030148368A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Inter- complementary peptide listing  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/572,270A  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 1144  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 948  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in PYRB. at 115-124 and may interact with  
US-09-572-270A-948

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
Db 5 EILK 8

RESULT 52  
US-09-572-270A-950  
; Sequence 950, Application US/09572270A  
; Publication No. US20030148368A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Inter- complementary peptide listing  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/572,270A  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 1144  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 950  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in PYRB. at 114-123 and may interact with  
US-09-572-270A-950

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
Db 6 EILK 9

RESULT 53  
US-09-942-052-152

; Sequence 152, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 152  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-152

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 7 LKSL 10

RESULT 54

US-09-942-052-269  
; Sequence 269, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 269  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-269

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 7 LKSL 10

RESULT 55



US-09-942-052-282  
; Sequence 282, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 282  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-282

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|||  
Db 2 LKSL 5

RESULT 56  
US-09-942-052-294  
; Sequence 294, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 294  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-294

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|||  
Db 5 LKSL 8

RESULT 57  
US-09-942-052-367  
; Sequence 367, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 367  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-367

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|||  
Db 5 LKSL 8

RESULT 58  
US-09-942-052-375  
; Sequence 375, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Faris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85PIB3  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 375  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-375

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|||  
Db 6 LKSL 9

```
RESULT 59
US-09-942-052-474
; Sequence 474, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 474
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-474

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
      |||||
Db      7 LKSL 10

RESULT 60
US-09-942-052-484
; Sequence 484, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 484
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-484

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
      |||||
Db      4 LKSL 7

RESULT 58
US-09-942-052-488
; Sequence 488, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 488
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-488

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
      |||||
Db      3 LKSL 6

RESULT 62
US-09-942-052-493
; Sequence 493, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 493
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-493

Query Match      22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
      |||||
```

```
Db          6 LKSL 9

RESULT 63
US-09-942-052-560
; Sequence 560, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 560
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-560

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 LKSL 18
          |||||
Db          7 LKSL 10

RESULT 64
US-09-942-052-566
; Sequence 566, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 566
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-566

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 LKSL 18
          |||||
Db          7 LKSL 10

RESULT 65
US-09-942-052-582
; Sequence 582, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-582

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 LKSL 18
          |||||
Db          6 LKSL 9

RESULT 66
US-09-942-052-597
; Sequence 597, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 597
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-942-052-597

Query Match          22.2%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          15 LKSL 18
          |||||
Db          6 LKSL 9
```

QY 15 LKSL 18  
|||  
Db 3 LKSL 6

## RESULT 67

US-09-942-052-667  
; Sequence 667, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 667  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-667

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 6 LKSL 9

## RESULT 68

US-09-942-052-681  
; Sequence 681, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 681  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-681

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 4 LKSL 7

## RESULT 69

US-09-942-052-682  
; Sequence 682, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 682  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-682

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
|||  
Db 7 LKSL 10

## RESULT 70

US-09-942-052-692  
; Sequence 692, Application US/09942052  
; Publication No. US20030170626A1  
; GENERAL INFORMATION:  
; APPLICANT: Raitano, Arthur B.  
; APPLICANT: Paris, Mary  
; APPLICANT: Hubert, Rene S.  
; APPLICANT: Afar, Daniel  
; APPLICANT: Ge, Wangmao  
; APPLICANT: Challita-Eid, Pia M.  
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3  
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER  
; FILE REFERENCE: 51158-20028.00  
; CURRENT APPLICATION NUMBER: US/09/942,052  
; CURRENT FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: 60/228,432  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 744  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 692  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
US-09-942-052-692

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
|||||  
Db 2 LKSL 5

## RESULT 71

US-10-239-313A-5  
; Sequence 5, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-239-313A-5

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
|||||  
Db 1 EILK 4

## RESULT 72

US-10-239-313A-80  
; Sequence 80, Application US/10239313A  
; Publication No. US20030175285A1  
; GENERAL INFORMATION:  
; APPLICANT: KLINGUER - HAMOUR, Christine  
; APPLICANT: CORVAIA, Nathalie  
; APPLICANT: BECK, Alain  
; APPLICANT: GOETSCH, Liliane  
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS  
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM  
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID  
; FILE REFERENCE: 343 727 - US  
; CURRENT APPLICATION NUMBER: US/10/239,313A  
; CURRENT FILING DATE: 2002-09-19  
; PRIOR APPLICATION NUMBER: FR 00/03711  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: PCT 01/70772  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 697  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 80  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-239-313A-80

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
|||||  
Db 7 EILK 10

## RESULT 73

US-10-200-708-29  
; Sequence 29, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-29

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
|||||  
Db 6 EILK 9

## RESULT 74

US-10-200-708-440  
; Sequence 440, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: DeGroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 440  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-440

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
|||||

Db 2 EILK 5

RESULT 75  
US-10-200-708-594  
; Sequence 594, Application US/10200708  
; Publication No. US20030180314A1  
; GENERAL INFORMATION:  
; APPLICANT: Degroot, Anne S.  
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES  
; FILE REFERENCE: 17999-001  
; CURRENT APPLICATION NUMBER: US/10/200,708  
; CURRENT FILING DATE: 2002-07-22  
; PRIOR APPLICATION NUMBER: US/09/351,036  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,346  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: 60/115,145  
; PRIOR FILING DATE: 1999-01-08  
; PRIOR APPLICATION NUMBER: 60/130,677  
; PRIOR FILING DATE: 1999-04-23  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 594  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-200-708-594

Query Match 22.2%; Score 4; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
|||  
Db 7 EILK 10

Search completed: November 25, 2003, 20:37:07  
Job time : 29.8837 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 25, 2003, 20:16:22 ; Search time 14.5465 Seconds  
(without alignments)  
52.356 Million cell updates/sec

Title: US-09-641-801-30

Perfect score: 18

Sequence: 1 ATFNRYQDDHGEEILKSL 18

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

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Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Listing first 100 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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Sequence 13, Appl  
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Sequence 32, Appl  
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; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
; US-08-665-220-23

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6

RESULT 9
US-08-665-220-33
; Sequence 33, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
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; US-08-665-220-33

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13
Db 3 HGEE 6

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US-08-665-220-38
; Sequence 38, Application US/08665220
; Patent No. 5786173
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, Apoptotic Proteases,
; Nucleic Acids Encoding and Methods of Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,220
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/618,408
; FILING DATE: 19-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
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; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "CED-3"
US-08-665-220-38

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Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 HGEE 6

RESULT 11
US-08-618-408B-23
; Sequence 23, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; NAME/KEY: Peptide
; LOCATION: 1..6
; OTHER INFORMATION: /note= "Mch3"
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QY 10 HGEE 13
DB 3 HGEE 6

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; Sequence 33, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
; APPLICANT: Fernandes-Alnemri, Teresa
; APPLICANT: Litwack, Gerald
; APPLICANT: Armstrong, Robert
; APPLICANT: Tomaselli, Kevin
; TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/618,408B
; FILING DATE: 19-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 1957
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; NAME/KEY: Peptide
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; OTHER INFORMATION: /note= "CPP32"
US-08-618-408B-33

Query Match 22.2%; Score 4; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13
DB 3 HGEE 6

RESULT 13
US-08-618-408B-38
; Sequence 38, Application US/08618408B
; Patent No. 5851815
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Emad S.
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APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: Mch4 and Mch5, No. 5851815el Apoptotic  
TITLE OF INVENTION: Proteases, Nucleic Acids Encoding and Methods of Use  
NUMBER OF SEQUENCES: 63  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell and Flores  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,408B  
FILING DATE: 19-MAR-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 1957  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
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US-08-618-408B-38  
Query Match 22.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
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Db 3 HGE 6  
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Sequence 205, Application US/08310912A  
Patent No. 5981730  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
NUMBER OF SEQUENCES: 208  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360

ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
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APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360  
FILING DATE: April 13, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/254001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 100254  
INFORMATION FOR SEQ ID NO: 205:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-310-912A-205  
Query Match 22.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 LKSL 18  
Db 3 LKSL 6  
RESULT 15  
US-08-310-912A-207  
Sequence 207, Application US/08310912A  
Patent No. 5981730  
GENERAL INFORMATION:  
APPLICANT: Ausubel, Frederick M.  
APPLICANT: Staskawicz, Brian J.  
APPLICANT: Brent, Andrew F.  
APPLICANT: Dahlbeck, Douglas  
APPLICANT: Katagiri, Fumiaki  
APPLICANT: Kunkel, Barbara N.  
APPLICANT: Mindrinos, Michael N.  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION  
NUMBER OF SEQUENCES: 208  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110-2904  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/310,912A  
FILING DATE: September 22, 1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/227,360

; FILING DATE: April 13, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lech, Karen F.  
; REGISTRATION NUMBER: 35,238  
; REFERENCE/DOCKET NUMBER: 00786/254001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 542-5070  
; TELEFAX: (617) 542-8906  
; TELEX: 100254  
; INFORMATION FOR SEQ ID NO: 207:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-310-912A-207

Query Match 22.2%; Score 4; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 LKSL 18  
Db 3 LKSL 6

RESULT 16  
US-09-301-085-205  
; Sequence 205, Application US/09301085  
; Patent No. 6262248  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.  
; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND  
; TITLE OF INVENTION: DETECTION METHODS  
; FILE REFERENCE: 00786/254002  
; CURRENT APPLICATION NUMBER: US/09/301,085  
; CURRENT FILING DATE: 1999-04-28  
; EARLIER APPLICATION NUMBER: 08/310,912  
; EARLIER FILING DATE: 1994-09-22  
; EARLIER APPLICATION NUMBER: 08/227,360  
; EARLIER FILING DATE: 1994-04-13  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 205  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-301-085-205

Query Match 22.2%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 LKSL 18  
Db 3 LKSL 6

RESULT 17  
US-09-301-085-207  
; Sequence 207, Application US/09301085  
; Patent No. 6262248  
; GENERAL INFORMATION:  
; APPLICANT: Ausubel, Frederick M.  
; APPLICANT: Staskawicz, Brian J.

; APPLICANT: Brent, Andrew F.  
; APPLICANT: Dahlbeck, Douglas  
; APPLICANT: Katagiri, Fumiaki  
; APPLICANT: Kunkel, Barbara N.  
; APPLICANT: Mindrinos, Michael N.  
; APPLICANT: Yu, Guo-Liang  
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND  
; TITLE OF INVENTION: DETECTION METHODS  
; FILE REFERENCE: 00786/254002  
; CURRENT APPLICATION NUMBER: US/09/301,085  
; CURRENT FILING DATE: 1999-04-28  
; EARLIER APPLICATION NUMBER: 08/310,912  
; EARLIER FILING DATE: 1994-09-22  
; EARLIER APPLICATION NUMBER: 08/227,360  
; EARLIER FILING DATE: 1994-04-13  
; NUMBER OF SEQ ID NOS: 208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 207  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-301-085-207

Query Match 22.2%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0;

Qy 15 LKSL 18  
Db 3 LKSL 6

RESULT 18  
US-09-257-218-34  
; Sequence 34, Application US/09257218  
; Patent No. 6271361  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease McHe, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/257,218  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-34

Query Match      22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGE 13
Db      3 HGE 6

RESULT 19
US-09-257-218-45
; Sequence 45, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Fernandes-Alnemri, Enad S.
; APPLICANT: Litwack, Gerald
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,579
; FILING DATE: 29-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-ID 2180
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-9849
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-257-218-50

Query Match      22.2%; Score 4; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 HGE 13
Db      3 HGE 6

RESULT 20
US-09-257-218-50
; Sequence 50, Application US/09257218
; Patent No. 6271361
; GENERAL INFORMATION:
; APPLICANT: Alnemri, Enad S.
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1 FILING DATE: 13-May-1999  
2 CLASSIFICATION: <Unknown>  
3 PRIOR APPLICATION DATA:  
4 APPLICATION NUMBER: 08/865,579  
5 FILING DATE: <Unknown>  
6 ATTORNEY/AGENT INFORMATION:  
7 NAME: Campbell, Cathryn A.  
8 REGISTRATION NUMBER: 31,815  
9 REFERENCE/DOCKET NUMBER: P-ID 2180  
10 TELECOMMUNICATION INFORMATION:  
11 TELEPHONE: (619) 535-9849  
12 TELEFAX: (619) 535-9849  
13 INFORMATION FOR SEQ ID NO: 34:  
14 SEQUENCE CHARACTERISTICS:  
15 LENGTH: 6 amino acids  
16 TYPE: amino acid  
17 TOPOLOGY: linear  
18 MOLECULE TYPE: peptide  
19 SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
20 US-09-311-760-34  
21  
22 Query Match 22.2%; Score 4; DB 3; Length 6;  
23 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
24 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
25  
26 QY 10 HGEE 13  
27 Db 3 HGEE 6  
28  
29 RESULT 22  
30 US-09-311-760-45  
31 Sequence 45, Application US/09311760  
32 Patent No. 6274318  
33 GENERAL INFORMATION:  
34 APPLICANT: Alnemri, Emad S.  
35 Fernandes-Alnemri, Teresa  
36 Litwack, Gerald  
37 TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
38 NUMBER OF SEQUENCES: 87  
39 CORRESPONDENCE ADDRESS:  
40 ADDRESSEE: Campbell & Flores LLP  
41 STREET: 4370 La Jolla Village Drive, Suite 700  
42 CITY: San Diego  
43 STATE: California  
44 COUNTRY: United States  
45 ZIP: 92122  
46 COMPUTER READABLE FORM:  
47 MEDIUM TYPE: Floppy disk  
48 COMPUTER: IBM PC compatible  
49 OPERATING SYSTEM: PC-DOS/MS-DOS  
50 SOFTWARE: Patent In Release #1.0, Version #1.25  
51 CURRENT APPLICATION DATA:  
52 APPLICATION NUMBER: US/09/311,760  
53 FILING DATE: 13-May-1999  
54 CLASSIFICATION: <Unknown>  
55 PRIOR APPLICATION DATA:  
56 APPLICATION NUMBER: 08/865,579  
57 FILING DATE: <Unknown>  
58 ATTORNEY/AGENT INFORMATION:  
59 NAME: Campbell, Cathryn A.  
60 REGISTRATION NUMBER: 31,815  
61 REFERENCE/DOCKET NUMBER: P-ID 2180  
62 TELECOMMUNICATION INFORMATION:  
63 TELEPHONE: (619) 535-9001  
64 TELEFAX: (619) 535-9849  
65 INFORMATION FOR SEQ ID NO: 45:  
66 SEQUENCE CHARACTERISTICS:  
67 LENGTH: 6 amino acids  
68 TYPE: amino acid  
69 TOPOLOGY: linear  
70 MOLECULE TYPE: peptide

1 SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
2 US-09-311-760-45  
3  
4 Query Match 22.2%; Score 4; DB 3; Length 6;  
5 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
6 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
7  
8 QY 10 HGEE 13  
9 Db 3 HGEE 6  
10  
11 RESULT 23  
12 US-09-311-760-50  
13 Sequence 50, Application US/09311760  
14 Patent No. 6274318  
15 GENERAL INFORMATION:  
16 APPLICANT: Alnemri, Emad S.  
17 Fernandes-Alnemri, Teresa  
18 Litwack, Gerald  
19 TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
20 NUMBER OF SEQUENCES: 87  
21 CORRESPONDENCE ADDRESS:  
22 ADDRESSEE: Campbell & Flores LLP  
23 STREET: 4370 La Jolla Village Drive, Suite 700  
24 CITY: San Diego  
25 STATE: California  
26 COUNTRY: United States  
27 ZIP: 92122  
28 COMPUTER READABLE FORM:  
29 MEDIUM TYPE: Floppy disk  
30 COMPUTER: IBM PC compatible  
31 OPERATING SYSTEM: PC-DOS/MS-DOS  
32 SOFTWARE: Patent In Release #1.0, Version #1.25  
33 CURRENT APPLICATION DATA:  
34 APPLICATION NUMBER: US/09/311,760  
35 FILING DATE: 13-May-1999  
36 CLASSIFICATION: <Unknown>  
37 PRIOR APPLICATION DATA:  
38 APPLICATION NUMBER: 08/865,579  
39 FILING DATE: <Unknown>  
40 ATTORNEY/AGENT INFORMATION:  
41 NAME: Campbell, Cathryn A.  
42 REGISTRATION NUMBER: 31,815  
43 REFERENCE/DOCKET NUMBER: P-ID 2180  
44 TELECOMMUNICATION INFORMATION:  
45 TELEPHONE: (619) 535-9001  
46 TELEFAX: (619) 535-9849  
47 INFORMATION FOR SEQ ID NO: 50:  
48 SEQUENCE CHARACTERISTICS:  
49 LENGTH: 6 amino acids  
50 TYPE: amino acid  
51 TOPOLOGY: linear  
52 MOLECULE TYPE: peptide  
53 SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
54 US-09-311-760-50  
55  
56 Query Match 22.2%; Score 4; DB 3; Length 6;  
57 Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
58 Matches 4; Conservative 0; Mismatches 0; Indels 0;  
59  
60 QY 10 HGEE 13  
61 Db 3 HGEE 6  
62  
63 RESULT 24  
64 US-09-291-692-23  
65 Sequence 23, Application US/09291692  
66 Patent No. 6287795  
67 GENERAL INFORMATION:  
68 APPLICANT: Alnemri, Emad S.

APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
NUCLEIC ACIDS ENCODING AND METHODS OF USE  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,692  
FILING DATE: 04-13-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION/DOCKET NUMBER: 480140.424C3  
TELEPHONE: (206) 622-6031  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "Mch3"  
US-09-291-692-23  
Query Match 22.2%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 HGEE 13  
Db 3 HGEE 6  
RESULT 25  
US-09-291-692-33  
Sequence 33, Application US/09291692  
Patent No. 6287795  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
NUCLEIC ACIDS ENCODING AND METHODS OF USE  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,692  
FILING DATE: 04-13-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION/DOCKET NUMBER: 480140.424C3  
TELEPHONE: (206) 622-6031  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "Mch3"  
US-09-291-692-23

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,692  
FILING DATE: 04-13-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION/DOCKET NUMBER: 480140.424C3  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 622-6031  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "CPP32"  
US-09-291-692-33  
Query Match 22.2%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 HGEE 13  
Db 3 HGEE 6  
RESULT 26  
US-09-291-692-38  
Sequence 38, Application US/09291692  
Patent No. 6287795  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
APPLICANT: Fernandes-Alnemri, Teresa  
APPLICANT: Litwack, Gerald  
APPLICANT: Armstrong, Robert  
APPLICANT: Tomaselli, Kevin  
TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
NUCLEIC ACIDS ENCODING AND METHODS OF USE  
NUMBER OF SEQUENCES: 75  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/291,692  
FILING DATE: 04-13-1999  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Christiansen, William T.  
REGISTRATION/DOCKET NUMBER: 480140.424C3  
TELEPHONE: (206) 622-6031  
TELEFAX: (206) 622-4900  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "CPP32"  
US-09-291-692-33



INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..6  
OTHER INFORMATION: /note= "CED-3"  
US-09-291-692-38

Query Match 22.2%; Score 4; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
|||||  
Db 3 HGEE 6

RESULT 27  
US-09-561-756-72  
; Sequence 72, Application US/09561756  
; Patent No. 6376226  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/561,756  
; CURRENT FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 09/227,721  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-561-756-72

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
|||||  
Db 3 HGEE 6

RESULT 28  
US-09-561-756-83  
; Sequence 83, Application US/09561756  
; Patent No. 6376226  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/561,756  
; CURRENT FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 09/227,721  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-561-756-83

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
|||||  
Db 3 HGEE 6

RESULT 29  
US-09-561-756-88  
; Sequence 88, Application US/09561756  
; Patent No. 6376226  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/561,756  
; CURRENT FILING DATE: 2000-04-26  
; PRIOR APPLICATION NUMBER: 09/227,721  
; PRIOR FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 88  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-561-756-88

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
|||||  
Db 3 HGEE 6

RESULT 30  
US-09-227-721-72  
; Sequence 72, Application US/09227721  
; Patent No. 6379950  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/227,721  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 72  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-227-721-72

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGEE 13  
|||||  
Db 3 HGEE 6

RESULT 31  
US-09-227-721-83  
; Sequence 83, Application US/09227721  
; Patent No. 6379950  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: THEREOF  
; FILE REFERENCE: 480140.431  
; CURRENT APPLICATION NUMBER: US/09/227,721  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 83  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-227-721-83

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13

Db 3 HGEE 6

## RESULT 32

US-09-227-721-88  
; Sequence 88, Application US/09227721  
; Patent No. 6379950

; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.

; TITLE OF INVENTION: RECOMBINANT, ACTIVE CASPASES AND USES  
; FILE REFERENCE: THEREOF  
; FILE REFERENCE: 480140.431

; CURRENT APPLICATION NUMBER: US/09/227,721  
; CURRENT FILING DATE: 1999-01-08  
; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 88  
; LENGTH: 6

; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-227-721-88

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13

Db 3 HGEE 6

## RESULT 33

US-08-865-579-34  
; Sequence 34, Application US/08865579  
; Patent No. 6455296

; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego

; STATE: California  
; COUNTRY: United States

; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-865-579-34

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13

Db 3 HGEE 6

## RESULT 34

US-08-865-579-45  
; Sequence 45, Application US/08865579  
; Patent No. 6455296

; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.

; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald

; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use

; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego

; STATE: California  
; COUNTRY: United States

; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579

; FILING DATE: 29-MAY-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849

; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids

; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-865-579-45

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGE 13  
Db 3 HGE 6

RESULT 35  
US-08-865-579-50  
; Sequence 50, Application US/08865579  
; Patent No. 6455296  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-865-579-50

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGE 13  
Db 3 HGE 6

RESULT 36  
US-10-059-749-34  
; Sequence 34, Application US/10059749  
; Patent No. 6566505  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California

; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/059,749  
; FILING DATE: 29-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-9849  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 34:  
US-10-059-749-34

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 HGE 13  
Db 3 HGE 6

RESULT 37  
US-10-059-749-45  
; Sequence 45, Application US/10059749  
; Patent No. 6566505  
; GENERAL INFORMATION:  
; APPLICANT: Alnemri, Emad S.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Litwack, Gerald  
; TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/059,749  
; FILING DATE: 29-Jan-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/865,579  
; FILING DATE: 29-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-9849  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
US-10-059-749-45

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13  
Db 3 HGEE 6

RESULT 38  
US-10-059-749-50  
Sequence 50, Application US/10059749  
Patent No. 6566505  
GENERAL INFORMATION:  
APPLICANT: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
TITLE OF INVENTION: Apoptotic Protease Mch6, Nucleic Acids  
Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 87  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/059,749  
FILING DATE: 29-Jan-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/865,579  
FILING DATE: 29-MAY-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-ID 2180

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-9849

INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-10-059-749-50

Query Match 22.2%; Score 4; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 HGEE 13  
Db 3 HGEE 6

Db 3 HGEE 6

## RESULT 39

US-08-615-181-19  
Sequence 19, Application US/08615181  
Patent No. 5756666  
GENERAL INFORMATION:

APPLICANT: MASAFUMI, TAKIGUCHI  
MIWA, KIYOSHI

TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE  
RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
CURING AIDS  
TITLE OF INVENTION: CURING AIDS  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,181  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01756  
FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 261302/1993  
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-796-0 PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

ORIGINAL SOURCE:  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-08-615-181-19

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
Db 6 LKSL 9

## RESULT 40

US-08-615-181-26  
Sequence 26, Application US/08615181  
Patent No. 5756666  
GENERAL INFORMATION:

APPLICANT: MASAFUMI, TAKIGUCHI  
MIWA, KIYOSHI

TITLE OF INVENTION: PEPTIDES CAPABLE OF INDUCING IMMUNE  
RESPONSE TO HIV AND ANTI-AIDS AGENT FOR PREVENTING AND  
CURING AIDS  
TITLE OF INVENTION: CURING AIDS  
NUMBER OF SEQUENCES: 115  
CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/615,181  
FILING DATE: 04-APR-1996  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01756  
FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 261302/1993  
FILING DATE: 19-OCT-1993

ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-796-0 PCT

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

ORIGINAL SOURCE:  
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-08-615-181-19

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;; TITLE OF INVENTION: CURING AIDS  
;; NUMBER OF SEQUENCES: 115  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MATER & NEUSTADT,  
;; ADDRESSEE: P.C.  
;; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
;; CITY: ARLINGTON  
;; STATE: VA  
;; COUNTRY: USA  
;; ZIP: 22202  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/615,181  
;; FILING DATE: 04-APR-1996  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/JP94/01756  
;; FILING DATE: 19-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 261302/1993  
;; FILING DATE: 19-OCT-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: OBLON, NORMAN F.  
;; REGISTRATION NUMBER: 24,618  
;; REFERENCE/DOCKET NUMBER: 10-796-0 PCT  
;; TELEPHONE: 703-413-3000  
;; TELEFAX: 703-413-2220  
;; INFORMATION FOR SEQ ID NO: 26:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 9 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; ORIGINAL SOURCE:  
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS  
US-08-615-181-26

Query Match 22.2%; Score 4; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
Db 6 LKSL 9

RESULT 41  
US-08-518-967-7  
; Sequence 7, Application US/08518967  
; Patent No. 5861307  
; GENERAL INFORMATION:  
; APPLICANT: Kuchino, Y. et al.  
; TITLE OF INVENTION: HUMAN s-MYC-LIKE POLYPEPTIDE AND  
; TITLE OF INVENTION: A GENE CODING FOR SAID POLYPEPTIDE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIELDS & LEWACK  
; STREET: 176 East Main Street, Suite 8  
; CITY: Westboro  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 01581  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent in Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/518,967  
;; FILING DATE: August 24, 1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: JP 6-207236  
;; FILING DATE: 31-AUG-94  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lemack, Kevin S.  
;; REGISTRATION NUMBER: 32,579  
;; REFERENCE/DOCKET NUMBER:  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (508) 898-1818  
;; TELEFAX: (508) 898-2020  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FRAGMENT TYPE: internal  
US-08-518-967-7

Query Match 22.2%; Score 4; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GEEI 14  
Db 5 GEEI 8

RESULT 42  
US-08-159-339A-287  
; Sequence 287, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses  
; NUMBER OF SEQUENCES: 1254  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/159,339A  
; FILING DATE: 29-NOV-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/926,666  
; FILING DATE: 07-AUG-1992  
; APPLICATION NUMBER: US 08/027,746  
; FILING DATE: 05-MAR-1993  
; APPLICATION NUMBER: US 08/103,396  
; FILING DATE: 06-AUG-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-005030US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200

```
;
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-287

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 7 EILK 10

RESULT 43
US-09-188-579-66
; Sequence 66, Application US/09188579B
; Patent No. 6107040
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185
; CURRENT APPLICATION NUMBER: US/09/188,579B
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 114
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-188-579-66

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 2 EILK 5

RESULT 44
US-09-315-444-66
; Sequence 66, Application US/09315444A
; Patent No. 6232070
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CDP
; CURRENT APPLICATION NUMBER: US/09/315,444A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/188,579
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-315-444-66

Query Match 22.2%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 13 EILK 16
Db 2 EILK 5

RESULT 45
US-09-319-730-8
; Sequence 8, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-8

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 6 LKSL 9

RESULT 46
US-09-319-730-9
; Sequence 9, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-9

Query Match 22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18
Db 6 LKSL 9

RESULT 47
US-09-311-236-3
; Sequence 3, Application US/09311236
; Patent No. 6376215
```

```

; GENERAL INFORMATION:
; APPLICANT: Lathangue, Nicholas B
; APPLICANT: Shikana, No. 6376215iko
; APPLICANT: The University Court of the University of Glasgow
; TITLE OF INVENTION: JMY, a co-activator for p300/CBP, nucleic acid encoding
; TITLE OF INVENTION: JMY and uses thereof
; FILE REFERENCE: AHB/LP5731500
; CURRENT APPLICATION NUMBER: US/09/311,236
; EARLIER APPLICATION NUMBER: GB 9722238.4
; EARLIER FILING DATE: 1997-10-21
; EARLIER FILING DATE: 1997-10-21
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-311-236-3

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```

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      13 EILK 16
        |||||
DB       5 EILK 8

```

```

RESULT 48
US-09-721-362-66
; Sequence 66, Application US/09721362
; Patent No. 6420163
; GENERAL INFORMATION:
; APPLICANT: Shuman, Stewart
; TITLE OF INVENTION: Pharmacological Targeting of mRNA Cap Formation
; FILE REFERENCE: D6185CIP/D
; CURRENT APPLICATION NUMBER: US/09/721,362
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/315,444
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: vaccinia virus
; FEATURE:
; OTHER INFORMATION: Motif VI of RNA guanylyltransferase.
US-09-721-362-66

```

```

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      13 EILK 16
        |||||
DB       2 EILK 5

```

```

RESULT 49
US-09-489-847-344
; Sequence 344, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031PI
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657

```

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; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 344
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-344

Query Match      22.2%; Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 LKSL 18
        |||||
DB       2 LKSL 5

RESULT 50
US-08-652-877-75
; Sequence 75, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESS: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Rd., 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.5.1
; SOFTWARE: Word 6.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,877
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15203
; FILING DATE: 22-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,314
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355E-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808

```

; INFORMATION FOR SEQ ID NO: 75:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-652-877-75

Query Match 22.2%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GBEI 14  
Db 2 GBEI 5

RESULT 51  
US-08-476-515A-75  
; Sequence 75, Application US/08476515A  
; Patent No. 6239270

; GENERAL INFORMATION:  
; APPLICANT: Akerstrom, Goran  
; APPLICANT: Juhlin, Claes  
; APPLICANT: Rask, Lars  
; APPLICANT: Crumley, Gregg R.  
; APPLICANT: Morse, Clarence C.  
; APPLICANT: Murray, Edward M.  
; APPLICANT: Hjal, Goran  
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
; TITLE OF INVENTION: Thereof and DNA Encoding Same  
; NUMBER OF SEQUENCES: 84  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Martin Savitzky  
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.;  
; CITY: Collegeville  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19426-0107  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Compaq PC  
; OPERATING SYSTEM: Windows 95  
; SOFTWARE: Word 7.0 (Patentin)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/476,515A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/344,836  
; FILING DATE: 23-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/SE94/00483  
; FILING DATE: 24-MAY-1994

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9301764-8  
; FILING DATE: 24-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Savitzky, Martin  
; REGISTRATION NUMBER: 29,699  
; REFERENCE/DOCKET NUMBER: A1355D  
; TELEPHONE: 610-454-3816  
; TELEFAX: 610-454-3808  
; INFORMATION FOR SEQ ID NO: 75:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:

; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: internal  
US-08-476-515A-75

Query Match 22.2%; Score 4; DB 3; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GBEI 14  
Db 2 GBEI 5

RESULT 52  
5194592-76  
; Patent No. 5194592  
; APPLICANT: YOSHIDA, HAJIME  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO NOVEL  
; POLYPEPTIDES DERIVATIVES OF HUMAN GRANULOCYTE COLONY  
; STIMULATING FACTOR  
; NUMBER OF SEQUENCES: 83  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/318,527  
; FILING DATE: 3-WAR-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 136,647  
; FILING DATE: 22-DEC-1987  
; SEQ ID NO:76:  
; LENGTH: 11  
5194592-76

Query Match 22.2%; Score 4; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 4 LKSL 7

RESULT 53  
5489533-12  
; Patent No. 5489533  
; APPLICANT: SPRINGER, TIMOTHY A.;STAUNTON, DONALD E.;  
; DUSTIN, MICHAEL L.  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ENCODING  
; ICAM-2  
; NUMBER OF SEQUENCES: 16  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/384,814  
; FILING DATE: 06-FEB-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 89,3075  
; FILING DATE: 12-JUL-1995  
; APPLICATION NUMBER: 89,307  
; FILING DATE: 12-JUL-1993  
; APPLICATION NUMBER: 454,294  
; FILING DATE: 22-DEC-1989  
; APPLICATION NUMBER: 45,963  
; FILING DATE: 04-MAY-1987  
; APPLICATION NUMBER: 115,798  
; FILING DATE: 02-NOV-1987  
; APPLICATION NUMBER: 155,943  
; FILING DATE: 16-FEB-1988  
; APPLICATION NUMBER: 189,815  
; FILING DATE: 03-MAY-1988  
; APPLICATION NUMBER: 250,446  
; FILING DATE: 28-SEP-1988  
; SEQ ID NO:12:  
; LENGTH: 12  
5489533-12



Query Match 22.2%; Score 4; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFN 4  
Db 2 ATFN 5

RESULT 54  
US-09-206-059-13  
; Sequence 13, Application US/09206059  
; Patent No. 6201104  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas  
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and  
; FILE REFERENCE: 05213-0370  
; CURRENT APPLICATION NUMBER: US/09/206,059  
; CURRENT FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-206-059-13  
Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Query Match 22.2%; Score 4; DB 6; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATFN 4  
Db 2 ATFN 5

RESULT 55  
US-09-206-059-13  
; Sequence 13, Application US/09206059  
; Patent No. 6201104  
; GENERAL INFORMATION:  
; APPLICANT: MacDonald, Nicholas  
; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Peptides and  
; FILE REFERENCE: 05213-0370  
; CURRENT APPLICATION NUMBER: US/09/206,059  
; CURRENT FILING DATE: 1998-12-04  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-206-059-13  
Query Match 22.2%; Score 4; DB 3; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 13 EILK 16  
Db 5 EILK 8

RESULT 56  
US-09-319-730-2  
; Sequence 2, Application US/09319730  
; Patent No. 6310176  
; GENERAL INFORMATION:  
; APPLICANT: Barra, Donatella  
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES  
; FILE REFERENCE: 003300-574  
; CURRENT APPLICATION NUMBER: US/09/319,730  
; CURRENT FILING DATE: 1999-08-24  
; PRIOR APPLICATION NUMBER: PCT/SE97/02075  
; PRIOR FILING DATE: 1997-12-12  
; PRIOR APPLICATION NUMBER: SE 9604593-5  
; PRIOR FILING DATE: 1996-12-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Rana Temporaria  
US-09-319-730-2

Query Match 22.2%; Score 4; DB 4; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
Db 9 LKSL 12

RESULT 57  
PCT-US93-06751-66  
; Sequence 66, Application PC/TUS9306751  
; GENERAL INFORMATION:  
; APPLICANT: P. Keller, A. J. Conley, A.R. Shaw, B.A. Arnold  
; TITLE OF INVENTION: Immunological Conjugates of OMP and  
; TITLE OF INVENTION: HIV-Specific Selected Principal Neutralization GXG Epitopes  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/06751  
; FILING DATE: 19930719  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meredith, Roy D.  
; REGISTRATION NUMBER: 30,777  
; REFERENCE/DOCKET NUMBER: 18614  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-4678  
; TELEFAX: (908) 594-4720  
; TELEX: 138825  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE: Random Epitope Library Delta  
PCT-US93-06751-66

Query Match 22.2%; Score 4; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 DHGE 12  
Db 10 DHGE 13

RESULT 58  
5498694-11  
; Patent No. 5498694  
; APPLICANT: RUOSLAHTI, ERKKI I.  
; TITLE OF INVENTION: PEPTIDES OF THE CYTOPLASMIC DOMAIN OF  
; INTEGRIN  
; NUMBER OF SEQUENCES: 12  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/240,967  
; FILING DATE: 10-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 973,547  
; FILING DATE: 09-NOV-1992  
; APPLICATION NUMBER: 357,824  
; FILING DATE: 25-MAY-1989  
; SEQ ID NO: 11  
; LENGTH: 13  
5498694-11

Query Match 22.2%; Score 4; DB 6; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LKSL 18  
Db 9 LKSL 12

RESULT 59  
US-09-231-159-2  
; Sequence 2, Application US/09231159  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,159  
; FILING DATE:  
; CLASSIFICATION:  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/231,159  
; FILING DATE: 05-MAR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 2  
; OTHER INFORMATION: /note= "Xaa is D-alanine"  
US-09-231-159-2

Query Match 22.2%; Score 4; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEIL 15  
Db 10 EEIL 13

RESULT 60  
US-08-611-307-2  
; Sequence 2, Application US/08611307  
; Patent No. 6271196  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, John S.  
; TITLE OF INVENTION: Methods of Alleviating Neuropathic Pain  
; TITLE OF INVENTION: Using Prosaposin-Derived Peptides  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/611,307  
; FILING DATE: 05-MAR-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-UD 1928  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: 2  
; OTHER INFORMATION: /note= "Xaa is D-alanine"  
US-08-611-307-2

Query Match 22.2%; Score 4; DB 3; Length 14;

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Best Local Similarity 100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 12 EIL 15
Db 10 EIL 13

RESULT 61
US-09-148-030-4
; Sequence 4, Application US/09148030C
; Patent No. 6458357
; GENERAL INFORMATION:
; APPLICANT: White, Michael T.
; APPLICANT: O'Brien, John S.
; APPLICANT: Wright, David E.
; TITLE OF INVENTION: RETRO-INVERSO NEUTROPHIC AND ANALGESIC
; FILE REFERENCE: MYELOS.004CPI
; CURRENT APPLICATION NUMBER: US/09/148,030C
; CURRENT FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 08/926,015
; PRIOR FILING DATE: 1997-09-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)...(2)
; OTHER INFORMATION: D-Ala
US-09-148-030-4

Query Match 22.2%; Score 4; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 EIL 15
Db 10 EIL 13

RESULT 62
US-08-467-083-32
; Sequence 32, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 6 EILK 9

RESULT 63
US-08-414-417B-32
; Sequence 32, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-414-417B-32

Query Match 22.2%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16
Db 6 EILK 9
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RESULT 64  
 US-08-486-348A-32  
 ; Sequence 32, Application US/08486348A  
 ; Patent No. 5846538  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,348A  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharkey, Richard G.  
 ; REGISTRATION NUMBER: 32,629  
 ; REFERENCE/DOCKET NUMBER: 920010.448C6  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-486-348A-32

Query Match 22.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
 Db 6 EILK 9

RESULT 65  
 US-08-468-545B-32  
 ; Sequence 32, Application US/08468545B  
 ; Patent No. 5876712  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/468,545B  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 424  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sharkey, Richard G.  
 REGISTRATION NUMBER: 32,629  
 REFERENCE/DOCKET NUMBER: 920010.448C5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 32:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-468-545B-32

Query Match 22.2%; Score 4; DB 2; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 EILK 16  
 Db 6 EILK 9

RESULT 66  
 US-08-466-680B-32  
 ; Sequence 32, Application US/08466680B  
 ; Patent No. 6075122  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cheever, Martin A.  
 ; APPLICANT: Disis, Mary L.  
 ; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN  
 ; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE  
 ; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED  
 ; NUMBER OF SEQUENCES: 69  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seed and Berry LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: US  
 ; ZIP: 98104-7092  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/466,680B  
 ; FILING DATE: 06-JUN-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharkey, Richard G.  
 ; REGISTRATION NUMBER: 32,629  
 ; REFERENCE/DOCKET NUMBER: 920010.448C4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 32:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 15 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-466-680B-32

Query Match 22.2%; Score 4; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
|||||  
Db 6 EILK 9

## RESULT 67

US-09-009-953-91  
; Sequence 91, Application US/09009953  
; Patent No. 6413517  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; TITLE OF INVENTION: Identification of Broadly  
; Reactive DR Restricted Epitopes  
; NUMBER OF SEQUENCES: 274  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/009,953  
; FILING DATE: 21-Jan-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/036,713  
; FILING DATE: 23-Jan-1997  
; APPLICATION NUMBER: US 60/037,432  
; FILING DATE: 07-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 018623-011520US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-576-0200  
; TELEFAX: 415-576-0300  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 91:  
US-09-009-953-91

Query Match 22.2%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
|||||  
Db 3 EILK 6

## RESULT 68

US-09-418-780A-5  
; Sequence 5, Application US/09418780A  
; Patent No. 6504009  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Michael H.  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR  
; FILE REFERENCE: 06501-043001  
; CURRENT APPLICATION NUMBER: US/09/418,780A  
; CURRENT FILING DATE: 1999-10-15

; PRIOR APPLICATION NUMBER: PCT/JP98/01782  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: JAPAN 9/116402  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-418-780A-5

Query Match 22.2%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
|||||  
Db 3 EILK 6

## RESULT 69

US-09-418-780A-8  
; Sequence 8, Application US/09418780A  
; Patent No. 6504009  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Michael H.  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR  
; FILE REFERENCE: 06501-043001  
; CURRENT APPLICATION NUMBER: US/09/418,780A  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: PCT/JP98/01782  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: JAPAN 9/116402  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-418-780A-8

Query Match 22.2%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
|||||  
Db 3 EILK 6

## RESULT 70

US-09-418-780A-24  
; Sequence 24, Application US/09418780A  
; Patent No. 6504009  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Michael H.  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR  
; FILE REFERENCE: 06501-043001  
; CURRENT APPLICATION NUMBER: US/09/418,780A  
; CURRENT FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: PCT/JP98/01782  
; PRIOR FILING DATE: 1998-04-17  
; PRIOR APPLICATION NUMBER: JAPAN 9/116402  
; PRIOR FILING DATE: 1997-04-18  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
US-09-418-780A-24

Query Match 22.2%; Score 4; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
    ||||  
Db 3 EILK 6

RESULT 71  
US-09-053-611-16  
; Sequence 16, Application US/09053611  
; Patent No. 6410245  
; GENERAL INFORMATION:  
; APPLICANT: No. 6410245throp, Jeffrey P.  
; APPLICANT: Hart, Charles P.  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Glaxo Group Limited  
; TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent  
; TITLE OF INVENTION: Nuclear Receptor and Coactivator Interactions  
; FILE REFERENCE: 2064  
; CURRENT APPLICATION NUMBER: US/09/053,611  
; CURRENT FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: lacI-fused  
; OTHER INFORMATION: peptide from focused 15mer library  
US-09-053-611-16

Query Match 22.2%; Score 4; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LKSL 18  
    ||||  
Db 8 LKSL 11

RESULT 72  
5183734-3  
; Patent No. 5183734  
; APPLICANT: MORIARTY, ANN M.  
; TITLE OF INVENTION: ANTIBODIES, DIAGNOSTIC SYSTEMS AND METHODS  
; FOR ASSAYING SV40 HEXAG  
; NUMBER OF SEQUENCES: 17  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/553,982  
; FILING DATE: 17-JUL-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 54,424  
; FILING DATE: 26-MAY-1987  
; APPLICATION NUMBER: 648,142  
; FILING DATE: 07-SEP-1984  
; APPLICATION NUMBER: 587,570  
; FILING DATE: 08-MAR-1984  
; SEQ ID NO: 3  
; LENGTH: 16  
5183734-3

Query Match 22.2%; Score 4; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GEEI 14  
    ||||  
Db 9 GEEI 12

## RESULT 73

US-08-795-430-9  
; Sequence 9, Application US/08795430  
; Patent No. 6130071  
; GENERAL INFORMATION:  
; APPLICANT: Alicato, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
; TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/795,430  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/FI96/00427  
; FILING DATE: 01-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/671,573  
; FILING DATE: 28-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/601,132  
; FILING DATE: 14-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/585,895  
; FILING DATE: 12-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/510,133  
; FILING DATE: 01-AUG-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/340,011  
; FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gass, David A.  
; REGISTRATION NUMBER: 38,153  
; REFERENCE/DOCKET NUMBER: 28967/33691  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/474-6300  
; TELEFAX: 312/474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-795-430-9

Query Match 22.2%; Score 4; DB 3; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 EILK 16  
    ||||  
Db 14 EILK 17

RESULT 74  
US-09-355-700-9

; Sequence 9, Application US/09355700  
; Patent No. 6361946  
; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research  
;     Helsinki University Licensing  
;     Alitalo, Kari (U.S. only)  
;     Joukov, Vladimir (U.S. only)  
; TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)  
;     Protein and Gene, Mutants Thereof, and Uses Thereof  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;     STREET: 6300 Sears Tower, 233 South Wacker Drive  
;     CITY: Chicago  
;     STATE: Illinois  
;     COUNTRY: United States of America  
;     ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Floppy disk  
;     COMPUTER: IBM PC compatible  
;     OPERATING SYSTEM: PC-DOS/MS-DOS  
;     SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
;     APPLICATION NUMBER: US/09/355,700  
;     FILING DATE: 05-NOV-1999  
;     CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
;     APPLICATION NUMBER: 08/795,430  
;     FILING DATE: 05-FEB-1997  
;     APPLICATION NUMBER: PCI/FI96/00427  
;     FILING DATE: 01-AUG-1996  
;     APPLICATION NUMBER: 08/671,573  
;     FILING DATE: 28-JUN-1996  
;     APPLICATION NUMBER: 08/601,132  
;     FILING DATE: 14-FEB-1996  
;     APPLICATION NUMBER: 08/585,895  
;     FILING DATE: 12-JAN-1996  
;     APPLICATION NUMBER: 08/510,133  
;     FILING DATE: 01-AUG-1995  
;     APPLICATION NUMBER: 08/340,011  
;     FILING DATE: 14-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
;     NAME: Gass, David A.  
;     REGISTRATION NUMBER: 38,153  
;     REFERENCE/DOCKET NUMBER: 28967/34140  
; TELECOMMUNICATION INFORMATION:  
;     TELEPHONE: 312/474-6300  
;     TELEFAX: 312/474-0448  
;     TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 9:  
;     SEQUENCE CHARACTERISTICS:  
;         LENGTH: 17 amino acids  
;         TYPE: amino acid  
;         STRANDEDNESS: not relevant  
;         TOPOLOGY: linear  
;     MOLECULE TYPE: peptide  
;     SEQUENCE DESCRIPTION: SEQ ID NO: 9:  
US-09-355-700-9

Query Match           22.2%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   13 BILK 16  
      |  
      |  
      |  
DB   14 BILK 17

RESULT 75  
US-08-601-132-39  
; Sequence 39, Application US/08601132  
; Patent No. 6403088  
; GENERAL INFORMATION:

; APPLICANT: Alitalo, Kari  
; APPLICANT: Joukov, Vladimir  
; TITLE OF INVENTION: Receptor Ligand  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
;     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
;     STREET: 6300 Sears Tower, 233 South Wacker Drive  
;     CITY: Chicago  
;     STATE: Illinois  
;     COUNTRY: United States of America  
;     ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
;     MEDIUM TYPE: Floppy disk  
;     COMPUTER: IBM PC compatible  
;     OPERATING SYSTEM: PC-DOS/MS-DOS  
;     SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
;     APPLICATION NUMBER: US/08/601,132  
;     FILING DATE:  
;     CLASSIFICATION: 530  
;     ATTORNEY/AGENT INFORMATION:  
;         NAME: Gass, David A.  
;         REGISTRATION NUMBER: 38,153  
;         REFERENCE/DOCKET NUMBER: 28113/33118  
;         TELECOMMUNICATION INFORMATION:  
;         TELEPHONE: 312/474-6300  
;         TELEFAX: 312/474-0448  
;         TELEX: 25-3856  
;     INFORMATION FOR SEQ ID NO: 39:  
;     SEQUENCE CHARACTERISTICS:  
;         LENGTH: 17 amino acids  
;         TYPE: amino acid  
;         STRANDEDNESS: single  
;         TOPOLOGY: linear  
;     MOLECULE TYPE: protein  
US-08-601-132-39

Query Match           22.2%; Score 4; DB 4; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.6e+02;  
Matches   4; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

QY   13 BILK 16  
      |  
      |  
      |  
DB   14 BILK 17

Search completed: November 25, 2003, 20:30:06  
Job time : 15.5465 secs